

METHODS OF IDENTIFYING OPTIMAL VARIANTS OF PEPTIDE EPITOPES

REFERENCE TO A SEQUENCE LISTING SUBMITTED ON A COMPACT DISC

[0001] This application includes a Sequence Listing, which is provided as an electronic document on a compact disc (CD-R). This compact disc contains the file "Final Sequence Listing.txt" (6,125,872 bytes, created on January 19, 2010), which is hereby incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

Field of the Invention

[0002] This invention relates to the field of biology. In a particular embodiment, it relates to peptides, polynucleotides, and compositions useful to monitor or elicit an immune response to selected antigens, and methods of identifying such peptides and polynucleotides.

Related Art

[0003] HLA class I molecules are expressed on the surface of almost all nucleated cells. Following intracellular processing of antigens, epitopes from the antigens are presented as a complex with the HLA class I molecules on the surface of such cells. CTL recognize the peptide-HLA class I complex, which then results in the destruction of the cell bearing the HLA-peptide complex directly by the CTL and/or via the activation of non-destructive mechanisms *e.g.*, the production of interferon, that inhibit viral replication.

[0004] **Human Immunodeficiency Virus.** Acquired immunodeficiency syndrome (AIDS) caused by infection with human immunodeficiency virus-1 (HIV-1) represents a major world health problem. Estimates indicate that about 16,000 people worldwide are infected with HIV each day.

[0005] The development of anti-viral drugs has been a major advancement in reducing viral loads in HIV infected patients. Highly active retroviral therapy (HAART) has been shown to reduce viremia to nearly undetectable levels. However, current drug therapies are not practicable as a

long term solution to the HIV epidemic. HAART therapy is severely limited due to poor tolerance for the drugs and the emergence of drug-resistant virus. Moreover, replication competent HIV persists in the lymphoid tissue of patients who have responded to HAART, thus serving as a reservoir of virus. Lastly, current anti-retroviral drug therapies have little impact upon the global epidemic: almost 90% of the world's HIV infected population resides within countries lacking financial resources for these drugs. Thus, a need exists for an efficacious vaccine to both prevent and treat HIV infection.

[0006] Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections in vivo (Oldstone *et al.*, *Nature* 321:239, 1989; Jamieson *et al.*, *J. Virol.* 61:3930, 1987; Yap *et al.*, *Nature* 273:238, 1978; Lukacher *et al.*, *J. Exp. Med.* 160:814, 1994; McMichael *et al.*, *N. Engl. J. Med.* 309:13, 1983; Sethi *et al.*, *J. Gen. Virol.* 64:443, 1983; Watari *et al.*, *J. Exp. Med.* 165:459, 1987; Yasukawa *et al.*, *J. Immunol.* 143:2051, 1989; Tigges *et al.*, *J. Virol.* 66:1622, 1993; Reddenhase *et al.*, *J. Virol.* 55:263, 1985; Quinnan *et al.*, *N. Engl. J. Med.* 307:6, 1982).

[0007] While immune correlates of protective immunity against HIV infection are not well defined, there is a growing body of evidence that suggests CTL are important in controlling HIV infection. HIV-specific CTL responses can be detected early in infection and the appearance of the responses corresponds to the time in infection at which initial viremia is reduced (Pantaleo *et al.*, *Nature* 370:463, 1994; Walker *et al.*, *Proc. Natl. Acad. Sci.* 86:9514, 1989). In addition, HIV replication in infected lymphocytes can be inhibited by incubation with autologous CTL (*see, e.g.*, Tsubota *et al.*, *J. Exp. Med.* 169:1421, 1989). These data are supported by recent studies that indicate CTL are required for controlling viral replication in a SIV/rhesus animal model (Schmitz *et al.*, *Science* 283:857, 1999), and additionally supported by studies that demonstrate that CTL exert selective pressure on HIV populations as evidenced by the eventual predominance of viruses with amino acid replacements in those regions of the virus to which CTL responses are directed (*see, e.g.*, Borrow *et al.*, *Nature Med.* 3:205-211, 1997; Price *et al.*, *Proc. Nat. Acad. Sci.* 94:12890-1895, 1997; Koenig *et al.*, *Nature Med.* 1:330-336, 1995; and Haas *et al.*, *J. Immunol.* 157:4212-4221, 1996).

[0008] Virus-specific T helper lymphocytes are also known to be critical for maintaining effective immunity in chronic viral infections. Historically, HTL responses were viewed as primarily supporting the expansion of specific CTL and B cell populations; however, more recent data indicate that HTL may directly contribute to the control of virus replication. For example, a decline in CD4⁺ T cells and a corresponding loss in HTL function characterize infection with HIV (Lane *et al.*, *New Engl. J. Med.* 313:79, 1985). Furthermore, studies in HIV infected patients have also shown that there is an inverse relationship between virus-specific HTL responses and viral load, suggesting that HTL play a role in viremia (*see, e.g.*, Rosenberg *et al.*, *Science* 278:1447, 1997).

[0009] A fundamental challenge in the development of an efficacious HIV vaccine is the heterogeneity observed in HIV. The virus, like some other infectious agents including retroviruses, rapidly mutates during replication resulting in the generation of virus that can escape anti-viral therapy and immune recognition (Borrow et al., *Nature Med.* 3:205, 1997). In addition, HIV can be classified into a variety of subtypes that exhibit significant sequence divergence (*see, e.g.,* Lukashov *et al.*, *AIDS* 12:S43, 1998). In view of the heterogeneous nature of HIV, and the heterogeneous immune response observed with HIV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple HIV epitopes appears to be important for the development of an efficacious vaccine against HIV. There is a need to establish such vaccine embodiments which elicit immune responses of sufficient breadth and vigor to prevent and/or clear HIV infection.

[0010] **Hepatitis B Virus.** Chronic infection by hepatitis B virus (HBV) affects at least 5% of the world's population and is a major cause of cirrhosis and hepatocellular carcinoma (Hoofnagle, J., *N. Engl. J. Med.* 323:337, 1990; Fields, B. and Knipe, D., In: *Fields Virology* 2:2137, 1990). The World Health Organization lists hepatitis B as a leading cause of death worldwide, close behind chronic pulmonary disease, and more prevalent than AIDS. Chronic HBV infection can range from an asymptomatic carrier state to continuous hepatocellular necrosis and inflammation, and can lead to hepatocellular carcinoma.

[0011] The immune response to HBV is believed to play an important role in controlling hepatitis B infection. A variety of humoral and cellular responses to different regions of the HBV nucleocapsid core and surface antigens have been identified. T cell mediated immunity, particularly involving class I human leukocyte antigen-restricted cytotoxic T lymphocytes (CTL), is believed to be crucial in combatting established HBV infection.

[0012] Several studies have emphasized the association between self-limiting acute hepatitis and multispecific CTL responses (Penna, A. et al., *J. Exp. Med.* 174:1565, 1991; Nayersina, R. et al., *J. Immunol.* 150:4659, 1993). Spontaneous and interferon-related clearance of chronic HBV infection is also associated with the resurgence of a vigorous CTL response (Guidotti, L. G. et al., *Proc. Natl. Acad. Sci. USA* 91:3764, 1994). In all such cases the CTL responses are polyclonal, and specific for multiple viral proteins including the HBV envelope, core and polymerase antigens. By contrast, in patients with chronic hepatitis, the CTL activity is usually absent or weak, and antigenically restricted.

- [0013] The crucial role of CTL in resolution of HBV infection has been further underscored by studies using HBV transgenic mice. Adoptive transfer of HBV-specific CTL into mice transgenic for the HBV genome resulted in suppression of virus replication. This effect was primarily mediated by a non-lytic, lymphokine-based mechanism (Guidotti, L. G. et al., *Proc. Natl. Acad. Sci. USA* 91:3764, 1994; Guidotti, L. G., Guilhot, S., and Chisari, F. V. *J. Virol.* 68:1265, 1994; Guidotti, L. G. et al., *J. Virol.* 69:6158, 1995; Gilles, P. N., Fey, G., and Chisari, F. V., *J. Virol.* 66:3955, 1992).
- [0014] As is the case for HLA class I restricted responses, HLA class II restricted T cell responses are usually detected in patients with acute hepatitis, and are absent or weak in patients with chronic infection (Chisari, F. V. and Ferrari, C., *Annu. Rev. Immunol.* 13:29, 1995). HLA Class II responses are tied to activation of helper T cells (HTLs) Helper T lymphocytes, which recognize Class II HLA molecules, may directly contribute to the clearance of HBV infection through the secretion of cytokines which suppress viral replication (Franco, A. et al., *J. Immunol.* 159:2001, 1997). However, their primary role in disease resolution is believed to be mediated by inducing activation and expansion of virus-specific CTL and B cells.
- [0015] In view of the heterogeneous immune response observed with HBV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple epitopes appears to be important for the development of an efficacious vaccine against HBV. There is a need to establish vaccine embodiments that elicit immune responses that correspond to responses seen in patients that clear HBV infection. Epitope-based vaccines appear useful.
- [0016] **Hepatitis C Virus.** Hepatitis C virus (HCV) infection is a global human health problem with approximately 150,000 new reported cases each year in the U.S. alone. HCV is a single stranded RNA virus, and is the etiological agent identified in most cases of non-A, non-B post-transfusion and post-transplant hepatitis, and is a common cause of acute sporadic hepatitis (Choo *et al.*, *Science* 244:359, 1989; Kuo *et al.*, *Science* 244:362, 1989; and Alter *et al.*, in: *Current Perspective in Hepatology*, p. 83, 1989). It is estimated that more than 50% of patients infected with HCV become chronically infected and, of those, 20% develop cirrhosis of the liver within 20 years (Davis *et al.*, *New Engl. J. Med.* 321:1501, 1989; Alter *et al.*, in: *Current Perspective in Hepatology*, p. 83, 1989; Alter *et al.*, *New Engl. J. Med.* 327:1899, 1992; and Dienstag, J. L. *Gastroenterology* 85:430,

1983). Moreover, the only therapy available for treatment of HCV infection is interferon- α . Most patients are unresponsive, however, and among the responders, there is a high recurrence rate within 6-12 months of cessation of treatment (Liang *et al.*, *J. Med. Virol.* 40:69, 1993). Ribavirin, a guanosine analog with a broad spectrum activity against many RNA and DNA viruses, has been shown in clinical trials to be effective against chronic HCV infection when used in combination with interferon- α (*see, e.g.,* Poynard *et al.*, *Lancet* 352:1426-1432, 1998; Reichard *et al.*, *Lancet* 351:83-87, 1998). However, the response rate is still well below 50%.

[0017] Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections *in vivo* (Oldstone *et al.*, *Nature* 321:239, 1989; Jamieson *et al.*, *J. Virol.* 61:3930, 1987; Yap *et al.*, *Nature* 273:238, 1978; Lukacher *et al.*, *J. Exp. Med.* 160:814, 1994; McMichael *et al.*, *N. Engl. J. Med.* 309:13, 1983; Sethi *et al.*, *J. Gen. Virol.* 64:443, 1983; Watari *et al.*, *J. Exp. Med.* 165:459, 1987; Yasukawa *et al.*, *J. Immunol.* 143:2051, 1989; Tigges *et al.*, *J. Virol.* 66:1622, 1993; Reddenhase *et al.*, *J. Virol.* 55:263, 1985; Quinnan *et al.*, *N. Engl. J. Med.* 307:6, 1982).

[0018] In view of the heterogeneous immune response observed with HCV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple HCV epitopes appears to be important for the development of an efficacious vaccine against HCV. There is a need, however, to establish vaccine embodiments that elicit immune responses that correspond to responses seen in patients that clear HCV infection.

[0019] **Human Papillomavirus.** Human papillomavirus (HPV) is a member of the papillomaviridae, a group of small DNA viruses that infect a variety of higher vertebrates. More than 80 types of HPVs have been identified. Of these, more than 30 can infect the genital tract. Some types, generally types 6 and 11, may cause genital warts, which are typically benign and rarely develop into cancer. Other strains of HPV, “cancer-associated”, or “high-risk” types, can more frequently lead to the development of cancer. The primary mode of transmission of these strains of HPV is through sexual contact.

[0020] The main manifestations of the genital warts are cauliflower-like condylomata acuminata that usually involve moist surfaces; keratotic and smooth papular warts, usually on dry surfaces; and subclinical “flat” warts, which are found on any mucosal or cutaneous

surface (Handsfield, H., *Am. J. Med.* 102(5A):16-20, 1997). These warts are typically benign but are a source of inter-individual spread of the virus (Ponten, J. & Guo, Z., *Cancer Surv.* 32:201-29, 1998). At least three HPV strains associated with genital warts have been identified: type 6a (see, *e.g.*, Hofmann, K.J., *et al.*, *Virology* 209(2):506-518, 1995), type 6b (see, *e.g.*, Hofmann *et al.*, *supra*) and type 11 (see, *e.g.*, Dartmann, K. *et al.*, *Virology* 151(1):124-130, 1986).

[0021] Cancer-associated HPVs have been linked with cancer in both men and women; they include, but are not limited to, HPV-16, HPV-18, HPV-31, HPV-45, HPV-33 and HPV-56. Other HPV strains, including types 6 and 11 as well as others, *e.g.*, HPV-5 and HPV-8, are less frequently associated with cancer. The high risk types are typically associated with the development of cervical carcinoma and premalignant lesions of the cervix in women, but are also associated with similar malignant and premalignant lesions at other anatomic sites within the lower genital or anogenital tract. These lesions include neoplasia of the vagina, vulva, perineum, the penis, and the anus. HPV infection has also been associated with respiratory tract papillomas, and rarely, cancer, as well as abnormal growth or neoplasia in other epithelial tissues. *See, e.g.* VIROLOGY, 2ND ED, Fields *et al.*, Eds. Raven Press, New York, 1990, Chapters 58 and 59, for a review of HPV association with cancer.

[0022] The HPV genome consists of three functional regions, the early region, the late region, and the “long control region”. The early region gene products control viral replication, transcription and cellular transformation. They include the HPV E1 and E2 proteins, which play a role in HPV DNA replication, and the E6 and E7 oncoproteins, which are involved in the control of cellular proliferation. The late region include the genes that encode the structural proteins L1 and L2, which are the major and minor capsid proteins, respectively. The “long control region” contains such sequences as enhancer and promoter regulatory regions.

[0023] HPV expresses different proteins at different stages of the infection, for example early, as well as late, proteins. Even in latent infections, however, early proteins are often expressed and are therefore useful targets for vaccine-based therapies. For example, high-grade dysplasia and cervical squamous cell carcinoma continue to express E6 and E7, which therefore can be targeted to treat disease at both early and late stages of infection.

[0024] Treatment for HPV infection is often unsatisfactory because of persistence of virus after treatment and recurrence of clinically apparent disease is common. The treatment may require frequent visits to clinics and is not directed at elimination of the virus but at

clearing warts. Because of persistence of virus after treatment, recurrence of clinically apparent disease is common.

- [0025] Thus, a need exists for an efficacious vaccine to both prevent and treat HPV infection and to treat cancer that is associated with HPV infection. Effective HPV vaccines would be a significant advance in the control of sexually transmissible infections and could also protect against clinical disease, particularly cancers such as cervical cancer. (see, e.g., Rowen, P. & Lacey, C., *Dermatologic Clinics* 16(4):835-838, 1998).
- [0026] Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections *in vivo* (Oldstone *et al.*, *Nature* 321:239, 1989; Jamieson *et al.*, *J. Virol.* 61:3930, 1987; Yap *et al.*, *Nature* 273:238, 1978; Lukacher *et al.*, *J. Exp. Med.* 160:814, 1994; McMichael *et al.*, *N. Engl. J. Med.* 309:13, 1983; Sethi *et al.*, *J. Gen. Virol.* 64:443, 1983; Watari *et al.*, *J. Exp. Med.* 165:459, 1987; Yasukawa *et al.*, *J. Immunol.* 143:2051, 1989; Tigges *et al.*, *J. Virol.* 66:1622, 1993; Reddenhase *et al.*, *J. Virol.* 55:263, 1985; Quinnan *et al.*, *N. Engl. J. Med.* 307:6, 1982).
- [0027] Virus-specific T helper lymphocytes are also known to be critical for maintaining effective immunity in chronic viral infections. Historically, HTL responses were viewed as primarily supporting the expansion of specific CTL and B cell populations; however, more recent data indicate that HTL may directly contribute to the control of virus replication. For example, a decline in CD4⁺ T cells and a corresponding loss in HTL function characterize infection with HIV (Lane *et al.*, *New Engl. J. Med.* 313:79, 1985). Furthermore, studies in HIV infected patients have also shown that there is an inverse relationship between virus-specific HTL responses and viral load, suggesting that HTL plays a role in viremia (see, e.g., Rosenberg *et al.*, *Science* 278:1447, 1997).
- [0028] The development of vaccines with prophylactic and therapeutic efficacy against HPV is ongoing. Early vaccine development was hampered by the inability to culture HPV. With the introduction of cloning techniques and protein expression, however, some attempts have been made to stimulate humoral and CTL response to HPV (See, e.g., Rowen, P. & Lacey, C., *Dermatologic Clinics* 16(4):835-838 (1998)). Studies to date, however, have been inconclusive.
- [0029] Activation of T helper cells and cytotoxic lymphocytes (CTLs) in the development of vaccines has also been analyzed. Lehtinen, M., *et al.* for instance, has shown that some peptides from the E2 protein of HPV type 16 activate T helper cells and CTLs (*Biochem. Biophys. Res. Commun.* 209(2):541-6 (1995)). Similarly, Tarpey *et al.*, has shown that

some peptides from HPV type 11 E7 protein can stimulate human HPV-specific CTLs *in vitro* (*Immunology* 81:222-227 (1994)) and Borysiewicz *et al.* have reported a recombinant vaccinia virus expressing HPV 16 and HPV 17 E6 and E7 that stimulated CTL responses in at least one patient (*Lancet* 347:1347-1357, 1996).

- [0030] ***Plasmodium falciparum* and Malaria.** Malaria, which is caused by infection with the parasite *Plasmodium falciparum* (PF), represents a major world health problem. Approximately 500 million people in the world are at risk from the disease, with approximately 200 million people actually harboring the parasites. An estimated 1 to 2 million deaths occur each year due to malaria. (Miller *et al.*, *Science* 234:1349, 1986).
- [0031] Fatal outcomes are not confined to first infections, and constant exposure is apparently a prerequisite for maintaining immunity. Naturally acquired sterile immunity is rare, if it exists at all. Accordingly, major efforts to develop an efficacious malaria vaccine have been undertaken.
- [0032] Human volunteers injected with irradiated PF sporozoites are resistant to subsequent sporozoite challenges, which demonstrates that development of a malaria vaccine is indeed immunologically feasible. Furthermore, these immune individuals developed a vigorous response, including antibodies, and cytotoxic T lymphocyte (CTL) and helper T lymphocyte (HTL) components, directed against multiple antigens. Reproducing the breadth and multiplicity of this response in a vaccine, however, is a task of large proportions. The epitope approach, as described herein, may represent a solution to this challenge, in that it allows the incorporation of various antibody, CTL and HTL epitopes, from various proteins, in a single vaccine composition.
- [0033] Anti-sporozoite antibodies are by themselves, in general, not completely efficacious in clearing the infection (Egan *et al.*, *Science* 236:453, 1987). However, high concentrations of antibodies directed against the repeated region of the major B cell antigen of the sporozoite/circumsporozoite protein (CSP) have been shown to prevent liver cell infection in certain experimental models (Egan *et al.*, *Science* 236:453, 1987; Potocnjak, P. *et al.*, *Science* 207:71, 1980). The present inventors have shown that constructs encompassing CSP-repeat B cell epitopes and the optimized helper epitope PADRE™ (San Diego, CA) are highly immunogenic, and can protect *in vitro* against sporozoite invasion in both mouse and human liver cells, and protect mice *in vivo* against live sporozoite challenge (Franke *et al.*, *Vaccine* 17:1201-1205, 1999)

- [0034] PF-specific CD4⁺ T cells also have a role in malarial immunity beyond providing help for B cell and CTL responses. Experiments by Renia *et al.* (Renia, *et al.*, *Proc. Natl. Acad. Sci. USA* 88:7963, 1991) demonstrated that HTLs directed against the *Plasmodium yoelli* CS protein could in fact adoptively transfer protection against malaria.
- [0035] Considerable data implicate CTLs in protection against pre-erythrocytic-stage malaria. CD8⁺ CTLs can eliminate *Plasmodium berghei*- or *Plasmodium yoelii*-infected mouse hepatocytes from in vitro culture in a major histocompatibility complex (MHC)-restricted and antigen-restricted manner (Hoffman *et al.*, *Science* 244:1078-1081, 1989; Weiss *et al.*, *J. Exp. Med.* 171:763-773, 1990). Further, it has also been shown that the immunity that developed in mice vaccinated with irradiated sporozoites is also dependent upon the presence of CD8⁺ T cells. These T cells accumulate in inflammatory liver infiltrates subsequent to challenge. Passive transfer of circumsporozoite (CSP)-specific CTL clones as long as three hours after inoculation of sporozoites (*i.e.*, after the parasites have left the bloodstream and infected liver cells) were capable of protecting animals against infection (Romero *et al.*, *Nature* 341:323, 1989).
- [0036] It is notable that CTL-restricted responses directed against a single antigen are insufficient to protect mice with different MHC alleles, and a combination of multiple antigens was required even to protect mice from the most common laboratory strains of *Plasmodium*. These data indicate that a combination of epitopes from several antigens is necessary to elicit a protective CTL response.
- [0037] Indirect evidence that CTLs are important in protective immunity against Pf in humans has also accumulated. It has been reported that cytotoxic CD8⁺ T cells can be identified in humans immunized with PF sporozoites (Moreno, *et al.*, *Int. Immunol.* 3:997, 1991). Further, humans immunized with irradiated sporozoites or naturally exposed to malaria can generate a CTL response to the pre-erythrocytic-stage antigens, CSP, sporozoite surface protein 2 (SSP2), liver-stage antigen-1 (LSA-1), and exported protein-1 (Exp-1) (*see, e.g.* Malik *et al.*, *Proc. Natl. Acad. Sci. USA* 88, 3300-3304, 1991; Doolan *et al.*, *Int. Immunol.* 3:511-516, 1991; Hill *et al.*, *Nature* 360:434-439, 1992). Additionally, there is evidence that the polymorphism within the CSP may be the result of selection by CTLs of parasites that express variant forms (McCutchan and Water, *Immunol. Lett.* 25:23-26, 1990). This is based on the observation that the variation is nonsynonymous at the nucleotide level, thereby indicating selective pressure at the protein level. The polymorphism primarily maps to identified CTL and T helper epitopes (Doolan *et al.*, *Int. Immunol.* 5:27-46, 1993); and CTL responses to some of the parasite variants do not cross-

react (Hill *et al.*, *supra*). Finally, the MHC class I human leukocyte antigen (HLA)-Bw53 has been associated with resistance to severe malaria in The Gambia, and CTLs to a conserved epitope restricted by the HLA-Bw53 allele have been identified on *P. falciparum* LSA-1 (Hill *et al.*, *Nature* 352:595-600, 1991; Hill *et al.*, *Nature* 340:434-439, 1992). Since HLA-Bw53 is found in 15%-40% of the population of sub-Saharan Africa but in less than 1% of Caucasians and Asians, these data suggest evolutionary selection on the basis of protection against severe malaria.

[0038] Thus, antibody, and both HLA class I and class II restricted responses directed against multiple sporozoite antigens appear to be involved in generating protective immunity to malaria. Furthermore, several important antigenic epitopes against which humoral and cellular immunity is focused have already been exactly delineated.

[0039] In view of the heterogeneous immune response observed with PF infection, induction of a multi-specific cellular immune response directed simultaneously against multiple PF epitopes appears to be important for the development of an efficacious vaccine against PF. There is a need, however, to establish vaccine embodiments that elicit immune responses that correspond to responses seen in patients that clear PF infection.

[0040] **Epitope-Based Vaccines.** The use of epitope-based vaccines has several advantages over current vaccines. The epitopes for inclusion in such a vaccine are to be selected from conserved regions of viral or tumor-associated antigens, in order to reduce the likelihood of escape mutants. The advantage of an epitope-based approach over the use of whole antigens is that there is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. Furthermore, immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-based vaccines.

[0041] Additionally, with an epitope-based vaccine approach, there is an ability to combine selected epitopes (CTL and HTL) and additionally to modify the composition of the epitopes, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches.

[0042] Another major benefit of epitope-based immune-stimulating vaccines is their safety. The possible pathological side effects caused by infectious agents or whole protein antigens, which might have their own intrinsic biological activity, is eliminated.

[0043] An epitope-based vaccine also provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Thus, patient-by-patient variability in the immune response to a particular pathogen may be alleviated by inclusion of epitopes from multiple antigens from that pathogen in a vaccine composition. A “pathogen” may be an infectious agent or a tumor associated molecule.

[0044] One of the most formidable obstacles to the development of broadly efficacious epitope-based immunotherapeutics has been the extreme polymorphism of HLA molecules. In the past, effective non-genetically biased coverage of a population has been a task of considerable complexity; such coverage has required that epitopes be used specific for HLA molecules corresponding to each individual HLA allele. Therefore, impractically large numbers of epitopes would be required in order to cover ethnically diverse populations. Recently, methods have been developed that allow the identification of epitopes that bind multiple HLA molecules. Therefore, epitope-based vaccines can be designed that contain epitopes which, either individually or in combination, bind a greater number of HLA molecules. The resulting epitope-based vaccines have a greater breadth of population coverage across one or more continents and even worldwide.

[0045] **Variation in Epitopes of Infectious Agents.** A challenge in the development of effective vaccines against infectious agents such as hepatitis B virus (HBV) (47, 60) hepatitis C virus (HCV) (61-63), human papilloma virus (HPV) (64, 65) *Plasmodium falciparum* (66), and human immunodeficiency virus (HIV-1) is the protein sequence variation associated with different isolates. This variation is the result of gene sequence mutations. When such mutations occur in regions encoding epitopes recognized by cytotoxic T-lymphocytes (CTL), they provide a mechanism for escape of the agent from immune system control.

[0046] HIV-1 represents an infectious agent with an especially high frequency of sequence variation. The sequence variation associated with HIV-1 proteins from related isolates, members of the same clades or types, as well as unrelated isolates, is well documented (1). Viral escape from CTL induced as the result of natural infection or vaccines was documented in nonhuman primate models where the mechanism behind this escape was mutation of the primary anchor residues in dominant CTL epitopes (5-9). Viral escape from HIV-specific CTL has also been strongly implied by data obtained from HIV-1 infected individuals whose disease status change, including the transition from

acute to chronic infection (10, 11), loss of stable control of viral replication and subsequent progression to AIDS (4, 12) or mother-to-child transmission (13). Thus, HIV-1 genetic and protein sequence variation represent a significant challenge to immune system-based control of viral replication, both within infected individuals and within populations.

[0047] While the public health need for a vaccine against HIV-1 is well recognized and accepted, the genetic variation of HIV-1 isolates represents a highly significant obstacle (1, 14-16). Several strategies have been proposed, some of which include:

- (1) Designing vaccines on HIV-1 types prevalent within small, well defined populations or geographical regions, such as individual countries or regions, and producing multiple different vaccines for exclusive use within these countries or regions (16).
- (2) Use of HIV-1 ancestral or consensus sequences based on HIV types present in larger target populations, such as groups of neighboring countries or continents (15, 17-19).
- (3) Incorporation of viral gene products obtained from multiple different virus isolates, representing diversely different types or clades, into a single 'multi-valent' vaccine.

[0048] Related vaccine design concepts that incorporate many of the advantages associated with the approaches described above are the use of highly conserved regions or epitopes derived from these regions as the basis of the vaccine. The logic behind this approach is that conserved regions of the viral genome are those that have been maintained through the evolution of HIV-1 because changes impact gene product function and general viral fitness. This theory is consistent with analyses of HIV-1 protein sequence data which demonstrated that CTL epitopes are concentrated in conserved regions and that regions devoid of CTL epitopes are the most variable (20). Additional support comes from published reports describing CTL responses, induced as the result of natural infection or vaccination, that recognize viral proteins or epitopes common to viral isolates from diverse types or clades (21-26). Broad function CTL responses are also known to be correlated with slower progression to AIDS, at least for certain carefully studied populations (27, 28). Despite these reports and the clustering of CTL epitopes in

conserved regions of HIV-1 gene products, amino acid sequence variation of analogous regions and epitopes from different viral isolates, both within the same type or clade and from different types, remains significant. There are currently no rules guiding the selection of conserved regions of CTL epitopes for use in vaccines other than the use of amino acid sequence identity (29).

[0049] A clear understanding of how CTL recognize pathogen infected cells has emerged over the past decade. It is now well established that small fragments of pathogen-derived proteins are generated, defined as peptide epitopes generally 8-11 amino acids in length, which bind to HLA-A, -B, or -C (human Class I Major Histocompatibility Molecules) molecules expressed on the cell surface. Sequencing of naturally processed peptides bound to HLA molecules provided a means to identify the amino acid residues required for allele-specific epitope-peptide binding (30-32). Data obtained from X-ray crystallographic analysis of HLA-epitope peptide complexes, allowed for the identification and structural characterization of 'binding pockets' within the peptide binding cleft of HLA molecules. More refined epitope anchor motif definitions were then developed using data obtained from *in vitro* peptide-MHC binding assays. It is now well known that the main anchor residues typically occur at position 2 and the carboxyl terminus of peptides 8-11 amino acids in length, thus positions 8, 9, 10 or 11 (33-40). The definition of epitope peptide binding anchor motifs is the key to most, if not all, epitope prediction methods.

[0050] Initial CTL epitope identification methods were developed using common HLA alleles, such as HLA-A2.1. Motifs defined using different HLA molecules were found to be similar and this led to the definition of HLA supertype families (41). The biological effect of this supertype relationship was first demonstrated for HIV-1 epitopes in a study where the HLA-A3 and -A11 epitope peptide binding patterns repertoires were demonstrated to be overlapping, not only with each other but also with HLA-A31, -A33 and -A*6801 (42). This binding specificity was defined as the HLA-A3 supertype. A significant overlap in peptide binding patterns was also demonstrated amongst several serologically distant HLA-B alleles (43, 44), and multiple HLA-A2 alleles (45, 46), resulting in the definition of the HLA-B7 and HLA-A2 supertype families. Recognition of epitopes by CTL in a supertype manner has since been demonstrated to occur naturally in infectious diseases and cancer (47-53).

[0051] While only two positions within CTL epitopes are typically characterized as the primary binding anchor positions, the amino acids that can serve as the anchor residues are

more variable. The preferred and tolerated amino acids that can serve as anchor residues for the HLA-A2, -A3 and -B7 supertype families of epitopes are listed in Table 1. It is possible for analogous HIV-1 epitope peptides derived from different isolates, which differ with respect to the amino acids used as anchor residues, to bind to HLA molecules similarly. This type of variation can be as conserved since it is likely that CTL produced against one epitope would recognize the related epitope. Thus, variation limited to changes in anchor residues that result in sufficient epitope peptide binding to HLA molecules does not result in immune escape from CTL. Epitopes that contain this type of variation can be identified using the appropriately designed motif search algorithms.

[0052] The TCR of CTL has been reported to be somewhat flexible or promiscuous with respect to recognition of epitope peptides bound to HLA molecules. For HIV-1, this flexibility was demonstrated as CTL recognition of related, but slightly variable, epitopes by single clones of CTL produced following natural infection (54, 55). Similar flexibility of CTL epitope recognition was demonstrated using rhesus macaques and natural infection with SIV or immunization (56, 57). This observation is not unique to HIV-1 and SIV but rather the TCR appears to have evolved to allow promiscuous recognition of peptide epitope bound to MHC molecules (58).

[0053] Selective replacement of certain amino acids in CTL epitope peptides, amino acids thought to represent TCR contact points, is not only tolerated but can increase the recognition of the epitopes by CTL clones (59). The types of amino acid substitutions that can be incorporated, typically amino acids that are similar in chemical properties are best tolerated, and their positions, independent of primary anchor positions, within a selected number of CTL epitopes from tumor associated antigens were also defined.

[0054] For HIV-1 and other infectious agents, reproducible methods for predicting the CTL recognition of related variant epitopes that occur amongst isolates have not been developed. Nor have methods for identifying CTL epitopes that are most likely to induce broadly functional responses when used in vaccine. Thus, there exists a need to develop such methods to overcome the challenge associated with protein sequence variation in HIV and other infectious agents.

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SUMMARY OF THE INVENTION

[0055] The present invention is directed to methods for selecting a variant of a peptide epitope which induces a CTL response against another variant(s) of the peptide epitope, by determining whether the variant comprises only conserved residues, as defined herein, at non-anchor positions in comparison to the other variant(s).

[0056] In some embodiments, antigen sequences from a population of an infectious agent, said antigens comprising variants of a peptide epitope, are optionally aligned (manually or by computer) along their length, preferably their full length. Variant(s) of a peptide epitope (preferably naturally occurring variants), each 8-11 amino acids in length and comprising the same MHC class I supermotif or motif, are identified manually or with the aid of a computer. In some embodiments, a variant is optionally chosen which comprises preferred anchor residues of said motif and/or which occurs with high frequency within the population of variants. In other embodiments, a variant is randomly chosen. The randomly or otherwise chosen variant is compared to from one to all the remaining variant(s) to determine whether it comprises only conserved residues in the non-anchor positions relative to from one to all the remaining variant(s).

[0057] The present invention is also directed to variants identified by the methods above; peptides comprising such variants; nucleic acids encoding such variants and peptides; cells comprising such variants, and/or peptides, and/or nucleic acids; compositions comprising such variants, and/or peptides, and/or nucleic acids, and/or cells; as well as therapeutic and diagnostic methods for using such variants, peptides, nucleic acids, cells, and compositions.

BRIEF DESCRIPTION OF THE DRAWINGS/FIGURES

[0058] FIGS. 1A-1E. Recognition of variant peptides by CTL generated against a single epitope. Variant peptides were identified from 167 HIV strains for 5 HIV epitopes, 3 HLA-A2 restricted (Env 134, A, Gag 386, B, and Vpr 62, C) and 2 HLA-A11 restricted (Pol 98, D, and Env 47, E). These are listed according to their relationship to a previously determined parent (P) into single anchor substitutions (A), single non-anchor substitutions (NA) or multiple substitutions (M). Binding of each variant peptide is also shown. The number of viral sequences containing each variant peptide is shown in the column labeled

Isolates, and is reported for the total sequences, Clade B sequences (B), and Clade C sequences (C). Finally, the ability of CTL primed against the parent peptide to recognize the variant peptides is shown in the bar graphs.

[0059] FIGS. 2A-2C. Characterization of the peptide-specific T cell lines. A. FACS analysis of the TCRs expressed by peptide -stimulated cells after 0, 1, and 5 peptide stimulations, using a panel of commercially available mAb for mouse TCR 2-14. B-C. Peptide affinity. Parent and variant peptides were titrated against CTL that had been stimulated 5 times with the parent peptide.

[0060] FIGS. 2A-2B. Recognition of a panel of variant peptides by PBL from an HIV-infected individual.

[0061] FIG 4. Prediction of immunological conservation. Gag 271 variants and their binding are shown, along with the number of isolates that express each variant. Immunological recognition was predicted for each variant based on two different choices in the immunizing peptide. On the right, the immunogenicity for each variant is shown.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

[0062] The invention can be better understood with reference to the following definitions:

[0063] An “antigen” refers to a polypeptide encoded by the genome of an infectious agent, or other another source, but preferably an infectious agent in the present invention. Examples of HIV antigens include Env, Gag, Nef, Pol, Tat, Rev, Vif, Vpr, Vpu, p17, p24, p2, p7, p1, p6, Protease, RT, Integrase, and gp160 (preferably Env, Gag, Nef, Pol, Tat, Rev, Vif, Vpr, Vpu). Examples of HBV antigens include Core, Env, and Pol. Examples of HCV antigens include Core, E1, E2, Ns1, Ns2, Ns3, Ns4, and Ns5. Examples of HPV antigens include E1, E2, E3, E4, E5, E6, E7, L1, and L2. Examples of *Plasmodium falciparum* antigens include CSP, SSP2, Exp1, and LSA1.

[0064] Throughout this disclosure, “binding data” results are often expressed in terms of “IC₅₀'s.” IC₅₀ is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e.*, limiting HLA proteins and labeled peptide concentrations), these values approximate K_D values. Assays for

determining binding are described in detail, *e.g.*, in PCT publications WO 94/20127 and WO 94/03205, and other publications such Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al.*, *J. Immunol.* 154:247 (1995); and Sette, *et al.*, *Mol. Immunol.* 31:813 (1994). It should be noted that IC₅₀ values can change, often dramatically, if the assay conditions are varied, and depending on the particular reagents used (*e.g.*, HLA preparation, *etc.*). For example, excessive concentrations of HLA molecules will increase the apparent measured IC₅₀ of a given ligand.

[0065] Alternatively, binding is expressed relative to a reference peptide. Although as a particular assay becomes more, or less, sensitive, the IC₅₀'s of the peptides tested may change somewhat, the binding relative to the reference peptide will not significantly change. For example, in an assay run under conditions such that the IC₅₀ of the reference peptide increases 10-fold, the IC₅₀ values of the test peptides will also shift approximately 10-fold. Therefore, to avoid ambiguities, the assessment of whether a peptide is a good (*i.e.* high), intermediate, weak, or negative binder is generally based on its IC₅₀, relative to the IC₅₀ of a standard peptide. The Tables included in this application present binding data in a preferred biologically relevant form of IC₅₀ nM.

[0066] Binding may also be determined using other assay systems including those using: live cells (*e.g.*, Ceppellini *et al.*, *Nature* 339:392 (1989); Christnick *et al.*, *Nature* 352:67 (1991); Busch *et al.*, *Int. Immunol.* 2:443 (1990); Hill *et al.*, *J. Immunol.* 147:189 (1991); del Guercio *et al.*, *J. Immunol.* 154:685 (1995)), cell free systems using detergent lysates (*e.g.*, Cerundolo *et al.*, *J. Immunol.* 21:2069 (1991)), immobilized purified MHC (*e.g.*, Hill *et al.*, *J. Immunol.* 152, 2890 (1994); Marshall *et al.*, *J. Immunol.* 152:4946 (1994)), ELISA systems (*e.g.*, Reay *et al.*, *EMBO J.* 11:2829 (1992)), surface plasmon resonance (*e.g.*, Khilko *et al.*, *J. Biol. Chem.* 268:15425 (1993)), high flux soluble phase assays (Hammer *et al.*, *J. Exp. Med.* 180:2353 (1994)), and measurement of class I MHC stabilization or assembly (*e.g.*, Ljunggren *et al.*, *Nature* 346:476 (1990); Schumacher *et al.*, *Cell* 62:563 (1990); Townsend *et al.*, *Cell* 62:285 (1990); Parker *et al.*, *J. Immunol.* 149:1896 (1992)).

[0067] As used herein, "high affinity" with respect to HLA class I molecules is defined as binding with an IC₅₀ or K_D value, of 50 nM or less, "intermediate affinity" is binding with an IC₅₀ or K_D value of between 50 and about 500 nM, weak affinity is binding with an IC₅₀ or K_D value of between about 500 and about 5000 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an IC₅₀ or K_D value of 100 nM or less; "intermediate affinity" is binding with an IC₅₀ or K_D value of between about 100 and about 1000 nM.

[0068] A "computer" or "computer system" generally includes: a processor and related computer programs; at least one information storage/retrieval apparatus such as a hard drive, a disk drive or a tape drive; at least one input apparatus such as a keyboard, a mouse, a touch screen, or a microphone; and display structure, such as a screen or a printer. Additionally, the computer may

include a communication channel in communication with a network. Such a computer may include more or less than what is listed above.

[0069] “Cross-reactive binding” indicates that a peptide is bound by more than one HLA molecule; a synonym is degenerate binding.

[0070] A “cryptic epitope” elicits a response by immunization with an isolated peptide, but the response is not cross-reactive *in vitro* when intact whole protein, which comprises the epitope, is used as an antigen.

[0071] The term “derived” when used to discuss an epitope is a synonym for “prepared.” A derived epitope can be isolated from a natural source, or it can be synthesized in accordance with standard protocols in the art. Synthetic epitopes can comprise artificial amino acids “amino acid mimetics,” such as D isomers of natural occurring L amino acids or non-natural amino acids such as cyclohexylalanine. A derived/prepared epitope can be an analog of a native epitope.

[0072] A “diluent” includes sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred diluent for pharmaceutical compositions. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as diluents, particularly for injectable solutions.

[0073] A “dominant epitope” is an epitope that induces an immune response upon immunization with a whole native antigen (see, *e.g.*, Sercarz, *et al.*, *Annu. Rev. Immunol.* 11:729-766, 1993). Such a response is cross-reactive *in vitro* with an isolated peptide epitope.

[0074] An “epitope” is the collective features of a molecule, such as primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an immunoglobulin, T cell receptor or HLA molecule. Alternatively, an epitope can be defined as a set of amino acid residues which is involved in recognition by a particular immunoglobulin, or in the context of T cells, those residues necessary for recognition by T cell receptor proteins and/or Major Histocompatibility Complex (MHC) receptors. Epitopes are present in nature, and can be isolated, purified or otherwise prepared/derived by humans. For example, epitopes can be prepared by isolation from a natural source, or they can be synthesized in accordance with standard protocols in the art. Synthetic epitopes can comprise artificial amino acids, “amino acid mimetics,” such as D isomers of naturally-occurring L amino acids or non-naturally-occurring amino acids such as cyclohexylalanine. Throughout this disclosure, epitopes may be referred to in some cases as peptides. The variants of the invention are set forth in Tables 6-9 and Figures 1A-4.

[0075] It is to be appreciated that proteins or peptides that comprise a variant of the invention as well as additional amino acid(s) are still within the bounds of the invention. In certain embodiments, the peptide comprises a fragment of an antigen. A “fragment of an antigen” or “antigenic fragment” or simply “fragment” is a portion of an antigen which has 100% identity with a wild type antigen or naturally-occurring variant thereof. The fragment may or may not comprise

an epitope of the invention. The fragment may be less than or equal to 600 amino acids, less than or equal to 500 amino acids, less than or equal to 400 amino acids, less than or equal to 250 amino acids, less than or equal to 100 amino acids, less than or equal to 85 amino acids, less than or equal to 75 amino acids, less than or equal to 65 amino acids, or less than or equal to 50 amino acids in length. In certain embodiments, a fragment is e.g., less than 101 or less than 51 amino acids in length, in any increment down to 5 amino acids in length. For example, the fragment may be 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length.

[0076] In certain embodiments, there is a limitation on the length of a peptide of the invention. The embodiment that is length-limited occurs when the protein/peptide comprising an epitope of the invention comprises a region (i.e., a contiguous series of amino acids) having 100% identity with a native sequence. In order to avoid the definition of epitope from reading, e.g., on whole natural molecules, there is a limitation on the length of any region that has 100% identity with a native peptide sequence. Thus, for a peptide comprising an epitope of the invention and a region with 100% identity with a native peptide sequence, the region with 100% identity to a native sequence generally has a length of: less than or equal to 600 amino acids, often less than or equal to 500 amino acids, often less than or equal to 400 amino acids, often less than or equal to 250 amino acids, often less than or equal to 100 amino acids, often less than or equal to 85 amino acids, often less than or equal to 75 amino acids, often less than or equal to 65 amino acids, and often less than or equal to 50 amino acids. In certain embodiments, an “epitope” of the invention is comprised by a peptide having a region with less than 51 amino acids that has 100% identity to a native peptide sequence, in any increment down to 5 amino acids.

[0077] Accordingly, peptide or protein sequences longer than 600 amino acids are within the scope of the invention, so long as they do not comprise any contiguous sequence of more than 600 amino acids that have 100% identity with a native peptide sequence. For any peptide that has five contiguous residues or less that correspond to a native sequence, there is no limitation on the maximal length of that peptide in order to fall within the scope of the invention. It is presently preferred that a peptide of the invention (e.g., a peptide comprising an epitope of the invention) be less than 600 residues long in any increment down to eight amino acid residues.

[0078] A peptide epitope occurring with “high frequency” is one that occurs in at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% of the infectious agents in a population. A “high frequency” peptide epitope is one of the more common in a population, preferably the first most common, second most common, third most common, or fourth most common in a population of variant peptide epitopes.

- [0079] "Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (*see, e.g., Stites, et al., IMMUNOLOGY, 8TH ED., Lange Publishing, Los Altos, CA (1994).*
- [0080] An "HLA supertype or HLA family", as used herein, describes sets of HLA molecules grouped on the basis of shared peptide-binding specificities. HLA class I molecules that share somewhat similar binding affinity for peptides bearing certain amino acid motifs are grouped into such HLA superotypes. The terms HLA superfamily, HLA supertype family, HLA family, and HLA xx-like molecules (where "xx" denotes a particular HLA type), are synonyms. See Tables 1-4.
- [0081] As used herein, "high affinity" with respect to HLA class I molecules is defined as binding with an IC₅₀, or K_D value, of 50 nM or less; "intermediate affinity" is binding with an IC₅₀ or K_D value of between about 50 and about 500 nM; "weak affinity" is binding with an IC₅₀ or K_D value between about 500 and about 5000 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an IC₅₀ or K_D value of 100 nM or less; "intermediate affinity" is binding with an IC₅₀ or K_D value of between about 100 and about 1000 nM. See "binding data."
- [0082] An "IC₅₀" is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e., limiting HLA proteins and labeled peptide concentrations*), these values approximate K_D values. See "binding data."
- [0083] The terms "identical" or percent "identity," in the context of two or more peptide sequences or antigen fragments, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using a sequence comparison algorithm or by manual alignment and visual inspection.
- [0084] An "immunogenic" peptide or an "immunogenic" epitope or "peptide epitope" is a peptide that comprises an allele-specific motif or supermotif such that the peptide will bind an HLA molecule and induce a CTL and/or HTL response. Thus, immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and thereafter inducing a cytotoxic T lymphocyte (CTL) response, or a helper T lymphocyte (HTL) response, to the peptide.
- [0085] An "infectious agent" refers to a disease-causing microorganism, including viruses, bacteria, fungi, and protozoa against which a cellular immune response, preferably a CTL response, plays a role in acquired immunity. Examples of infectious agents include viruses such as human immunodeficiency virus (HIV), hepatitis B virus (HBV), hepatitis C virus (HCV), human papillomoma virus (HPV), Influenza virus, Dengue virus, Epstein-Barr virus, bacteria such as *Mycobacterium tuberculosis* and *Chlamydia*, fungi such as *Candida albicans*, *Cryptococcus neoformans*, *Coccidioides spp.*, *Histoplasma spp.*, and *Aspergillus*

fumigatis, protozoa such as *Plasmodium spp.*, including *P. falciparum*, *Trypanosoma spp.*, *Schistosoma spp.*, *Leishmania spp* and the like. Preferred infectious agents include HIV, HBV, HCV, HPV, Epstein-Barr virus, *Plasmodium falciparum*, Influenza virus and Dengue virus.

[0086] The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment. An "isolated" epitope refers to an epitope that does not include the whole sequence of the antigen or polypeptide from which the epitope was derived. Typically the "isolated" epitope does not have attached thereto additional amino acids that result in a sequence that has 100% identity with a native sequence. The native sequence can be a sequence such as a tumor-associated antigen from which the epitope is derived. Thus, the term "isolated" means that the material is removed from its original environment (*e.g.*, the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or peptide present in a living animal is not isolated, but the same polynucleotide or peptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such a polynucleotide could be part of a vector, and/or such a polynucleotide or peptide could be part of a composition, and still be "isolated" in that such vector or composition is not part of its natural environment. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the DNA molecules of the present invention, and further include such molecules produced synthetically.

[0087] "Major Histocompatibility Complex" or "MHC" is a cluster of genes that plays a role in control of the cellular interactions responsible for physiologic immune responses. In humans, the MHC complex is also known as the human leukocyte antigen (HLA) complex. For a detailed description of the MHC and HLA complexes, see, Paul, FUNDAMENTAL IMMUNOLOGY, 3RD ED., Raven Press, New York (1993).

[0088] The term "motif" refers to a pattern of residues in an amino acid sequence of defined length, preferably a peptide of less than about 15 amino acids in length, or less than about 13 amino acids in length, usually from about 8 to about 13 amino acids (*e.g.*, 8, 9, 10, 11, 12, or 13) for a class I HLA motif and from about 6 to about 25 amino acids (*e.g.*, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) for a class II HLA motif, which is recognized by a particular HLA molecule. Motifs are typically different for each HLA protein encoded by a given human HLA allele. These motifs often differ in their pattern of the primary and secondary anchor residues. See Tables 1-3.

[0089] A "native" or a "wild type" sequence refers to a sequence found in nature.

- [0090] A "negative binding residue" or "deleterious residue" is an amino acid which, if present at certain positions (typically not primary anchor positions) in a peptide epitope, results in decreased binding affinity of the peptide for the peptide's corresponding HLA molecule.
- [0091] The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the α -amino and carboxyl groups of adjacent amino acids.
- [0092] A "PanDR binding" peptide or "PADRE[®]" peptide (Epimmune, San Diego, CA) is a member of a family of molecules that binds more than one HLA class II DR molecule. The pattern that defines the PADRE[®] family of molecules can be referred to as an HLA Class II supermotif. A PADRE[®] molecule binds to HLA-DR molecules and stimulates *in vitro* and *in vivo* human helper T lymphocyte (HTL) responses. For a further definition of the PADRE[®] family, see copending application US serial Nos. 09/709,774, filed November 11, 2000; and 09/707,738, filed November 6, 2000; PCT publication Nos WO 95/07707, and WO 97/26784; U.S. Patent Nos. 5,736,142 issued April 7, 1998; 5,679,640, issued October 21, 1997; and 6,413,935, issued July 2, 2002.
- [0093] "Pharmaceutically acceptable" refers to a generally non-toxic, inert, and/or physiologically compatible composition or component of a composition.
- [0094] A "pharmaceutical excipient" or "excipient" comprises a material such as an adjuvant, a carrier, pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like. A "pharmaceutical excipient" is an excipient which is pharmaceutically acceptable.
- [0095] A "primary anchor residue" is an amino acid at a specific position along a peptide sequence which is understood to provide a contact point between the immunogenic peptide and the HLA molecule. One, two or three, primary anchor residues within a peptide of defined length generally defines a "motif" for an immunogenic peptide. These residues are understood to fit in close contact with peptide binding grooves of an HLA molecule, with their side chains buried in specific pockets of the binding grooves themselves. In one embodiment of an HLA class I motif, the primary anchor residues are located at position 2 (from the amino terminal position) and at the carboxyl terminal position of a peptide epitope in accordance with the invention. The primary anchor positions for each motif and supermotif of HLA Class I are set forth in Tables 1-2. For example, analog peptides can be created by altering the presence or absence of particular residues in these anchor positions. Such analogs are used to modulate the binding affinity of an epitope comprising a particular motif or supermotif. A "preferred primary anchor residue" is an anchor residue of a motif or supermotif that is associated with optimal binding. Preferred primary anchor residues are indicated in bold-face in Tables 1-2. A "tolerated primary anchor residue" is an anchor residue of a motif or supermotif that is associated with

binding to a lesser extent than a preferred residue. Tolerated primary anchor residues are indicated in italicized text in Tables 1-2.

- [0096] “Promiscuous recognition” by a TCR is where a distinct peptide is recognized by the various T cell clones in the context of various HLA molecules. Promiscuous binding by an HLA molecule is synonymous with cross-reactive binding.
- [0097] A “protective immune response” or “therapeutic immune response” refers to a CTL and/or an HTL response to an antigen derived from an antigen of an infectious agent, which in some way prevents or at least partially arrests disease symptoms, side effects or progression. The immune response may also include an antibody response which has been facilitated by the stimulation of helper T cells.
- [0098] By “ranking” the variants in a population of peptide epitopes is meant ordering each variant by its frequency of occurrence relative to the other variants.
- [0099] The term “residue” refers to an amino acid or amino acid mimetic incorporated into a peptide or protein by an amide bond or amide bond mimetic.
- [00100] A “secondary anchor residue” is an amino acid at a position other than a primary anchor position in a peptide which may influence peptide binding. A secondary anchor residue occurs at a significantly higher frequency amongst HLA-bound peptides than would be expected by random distribution of amino acids at a given position. A secondary anchor residue can be identified as a residue which is present at a higher frequency among high or intermediate affinity binding peptides, or a residue otherwise associated with high or intermediate affinity binding. The secondary anchor residues are said to occur at “secondary anchor positions.” For example, analog peptides can be created by altering the presence or absence of particular residues in these secondary anchor positions. Such analogs are used to finely modulate the binding affinity of an epitope comprising a particular motif or supermotif. The terminology “fixed peptide” is generally used to refer to an analog peptide that has changes in primary anchor position; not secondary.
- [00101] A “subdominant epitope” is an epitope which evokes little or no response upon immunization with a whole antigen or a fragment of the whole antigen comprising a subdominant epitope and a dominant epitope, which comprise the epitope, but for which a response can be obtained by immunization with an isolated peptide, and this response (unlike the case of cryptic epitopes) is detected when whole antigen or a fragment of the whole antigen comprising a subdominant epitope and a dominant epitope is used to recall the response *in vitro* or *in vivo*.
- [00102] A “supermotif” is a peptide binding specificity shared by HLA molecules encoded by two or more HLA alleles. Preferably, a supermotif-bearing peptide is recognized with high or intermediate affinity (as defined herein) by two or more HLA antigens.

[00103] “Synthetic peptide” refers to a peptide that is obtained from a non-natural source, *e.g.*, is man-made. Such peptides may be produced using such methods as chemical synthesis or recombinant DNA technology. “Synthetic peptides” include “fusion proteins.”

[00104] As used herein, a “vaccine” is a composition used for vaccination, *e.g.*, for prophylaxis or therapy, that comprises one or more peptides of the invention. There are numerous embodiments of vaccines in accordance with the invention, such as by a cocktail of one or more peptides; one or more peptides of the invention comprised by a polyepitopic peptide; or nucleic acids that encode such peptides or polypeptides, *e.g.*, a minigene that encodes a polyepitopic peptide. The “one or more peptides” can include any whole unit integer from 1-150, *e.g.*, at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 or more peptides of the invention. The peptides or polypeptides can optionally be modified, such as by lipidation, addition of targeting or other sequences. HLA class I-binding peptides of the invention can be linked to HLA class II-binding peptides, *e.g.*, a PADRE® universal HTL-binding peptide; to facilitate activation of both cytotoxic T lymphocytes and helper T lymphocytes. Vaccines can comprise peptide pulsed antigen presenting cells, *e.g.*, dendritic cells.

[00105] A “variant of a peptide epitope” refers to a peptide that is identified from a different viral strain at the same position in an aligned sequence, and that varies by one or more amino acids from the parent peptide epitope. Examples of peptide epitope variants include those shown in Tables 6-9 and Figures 1A-4. A “variant of an antigen” refers to an antigen that comprises at least one variant of a peptide epitope. Examples of antigen variants include those listed by sequence and/or accession number in Tables 10-22. A “variant of an infectious agent” refers to an infectious agent whose genome encodes at least one variant of an antigen. Variants of infectious agents are related viral, bacterial, fungal, or protozoan strains or isolates that vary in sequence but cause the same disease symptoms. Examples of infectious agent variants include HIV Clade A, B, and C subtypes, HBV subtypes adr, ayr, adw, and ayw, HCV types 1, 2, 3, 4, 5, and 6, HPV strains 1-92 (preferably strains 16, 18, 31, 33, 45, 52, 56, and 58) (see Table 10, listing accession numbers for the complete genome sequences of 167 HIV variants; Table 22, showing an alignment of the complete polyprotein sequences of 50 HCV variants) (see also, *Human Retroviruses and AIDS 2000: A Compilation and Analysis of Nucleic Acid and Amino Acid Sequences*, Kuiken CL, et al., Eds. Theoretical Biology and Biophysics Group, Los Alamos National Laboratory, Los Alamos, NM).

[00106] The nomenclature used to describe peptides/proteins follows the conventional practice wherein the amino group is presented to the left (the N-terminus) and the carboxyl group to the right (the C-terminus) of each amino acid residue. When amino acid residue positions are referred to in a peptide epitope they are numbered in an amino to carboxyl direction with position one being the position closest to the amino terminal end of the epitope, or the peptide or protein of which it may be a part. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. However, when three letter symbols or full names are used without capitals, they may refer to L amino acids. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or "G". The amino acid sequences of peptides set forth herein are generally designated using the standard single letter symbol. (A, Alanine; C, Cysteine; D, Aspartic Acid; E, Glutamic Acid; F, Phenylalanine; G, Glycine; H, Histidine; I, Isoleucine; K, Lysine; L, Leucine; M, Methionine; N, Asparagine; P, Proline; Q, Glutamine; R, Arginine; S, Serine; T, Threonine; V, Valine; W, Tryptophan; and Y, Tyrosine.) In addition to these symbols, "B" in the single letter abbreviations used herein designates α -amino butyric acid. In some embodiments, α -amino butyric acid may be replaced with cysteine.

Acronyms used herein are as follows:

APC:	Antigen presenting cell
CD3:	Pan T cell marker
CD4:	Helper T lymphocyte marker
CD8:	Cytotoxic T lymphocyte marker
CEA:	Carcinoembryonic antigen (see, e.g., SEQ ID NO: 363)
CTL:	Cytotoxic T lymphocyte
DC:	Dendritic cells. DC functioned as potent antigen presenting cells by stimulating cytokine release from CTL lines that were specific for a model peptide derived from hepatitis B virus. <i>In vivo</i> experiments using DC pulsed <i>ex vivo</i> with an HBV peptide epitope have stimulated CTL immune responses <i>in vivo</i> following delivery to naïve mice.
DLT:	Dose-limiting toxicity, an adverse event related to therapy.
DMSO:	Dimethylsulfoxide
ELISA:	Enzyme-linked immunosorbant assay
E:T:	Effector:Target ratio
G-CSF:	Granulocyte colony-stimulating factor
GM-CSF:	Granulocyte-macrophage (monocyte)-colony stimulating factor
HBV:	Hepatitis B virus
HER2/neu:	A tumor associated antigen; c-erbB-2 is a synonym (see, e.g., SEQ ID NO: 364)
HLA:	Human leukocyte antigen

HLA-DR:	Human leukocyte antigen class II
HPLC:	High Performance Liquid Chromatography
HTC:	Helper T Cell
HTL:	Helper T Lymphocyte. A synonym for HTC.
ID:	Identity
IFN γ :	Interferon gamma
IL-4:	Interleukin-4
IV:	Intravenous
LU _{30%} :	Cytotoxic activity for 10 ⁶ effector cells required to achieve 30% lysis of a target cell population, at a 100:1 (E:T) ratio.
MAb:	Monoclonal antibody
MAGE:	Melanoma antigen (see, e.g., SEQ ID NO: 365 and 366 for MAGE2 and MAGE3)
MLR:	Mixed lymphocyte reaction
MNC:	Mononuclear cells
PB:	Peripheral blood
PBMC:	Peripheral blood mononuclear cell
ProGP TM :	Progenipointin TM product (Searle, St. Louis, MO), a chimeric flt3/G-CSF receptor agonist.
SC:	Subcutaneous
S.E.M.:	Standard error of the mean
QD:	Once a day dosing
TAA:	Tumor Associated Antigen
TNF:	Tumor necrosis factor
WBC:	White blood cells

[00107] The following describes the peptides, nucleic acid molecules, compositions, and methods of the invention in more detail.

Methods of Identifying Candidate Peptide Epitopes

[00108] The present invention is directed to methods for selecting a variant of a peptide epitope which induces a CTL response against another variant(s) of the peptide epitope, by determining whether the variant comprises only conserved residues, as defined herein, at non-anchor positions in comparison to the other variant(s).

[00109] In some embodiments, antigen sequences from a population of an infectious agent, said antigens comprising variants of a peptide epitope, are optionally aligned (manually or by computer) along their length, preferably their full length. Variant(s) of a peptide epitope (preferably naturally occurring variants), each 8-11 amino acids in length and comprising the same MHC class I supermotif or motif, are identified manually or with the aid of a computer. In some embodiments, a variant is optionally chosen which comprises preferred anchor residues of said motif and/or which occurs with high frequency within the population of variants. In other embodiments, a variant is randomly chosen. The

randomly or otherwise chosen variant is compared to from one to all the remaining variant(s) to determine whether it comprises only conserved residues in the non-anchor positions relative to from one to all the remaining variant(s).

[00110] The present invention is also directed to variants identified by the methods above; peptides comprising such variants; nucleic acids encoding such variants and peptides; cells comprising such variants, and/or peptides, and/or nucleic acids; compositions comprising such variants, and/or peptides, and/or nucleic acids, and/or cells; as well as therapeutic and diagnostic methods for using such variants, peptides, nucleic acids, cells, and compositions.

[00111] In some embodiments, the invention is directed to a method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

- a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif; and
- b) determining whether one of said variants comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.

[00112] In some embodiments, (b) comprises identifying a variant which comprises only conserved non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

[00113] In some embodiments, the invention is directed to a method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

- a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif;
- b) determining whether each of said variants comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and
- c) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.

[00114] In some embodiments, (c) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

[00115] In some embodiments, the invention is directed to a method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

- a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;
- b) choosing a variant selected from the group consisting of:
 - i) a variant which comprises preferred primary anchor residues of said motif; and
 - ii) a variant which occurs with high frequency within the population of variants; and
- c) determining whether the variant of (b) comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.

[00116] In some embodiments, (c) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

[00117] In some embodiments, the invention is directed to method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

- a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;
- b) choosing a variant selected from the group consisting of:
 - i) a variant which comprises preferred primary anchor residues of said motif; and

- ii) a variant which occurs with high frequency within the population of variants; and
- c) determining whether the variant of (b) comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and
- d) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.

[00118] In some embodiments, (d) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

[00119] In some embodiments, (a) comprises aligning the sequences of said antigens.

[00120] In some embodiments, (b) comprises choosing a variant which comprises preferred primary anchor residues of said motif.

[00121] In some embodiments, (b) comprises choosing a variant which occurs with high frequency within said population.

[00122] In some embodiments, (b) comprises ranking said variants by frequency of occurrence within said population.

[00123] In some embodiments, (b) comprises choosing a variant which comprises preferred primary anchor residues of said motif and which occurs with high frequency within said population.

[00124] In some embodiments, (b) comprises ranking said variants by frequency of occurrence within said population.

[00125] In some embodiments, the identified variant comprises the fewest conserved anchor residues in comparison to each of the remaining variants.

[00126] In some embodiments, the remaining variants comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 27, 28, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 240, 260, 280, or 300 variants.

[00127] In some embodiments, the infectious agent is selected from the group consisting of: HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, and Dengue virus, Epstein-Barr virus, *Mycobacterium tuberculosis*, *Chlamydia*, *Candida albicans*, *Cryptococcus*

neoformans, *Coccidioides spp.*, *Histoplasma spp.*, *Aspergillus fumigatis*, *Plasmodium spp.*, *Trypanosoma spp.*, *Schistosoma spp.*, and *Leishmania spp.*

- [00128] In some embodiments, the infectious agent is selected from the group consisting of: HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, and Dengue virus.
- [00129] In some embodiments, the infectious agent is HIV and the antigen is selected from the group consisting of: Gag, Env, Pol, Nef, Rev, Tat, Vif, Vpr, and Vpu.
- [00130] In some embodiments, the infectious agent is HBV and the antigen is selected from the group consisting of: Pol, Env, Core, and NS1/Env2.
- [00131] In some embodiments, the infectious agent is HCV and the antigen is selected from the group consisting of: Core, E1, E2, NS1, NS2, NS3, NS4, and NS5.
- [00132] In some embodiments, the infectious agent is HPV and the antigen is selected from the group consisting of: E1, E2, E3, E4, E5, E6, E7, L1, and L2.
- [00133] In some embodiments, the infectious agent is *Plasmodium falciparum* and the antigen is selected from the group consisting of: CSP, SSP2, EXP1, LSA1.
- [00134] In some embodiments, the selected variant and the at least one remaining variant comprise different primary anchor residues of the same motif or supermotif.
- [00135] In some embodiments, the motif or supermotif is selected from the group consisting of those in Tables 1-2.
- [00136] In some embodiments, the conserved non-anchor residues are at any of positions 3-7 of said variant.
- [00137] In some embodiments, the variant comprises only 1-3 conserved non-anchor residues compared to at least one remaining variant.
- [00138] In some embodiments, the variant comprises only 1-2 conserved non-anchor residues compared to at least one remaining variant.
- [00139] In some embodiments, the variant comprises only 1 conserved non-anchor residue compared to at least one remaining variant.
- [00140] In some embodiments, the infectious agent is HPV, and further wherein, the HPV infectious agent is selected from the group consisting of HPV strains 16, 18, 31, 33, 45, 52, 56, and 58.
- [00141] In some embodiments, the variants are a population of naturally occurring variants.
- [00142] **Optional Alignment.** Optionally, antigen sequences, either full-length or partial, may be aligned manually or by computer. Convenient computer programs for aligning multiple sequences include Omega, Oxford software, version 1.1.3, using ClustalW

alignment, using an open gap penalty of 10.0, extend gap penalty of 0.05, and delay divergent sequences of 40.0 (See, e.g., Table 21); and BLASTP 2.2.5 (Nov-16-2002) (Altschul, S.F., et al., Nucleic Acids Res. 25:3389-3402 (1997)) using a cutoff = 3e-88 (to select human sequences) (see, e.g., Table 20). Alternatively, alignments may be obtained through publicly available sources such as published journal articles and published patent documents or as disclosed herein (see, e.g., Tables 10-22).

[00143] **HLA Class I Motifs Indicative of CTL Inducing Peptide Epitopes.** A large fraction of HLA class I and class II molecules can be classified into a relatively few supertypes, each respective supertype characterized by largely overlapping peptide binding repertoires, and consensus structures of the main peptide binding pockets. Thus, peptides of the present invention are preferably identified by the primary residues of any one of several HLA-specific amino acid motifs, or if the presence of the motif corresponds to the ability to bind several allele-specific HLA antigens, a supermotif (*see, e.g.*, Tables 1-2). The preferred primary residues are indicated in bold, while the tolerated primary residues are indicated by italics.

[00144] The primary anchor residues of the HLA class I peptide epitope supermotifs and motifs are summarized in Tables 1-2. Preferred primary anchors are shown in bold, while tolerated primary anchors are shown in italics. Primary and secondary anchor positions for HLA Class I are summarized in Table 3. Allele-specific HLA molecules that fall within the various HLA class I supertypes are listed in Table 4. In some cases, patterns of amino acid residues are present in both a motif and a supermotif. The relationship of a particular motif and any related supermotif is indicated in the description of the individual motifs.

[00145] Thus, the peptide motifs and supermotifs described below, and summarized in Tables 1-2, provide guidance for the identification and use of peptide epitopes comprising primary anchor residues of motifs or supermotifs in accordance with the invention.

[00146] Allele-specific HLA molecules that comprise HLA class I supertype families are listed in Table 4.

[00147] **HLA-A1 supermotif.** The HLA-A1 supermotif is characterized by the presence in peptide ligands of a small (T or S) or hydrophobic (L, I, V, or M) primary anchor residue in position 2, and an aromatic (Y, F, or W) primary anchor residue at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind to the A1 supermotif (*i.e.*, the HLA-A1 supertype) is comprised of at least A*0101, A*2601,

A*2602, A*2501, and A*3201 (*see, e.g., DiBrino, M. et al., J. Immunol.* 151:5930, 1993; DiBrino, M. et al., *J. Immunol.* 152:620, 1994; Kondo, A. et al., *Immunogenetics* 45:249, 1997). Other allele-specific HLA molecules predicted to be members of the A1 superfamily are shown in Table 4. Peptides binding to each of the individual HLA proteins can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00148] HLA-A2 supermotif. Primary anchor specificities for allele-specific HLA-A2.1 molecules (*see, e.g., Falk et al., Nature* 351:290-296, 1991; Hunt et al., *Science* 255:1261-1263, 1992; Parker et al., *J. Immunol.* 149:3580-3587, 1992; Ruppert et al., *Cell* 74:929-937, 1993) and cross-reactive binding among HLA-A2 and -A28 molecules have been described. (*See, e.g., Fruci et al., Human Immunol.* 38:187-192, 1993; Tanigaki et al., *Human Immunol.* 39:155-162, 1994; Del Guercio et al., *J. Immunol.* 154:685-693, 1995; Kast et al., *J. Immunol.* 152:3904-3912, 1994 for reviews of relevant data.) These primary anchor residues define the HLA-A2 supermotif; which presence in peptide ligands corresponds to the ability to bind several different HLA-A2 and -A28 molecules. The HLA-A2 supermotif comprises peptide ligands with L, I, V, M, A, T, or Q as a primary anchor residue at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope.

[00149] The corresponding family of HLA molecules (*i.e., the HLA-A2 supertype that binds these peptides*) is comprised of at least: A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, and A*6901. Other allele-specific HLA molecules predicted to be members of the A2 superfamily are shown in Table 4. As explained in detail below, binding to each of the individual allele-specific HLA molecules can be modulated by substitutions at the primary anchor and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00150] The motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

[00151] HLA-A3 supermotif. The HLA-A3 supermotif is characterized by the presence in peptide ligands of A, L, I, V, M, S, or, T as a primary anchor at position 2, and a positively charged residue, R or K, at the C-terminal position of the epitope, *e.g., in position 9 of 9-mers* (*see, e.g., Sidney et al., Hum. Immunol.* 45:79, 1996). Exemplary members of the corresponding family of HLA molecules (the HLA-A3 supertype) that bind the A3 supermotif include at least A*0301, A*1101, A*3101, A*3301, and A*6801. Other allele-

specific HLA molecules predicted to be members of the A3 supertype are shown in Table 4. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions of amino acids at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

[00152] HLA-A24 supermotif. The HLA-A24 supermotif is characterized by the presence in peptide ligands of an aromatic (F, W, or Y) or hydrophobic aliphatic (L, I, V, M, or T) residue as a primary anchor in position 2, and Y, F, W, L, I, or M as primary anchor at the C-terminal position of the epitope (*see, e.g.,* Sette and Sidney, *Immunogenetics*, in press, 1999). The corresponding family of HLA molecules that bind to the A24 supermotif (*i.e.,* the A24 supertype) includes at least A*2402, A*3001, and A*2301. Other allele-specific HLA molecules predicted to be members of the A24 supertype are shown in Table 4. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00153] HLA-B7 supermotif. The HLA-B7 supermotif is characterized by peptides bearing proline in position 2 as a primary anchor, and a hydrophobic or aliphatic amino acid (L, I, V, M, A, F, W, or Y) as the primary anchor at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind the B7 supermotif (*i.e.,* the HLA-B7 supertype) is comprised of at least twenty six HLA-B proteins including: B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, and B*7801 (*see, e.g.,* Sidney, *et al., J. Immunol.* 154:247, 1995; Barber, *et al., Curr. Biol.* 5:179, 1995; Hill, *et al., Nature* 360:434, 1992; Rammensee, *et al., Immunogenetics* 41:178, 1995 for reviews of relevant data). Other allele-specific HLA molecules predicted to be members of the B7 supertype are shown in Table 4. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

[00154] HLA-B27 supermotif. The HLA-B27 supermotif is characterized by the presence in peptide ligands of a positively charged (R, H, or K) residue as a primary anchor at position 2, and a hydrophobic (F, Y, L, W, M, I, A, or V) residue as a primary anchor at the C-terminal position of the epitope (*see, e.g.,* Sidney and Sette, *Immunogenetics*, in

press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B27 supermotif (*i.e.*, the B27 supertype) include at least B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, and B*7301. Other allele-specific HLA molecules predicted to be members of the B27 supertype are shown in Table 4. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00155] **HLA-B44 supermotif.** The HLA-B44 supermotif is characterized by the presence in peptide ligands of negatively charged (D or E) residues as a primary anchor in position 2, and hydrophobic residues (F, W, Y, L, I, M, V, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney et al., *Immunol. Today* 17:261, 1996). Exemplary members of the corresponding family of HLA molecules that bind to the B44 supermotif (*i.e.*, the B44 supertype) include at least: B*1801, B*1802, B*3701, B*4001, B*4002, B*4006, B*4402, B*4403, and B*4006. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions; preferably choosing respective residues specified for the supermotif.

[00156] **HLA-B58 supermotif.** The HLA-B58 supermotif is characterized by the presence in peptide ligands of a small aliphatic residue (A, S, or T) as a primary anchor residue at position 2, and an aromatic or hydrophobic residue (F, W, Y, L, I, V, M, or A) as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999 for reviews of relevant data). Exemplary members of the corresponding family of HLA molecules that bind to the B58 supermotif (*i.e.*, the B58 supertype) include at least: B*1516, B*1517, B*5701, B*5702, and B*5801. Other allele-specific HLA molecules predicted to be members of the B58 supertype are shown in Table 4. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00157] **HLA-B62 supermotif.** The HLA-B62 supermotif is characterized by the presence in peptide ligands of the polar aliphatic residue Q or a hydrophobic aliphatic residue (L, V, M, I, or P) as a primary anchor in position 2, and a hydrophobic residue (F, W, Y, M, I, V, L, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B62 supermotif (*i.e.*, the B62 supertype) include at least: B*1501, B*1502, B*1513, and B5201. Other allele-specific HLA molecules

predicted to be members of the B62 supertype are shown in Table 4. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00158] HLA-A1 motif. The HLA-A1 motif is characterized by the presence in peptide ligands of T, S, or M as a primary anchor residue at position 2 and the presence of Y as a primary anchor residue at the C-terminal position of the epitope. An alternative allele-specific A1 motif is characterized by a primary anchor residue at position 3 rather than position 2. This motif is characterized by the presence of D, E, A, or S as a primary anchor residue in position 3, and a Y as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.,* DiBrino *et al.*, *J. Immunol.*, 152:620, 1994; Kondo *et al.*, *Immunogenetics* 45:249, 1997; and Kubo *et al.*, *J. Immunol.* 152:3913, 1994 for reviews of relevant data). Peptide binding to HLA A1 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

[00159] Those epitopes comprising T, S, or M at position 2 and Y at the C-terminal position are also HLA-A1 supermotif-bearing peptide epitopes, as these residues are a subset of the A1 supermotif primary anchors.

[00160] HLA-A*0201 motif. An HLA-A2*0201 motif was determined to be characterized by the presence in peptide ligands of L or M as a primary anchor residue in position 2, and L or V as a primary anchor residue at the C-terminal position of a 9-residue peptide (*see, e.g.,* Falk *et al.*, *Nature* 351:290-296, 1991) and was further found to comprise an I at position 2 and I or A at the C-terminal position of a nine amino acid peptide (*see, e.g.,* Hunt *et al.*, *Science* 255:1261-1263, March 6, 1992; Parker *et al.*, *J. Immunol.* 149:3580-3587, 1992). The A*0201 allele-specific motif has also been defined by the present inventors to additionally comprise V, A, T, or Q as a primary anchor residue at position 2, and M or T as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.,* Kast *et al.*, *J. Immunol.* 152:3904-3912, 1994). Thus, the HLA-A*0201 motif comprises peptide ligands with L, I, V, M, A, T, or Q as primary anchor residues at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope. The preferred and tolerated residues that characterize the primary anchor positions of the HLA-A*0201 motif are identical to the residues describing the A2 supermotif. (For reviews of relevant data, *see, e.g.,* Del Guercio *et al.*, *J. Immunol.* 154:685-693, 1995; Ruppert *et al.*, *Cell* 74:929-937, 1993; Sidney *et al.*, *Immunol. Today* 17:261-266, 1996; Sette and

Sidney, *Curr. Opin. in Immunol.* 10:478-482, 1998). Secondary anchor residues that characterize the A*0201 motif have additionally been defined (*see, e.g., Ruppert et al., Cell* 74:929-937, 1993). These are shown in Table 3. Peptide binding to HLA-A*0201 molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

[00161] **HLA-A3 motif.** The HLA-A3 motif is characterized by the presence in peptide ligands of L, M, V, I, S, A, T, F, C, G, or D as a primary anchor residue at position 2, and the presence of K, Y, R, H, F, or A as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., DiBrino et al., Proc. Natl. Acad. Sci USA* 90:1508, 1993; and Kubo *et al., J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

[00162] The A3 supermotif primary anchor residues comprise a subset of the A3- and A11-allele specific motif primary anchor residues.

[00163] **HLA-A11 motif.** The HLA-A11 motif is characterized by the presence in peptide ligands of V, T, M, L, I, S, A, G, N, C, D, or F as a primary anchor residue in position 2, and K, R, Y, or H as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., Zhang et al., Proc. Natl. Acad. Sci USA* 90:2217-2221, 1993; and Kubo *et al., J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A11 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

[00164] There is extensive overlap between the A3 and A11 motif primary anchor specificities.

[00165] **HLA-A24 motif.** The HLA-A24 motif is characterized by the presence in peptide ligands of Y, F, W, or M as a primary anchor residue in position 2, and F, L, I, or W as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., Kondo et al., J. Immunol.* 155:4307-4312, 1995; and Kubo *et al., J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A24 molecules can be modulated by substitutions at primary and/or secondary anchor positions; preferably choosing respective residues specified for the motif.

[00166] The primary anchor residues characterizing the A24 allele-specific motif comprise a subset of the A24 supermotif primary anchor residues.

[00167] Computer or Manual Screening. Peptides bearing HLA Class I or Class II supermotifs or motifs may be identified by computer searches or manually, e.g., as follows. In utilizing computer screening to identify peptide epitopes, a protein sequence or translated sequence may be analyzed using software developed to search for motifs, for example the "FINDPATTERNS" program (Devereux, *et al. Nucl. Acids Res.* 12:387-395, 1984) or MotifSearch 1.4 software program (D. Brown, San Diego, CA) to identify potential peptide sequences containing appropriate HLA binding motifs. The identified peptides can be scored using customized polynomial algorithms to predict their capacity to bind specific HLA class I or class II alleles. As appreciated by one of ordinary skill in the art, a large array of computer programming software and hardware options are available in the relevant art which can be employed to implement the motifs in order to evaluate (*e.g.*, without limitation, to identify epitopes, identify epitope concentration per peptide length, or to generate analogs) known or unknown peptide sequences.

[00168] Translated antigen protein sequences may be analyzed using a text string search software program, *e.g.*, MotifSearch 1.4 (D. Brown, San Diego) to identify potential peptide sequences containing appropriate HLA binding motifs; alternative programs are readily produced in accordance with information in the art in view of the motif/supermotif disclosure herein. Furthermore, such calculations can be made mentally.

[00169] Identified supermotif or motif sequences may be scored using polynomial algorithms to predict their capacity to bind to specific HLA-Class I or Class II molecules. These polynomial algorithms take into account both extended and refined motifs (that is, to account for the impact of different amino acids at different positions), and are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA molecule interactions can be approximated as a linear polynomial function of the type:

$$"\Delta G" = a_{1i} \times a_{2i} \times a_{3i} \dots \times a_{ni}$$

where a_{ji} is a coefficient which represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. The crucial assumption of this method is that the effects at each position are essentially independent of each other (*i.e.*, independent binding of individual side-chains). When residue j occurs at position i in the peptide, it is assumed to contribute a constant amount j_i to the free energy of binding of the peptide irrespective of the sequence of the rest of the peptide. This assumption is justified by studies from our laboratories that demonstrated that peptides are

bound to MHC and recognized by T cells in essentially an extended conformation (data omitted herein).

[00170] The method of derivation of specific algorithm coefficients has been described in Gulukota *et al.*, *J. Mol. Biol.* 267:1258-126, 1997; (see also Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; and Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). Briefly, for all i positions, anchor and non-anchor alike, the geometric mean of the average relative binding (ARB) of all peptides carrying j is calculated relative to the remainder of the group, and used as the estimate of j_i . For Class II peptides, if multiple alignments are possible, only the highest scoring alignment is utilized, following an iterative procedure. To calculate an algorithm score of a given peptide in a test set, the ARB values corresponding to the sequence of the peptide are multiplied. If this product exceeds a chosen threshold, the peptide is predicted to bind. Appropriate thresholds are chosen as a function of the degree of stringency of prediction desired.

[00171] Additional methods to identify preferred peptide sequences, which also make use of specific motifs, include the use of neural networks and molecular modeling programs (see, e.g., Milik *et al.*, *Nature Biotechnology* 16:753, 1998; Altuvia *et al.*, *Hum. Immunol.* 58:1, 1997; Altuvia *et al.*, *J. Mol. Biol.* 249:244, 1995; Buus, S. *Curr. Opin. Immunol.* 11:209-213, 1999; Brusic, V. *et al.*, *Bioinformatics* 14:121-130, 1998; Parker *et al.*, *J. Immunol.* 152:163, 1993; Meister *et al.*, *Vaccine* 13:581, 1995; Hammer *et al.*, *J. Exp. Med.* 180:2353, 1994; Sturniolo *et al.*, *Nature Biotechnol.* 17:555 1999).

[00172] **Conserved, Semi-conserved, and Non-conserved Non-anchor Residues.** The determination of non-anchor residues as being conserved (conservative) or semi-conserved (semi-conservative) or non-conserved (non-conservative) in comparison to the non-anchor positions of from one to all of the remaining variant(s) is defined by as follows, the results of which are summarized in Table 5.

[00173] Table 5 shows the similarity assignments between any given amino acid pair so that a given amino acid substitution could be characterized as being a (conservative) or semi-conserved (semi-conservative) or non-conserved (non-conservative) residue.

[00174] The degree of similarity between amino acid pairs was quantified by averaging, for each amino acid pair, the rank coefficient scores for PAM250, hydrophobicity, and side chain volume as described below. Based on the average values of these composite rankings, Table 5 shows each pair to be conserved, semi-conserved or non-conserved.

- [00175] The Dayhoff PAM250 score (Dayhoff, M.O., *et al.*, *Atlas of Protein Sequence and Structure*, Vol. 5, suppl.3. (1978) M.O. Dayhoff, ed. National Biomedical Research Foundation, Washington DC, p. 345; Creighton, T.E., *Proteins: structures and molecular properties* (1993) (2nd edition) W.H. Freeman and Company, NY; is a commonly utilized protein alignment scoring matrix which measures the percentage of acceptable point mutations (PAM) within a defined time frame. The frequencies of these mutations are different from what would be expected from the probability of random mutations, and presumably reflect a bias due to the degree of physical and chemical similarity of the amino acid pair involved in the substitution. To obtain a score of amino acid similarity that could be standardized with other measures of similarity, the PAM250 scores were converted to a rank value, where 1 indicates the highest probability of being an accepted mutation.
- [00176] The most commonly utilized scales to represent the relative hydrophobicity of the 20 naturally occurring amino acids (Cornette, J., *et al.*, *J. Mol. Biol.* (1987) 195:659) are those developed on the basis of experimental data by Kyte and Doolittle (Kyte, J. and R.F. Doolittle, *J. Mol. Biol.* (1982) 157:105), and by Fauchere and Pliska (Fauchere, J. and V. Pliska, *Eur. J. Med. Chem.* (1983) 18:369). The Kyte/Doolittle scale measures the H₂O/organic solvent partition of individual amino acids. Because it considers the position of amino acids in folded proteins, it may most accurately reflect native hydrophobicity in the context of proteins. The Fauchere/Pliska scale measures the octanol/H₂O partitioning of N-acetyl amino acid amides, and most accurately reflects hydrophobicity in the context of denatured proteins and/or small synthetic peptides. To obtain scores for hydrophobicity, each amino acid residue was ranked on both the Kyte/Doolittle and Fauchere/Pliska hydrophobicity scales. An average rank between the two scales was calculated and the average difference in hydrophobicity for each pair was calculated.
- [00177] Finally, for calculating amino acid side-chain volume, the partial volume in solution obtained by noting the increase in volume of water after adding either one molecule or one gram of amino acid residue was considered (Zamyatnin, A.A., *Ann. Rev. Biophys. Bioeng.* (1984) 13:145; Zamyatnin, A.A., *Prog. Biophys. Mol. Biol.* (1972) 24:107). The absolute difference in the partial volume of each possible pairing of the 20 naturally occurring amino acids was calculated and ranked, where 1 indicated residues with the most similar volumes, and 20 the most dissimilar.
- [00178] Thus, by consulting Table 5, one can determine whether a residue in a variant is considered to be conserved, semi-conserved, or non-conserved in comparison to a residue

in another variant(s). The residue of the parent variant (randomly or otherwise chosen variant) is shown across the top of Table 5, and the residue of the variant(s) it is compared with is shown below the parent residue.

[00179] As shown in Table 5, each of the amino acids shown across the top of the table bears a numerically defined relationship to the remaining 19 genetically encoded amino acids. The lower the index, the higher the conservation; the same amino acid will have a similarity assignment of 1.0; maximally different amino acids will have similarity assignments approaching 20. Using the method set forth above, amino acids which are not gene-encoded can also be assigned similarity indices and can be classified with respect to any natively occurring amino acid as conserved (conservative) or semi-conserved (semi-conservative) or non-conserved (non-conservative).

Variant Peptide Epitopes

[00180] In some embodiments, the invention is directed to an isolated peptide comprising or consisting of a variant. In some embodiments, the invention is directed to an isolated polynucleotide encoding such a peptide.

[00181] The isolated variants of the invention are all class I binding peptides, i.e., CTL peptides. In particular, the variants of the invention comprise a motif or supermotif, as described above. Variants of the invention are those set forth in Tables 6-9 and Figures 1A-4 (SEQ ID Nos: 1,2, 9-13, 15,16,18-26, 56-60, 69, 71, 72, 74,77-89, 91-96,99-101, 103, 105, 108, 109, 112-117, 119, 120, 123-127, 129, 130, 132, 133, 136-142, 145-152, 154-158, 160-165, 167, 168, 172-175, 177-179, 181, 182, 184-186, 188, 189, 191-212, 222-237, 262-277). Variants of the invention may be referred to herein as “variants” and “variant peptide epitopes” or referred to by Table or referred to by SEQ ID NO. Other peptide epitopes are referred to herein as CTL epitopes or CTL peptides and HTL epitopes or HTL peptides.

[00182] **Peptides and Polynucleotides.** In some embodiments, the invention is directed to an isolated peptide comprising or consisting of a variant, wherein the variant consists of a sequence selected from those in Tables 6-9 and Figures 1A-4 (SEQ ID Nos: 1,2, 9-13, 15,16,18-26, 56-60, 69, 71, 72, 74,77-89, 91-96,99-101, 103, 105, 108, 109, 112-117, 119, 120, 123-127, 129, 130, 132, 133, 136-142, 145-152, 154-158, 160-165, 167, 168, 172-175, 177-179, 181, 182, 184-186, 188, 189, 191-212, 222-237, 262-277).

[00183] Peptides of the invention may be fusion proteins of variant(s) to CTL epitope(s), and/or HTL epitope(s), and/or linker(s), and/or spacer(s), and/or carrier(s), and/or additional amino acid(s), and/or may comprise or consist of homopolymers of a variant or heteropolymers of more than one variant, as is described in detail below.

- [00184]** Peptides which comprise a variant of the invention may comprise or consist of a fragment of an antigen (“fragment” or “antigenic fragment”), wherein the fragment comprises a variant. The fragment may be a portion of any antigen of an infectious agent, e.g., the sequences in Tables 11-22 (SEQ ID Nos: 302-1755, respectively). The variant of the invention may be within the fragment or may be linked, directly or indirectly, to the fragment.
- [00185]** The fragment may comprise or consist of a region of a native antigen that contains a high concentration of class I and/or class II epitopes, preferably it contains the greatest number of epitopes per amino acid length. Such epitopes can be present in a frame-shifted manner, *e.g.* a 10 amino acid long peptide could contain two 9 amino acid long epitopes and one 10 amino acid long epitope.
- [00186]** The fragment may be less than or equal to 600 amino acids, less than or equal to 500 amino acids, less than or equal to 400 amino acids, less than or equal to 250 amino acids, less than or equal to 100 amino acids, less than or equal to 85 amino acids, less than or equal to 75 amino acids, less than or equal to 65 amino acids, or less than or equal to 50 amino acids in length. In certain embodiments, a fragment is less than 101 amino acids in length, in any increment down to 5 amino acids in length. For example, the fragment may be 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length. Fragments of full length antigens may be fragments from about residue 1-20, 21-40, 41-60, 61-80, 81-100, 101-120, 121-140, 141-160, 161-180, 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-680, 681-700, 701-720, 721-740, 741-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981 to the C-terminus of the antigen.
- [00187]** Peptides which comprise a variant of the invention may be a fusion protein comprising one or more amino acid residues in addition to the variant or fragment. Fusion proteins include homopolymers and heteropolymers, as described below.
- [00188]** In some embodiments, the peptide comprises or consists of multiple variants, *e.g.*, 2, 3, 4, 5, 6, 7, 8, or 9 variants of the invention. In some embodiments, the peptide comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 variants of the invention.
- [00189]** The peptide may also be a homopolymer of one variant or the peptide may be a heteropolymer which contains at least two different variants. Polymers have the advantage of increased probability for immunological reaction and, where different variants are used to make up the polymer, the ability to induce antibodies and/or T cells that react with different antigenic determinants of the antigen(s) targeted for an immune response.

[00190] A homopolymer may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 copies of the same variant.

[00191] A heteropolymer may comprise one or more copies of an individual variant and one or more copies of one or more different variants of the invention. The variants that form a heteropolymer may all be from the same antigen, e.g., may be from any of those in Tables 11-22 (SEQ ID NOS: 302-1755) or other antigens herein or known in the art, or may be from different antigens, preferably from infectious agents. Combinations of variants that may form a heteropolymer include, for example, Gag 545 variants EPLTSLKSLF (SEQ ID NO: 1) and YPLASLKSLF (SEQ ID NO: 2), or combinations of peptides from different tables in Tables 6-9 (SEQ ID NOS: 1, 2, 9-13, 15, 16, 18-26, 56-60, 69, 71, 72, 74, 77-89, 91-96, 99-101, 103, 105, 108, 109, 112-117, 119, 120, 123-127, 129, 130, 132, 133, 136-142, 145-152, 154-158, 160-165, 167, 168, 172-175, 177-179, 181, 182, 184-186, 188, 189, 191-212, 222-237, 262-277) and/or Figures 1A-4 (Figure 1A, SEQ ID NOS: 1756-1775; Figure 1B, SEQ ID NOS: 1776-1796; Figure 1C, SEQ ID NOS: 1797-1820; Figure 1D, SEQ ID NOS: 1821-1851; Figure 1E, SEQ ID NOS: 1852-1861; and Figure 4, SEQ ID NOS: 1919-1933) or those combinations in Tables 23-28 (SEQ ID NOS: 1934 - 1946). Heteropolymers may contain multiple copies of one or more variants.

[00192] Thus, peptides of the invention such as heteropolymers may comprise a first variant and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 other (different) variants.

[00193] In some embodiments, the peptide comprising a variant may also comprise a number of CTL and/or HTL epitopes, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 CTL and/or HTL epitopes.

[00194] The CTL and/or HTL epitope and the variant of the invention may be from the same antigen of an infectious agent or from different antigens. Thus, for example, if the variant is from HIV pol, the CTL peptide and/or HTL peptide may also be from HIV pol. Alternatively, if the variant is from HIV pol, the CTL peptide and/or HTL peptide may be from another antigen such as HIV env or HIV vpr. As another example, if the variant is from HBV E6, the CTL peptide and/or HTL peptide may be from HBV E7. The CTL and/or HTL epitope and the variant of the invention may be from the same infectious agent or different infectious agents. Thus, for example, the variant may be from HIV, and the CTL and/or HTL epitope may be from HIV or may be from another infectious agent such as HBV, HCV, HPV, or *Plasmodium falciparum*.

- [00195] The CTL peptide and/or HTL peptide may be from other antigens including hepatitis B core and surface antigens (HBVc, HBVs), hepatitis C antigens, Epstein-Barr virus antigens, human immunodeficiency virus (HIV) antigens and human papilloma virus (HPV) antigens (in particular antigens from HPV-16, HPV-18, HPV-31, HPV-33, HPV-45, HPV-52, HPV-56 and HPV-58, *Mycobacterium tuberculosis* and *Chlamydia*. Examples of suitable fungal antigens include those derived from *Candida albicans*, *Cryptococcus neoformans*, *Coccidioides spp.*, *Histoplasma spp.*, and *Aspergillus fumigatis*. Examples of suitable protozoan parasitic antigens include those derived from *Plasmodium spp.*, including *P. falciparum*, *Trypanosoma spp.*, *Schistosoma spp.*, *Leishmania spp* and the like.
- [00196] Alternatively, the CTL peptide and/or HTL peptide may be from tumor-associated antigens such as but not limited to, melanoma antigens MAGE-1, MAGE-2, MAGE-3, MAGE-11, MAGE-A10, as well as BAGE, GAGE, RAGE, MAGE-C1, LAGE-1, CAG-3, DAM, MUC1, MUC2, MUC18, NY-ESO-1, MUM-1, CDK4, BRCA2, NY-LU-1, NY-LU-7, NY-LU-12, CASP8, RAS, KIAA-2-5, SCCs, p53, p73, CEA, HER2/neu, Melan-A, gp100, tyrosinase, TRP2, gp75/TRP1, kallikrein, prostate-specific membrane antigen (PSM), prostatic acid phosphatase (PAP), prostate-specific antigen (PSA), PT1-1, β -catenin, PRAME, Telomerase, FAK, cyclin D1 protein, NOEY2, EGF-R, SART-1, CAPB, HPVE7, p15, Folate receptor CDC27, PAGE-1, and PAGE-4.
- [00197] Examples of CTL peptides and HTL peptides are disclosed in WO 01/42270, published 14 June 2001; WO 01/41788, published 14 June 2001; WO 01/42270, published 14 June 2001; WO 01/45728, published 28 June 2001; and WO 01/41787, published 14 June 2001.
- [00198] The HTL peptide may comprise a "loosely HLA-restricted" or "promiscuous" sequence. Examples of amino acid sequences that are promiscuous include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; SEQ ID NO: 3), *Plasmodium falciparum* CS protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; SEQ ID NO: 5), and Streptococcus 18kD protein at positions 116-131 (GAVDSILGGVATYGAA; SEQ ID NO: 5). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.
- [00199] The HTL peptide may comprise a synthetic peptide such as a Pan-DR-binding epitope (e.g., a PADRE[®] peptide, Epimmune Inc., San Diego, CA, described, for example, in U.S. Patent Number 5,736,142), for example, having the formula aKXVAAZTLKAAa, where "X" is either cyclohexylalanine, phenylalanine, or tyrosine; "Z" is either tryptophan, tyrosine, histidine or asparagine; and "a" is either D-alanine or L-alanine (SEQ ID NO: 746). Certain pan-DR binding epitopes comprise all "L" natural amino acids;

these molecules can be provided as peptides or in the form of nucleic acids that encode the peptide. See also, U.S. Patent Nos. 5,679,640 and 6,413,935.

[00200] The peptide comprising a variant may comprise additional amino acid(s). Such additional amino acids may be Ala, Arg, Asn, Asp, Cys, Gln, Gly, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr, Trp, Val, amino acid mimetics, and other unnatural amino acids such as those described below. Additional amino acids may provide for ease of linking peptides one to another, for linking variants to one another, for linking variants to CTL and/or HTL epitopes, for coupling to a carrier support or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as Ala, Arg, Asn, Asp, Cys, Gln, Gly, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr, Trp, or Val, or the like, can be introduced at the C- and/or N-terminus of the peptide and/or can be introduced internally.

[00201] The peptide comprising a variant may comprise an amino acid spacer(s), which may be joined to the variants, CTL epitopes, HTL epitopes, carriers, etc. within a peptide or may be joined to the peptide at the N-and/or C-terminus. Thus, spacers may be at the N-terminus or C-terminus of peptide, or may be internal such that they link or join variants, CTL epitopes, HTL epitopes, carriers, additional amino acids, and/or antigenic fragments one to the other.

[00202] The spacer is typically comprised of one or more relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, *e.g.*, Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer may be composed of the same residues or may be composed of one or more different residues and thus may be a homo- or hetero-oligomer of spacer residues. Thus, the spacer may contain more than one Ala residue (poly-alanine) or more than one Gly residue (poly-glycine), or may contain both Ala and Gly residues, *e.g.*, Gly, Gly-Gly-, Ser, Ser-Ser-, Gly-Ser-, Ser-Gly-, etc. When present, the spacer will usually be at least one or two residues, more usually three to six residues and sometimes 10 or more residues, *e.g.*, 3, 4, 5, 6, 7, 8, 9, or 10, or even more residues. (Livingston, B.D. *et al. Vaccine* 19:4652-4660 (2000)).

[00203] Peptides comprising a variant may comprise carrier(s) such as those well known in the art, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid,

polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza virus proteins, hepatitis B virus core protein, and the like. (See Table 29).

[00204] In addition, the peptide comprising or consisting of a variant may be modified by terminal-NH₂ acylation, *e.g.*, by alkanoyl (C₁-C₂₀) or thioglycolyl acetylation, terminal-carboxyl amidation, *e.g.*, ammonia, methylamine, *etc.* In some instances these modifications may provide sites for linking to a support or other molecule.

[00205] The peptides in accordance with the invention can contain modifications such as but not limited to glycosylation, side chain oxidation, biotinylation, phosphorylation, addition of a surface active material, *e.g.* a lipid, or can be chemically modified, *e.g.*, acetylation, *etc.* Moreover, bonds in the peptide can be other than peptide bonds, *e.g.*, covalent bonds, ester or ether bonds, disulfide bonds, hydrogen bonds, ionic bonds, *etc.*

[00206] Peptides of the present invention may contain substitutions to modify a physical property (*e.g.*, stability or solubility) of the resulting peptide. For example, peptides may be modified by the substitution of a cysteine (C) with α -amino butyric acid ("B"). Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Substituting α -amino butyric acid for C not only alleviates this problem, but actually improves binding and crossbinding capability in certain instances. Substitution of cysteine with α -amino butyric acid may occur at any residue of a peptide, *e.g.*, at either anchor or non-anchor positions of a variant within a peptide, or at other positions of a peptide.

[00207] The peptides comprising a variant can comprise amino acid mimetics or unnatural amino acids, *e.g.* D- or L-naphylalanine; D- or L-phenylglycine; D- or L-2-thieneylalanine; D- or L-1, -2, 3, or 4-pyreneylalanine; D- or L-3 thieneylalanine; D- or L-(2-pyridinyl)-alanine; D- or L-(3-pyridinyl)-alanine; D- or L-(2-pyrazinyl)-alanine; D- or L-(4-isopropyl)-phenylglycine; D-(trifluoromethyl)-phenylglycine; D-(trifluoromethyl)-phenylalanine; D-p-fluorophenylalanine; D- or L-p-biphenylphenylalanine; D- or L-p-methoxybiphenylphenylalanine; D- or L-2-indole(alkyl)alanines; and, D- or L-alkylalanines, where the alkyl group can be a substituted or unsubstituted methyl, ethyl, propyl, hexyl, butyl, pentyl, isopropyl, iso-butyl, sec-isotyl, iso-pentyl, or a non-acidic amino acids. Aromatic rings of a non-natural amino acid include, *e.g.*, thiazolyl, thiophenyl, pyrazolyl, benzimidazolyl, naphthyl, furanyl, pyrrolyl, and pyridyl aromatic rings. Modified peptides that have various amino acid mimetics or unnatural amino acids

are particularly useful, as they tend to manifest increased stability *in vivo*. Such peptides may also possess improved shelf-life or manufacturing properties.

[00208] Peptide stability can be assayed in a number of ways. For instance, peptidases and various biological media, such as human plasma and serum, have been used to test stability. *See, e.g., Verhoef, et al., Eur. J. Drug Metab. Pharmacokinetics* 11:291 (1986). Half-life of the peptides of the present invention is conveniently determined using a 25% human serum (v/v) assay. The protocol is generally as follows: Pooled human serum (Type AB, non-heat inactivated) is delipidated by centrifugation before use. The serum is then diluted to 25% with RPMI-1640 or another suitable tissue culture medium. At predetermined time intervals, a small amount of reaction solution is removed and added to either 6% aqueous trichloroacetic acid (TCA) or ethanol. The cloudy reaction sample is cooled (4°C) for 15 minutes and then spun to pellet the precipitated serum proteins. The presence of the peptides is then determined by reversed-phase HPLC using stability-specific chromatography conditions.

[00209] As indicated above, the peptides in accordance with the invention can be a variety of lengths, and either in their neutral (uncharged) forms or in forms which are salts. The peptides in accordance with the invention can contain modifications such as glycosylation, side chain oxidation, or phosphorylation, generally subject to the condition that modifications do not destroy the biological activity of the peptides.

[00210] The peptides of the invention may be lyophilized, or may be in crystal form.

[00211] It is generally preferable that the variant peptide epitope be as small as possible while still maintaining substantially all of the immunologic activity of the native protein. When possible, it may be desirable to optimize HLA class I binding epitopes of the invention to a length of about 8 to about 13 amino acid residues, for example, 8, 9, 10, 11, 12 or 13, preferably 8 to 11 or 9 to 10. It is to be appreciated that one or more epitopes in this size range can be comprised by a longer peptide (see the Definition Section for the term "epitope" for further discussion of peptide length). HLA class II binding epitopes are preferably optimized to a length of about 6 to about 30 amino acids in length, *e.g.*, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30, preferably to between about 13 and about 20 residues, *e.g.*, 13, 14, 15, 16, 17, 18, 19 or 20. Preferably, the epitopes are commensurate in size with endogenously processed pathogen-derived peptides or tumor cell peptides that are bound to the relevant HLA molecules. The identification and preparation of peptides of various lengths can be carried out using the techniques described herein.

[00212] Peptides in accordance with the invention can be prepared synthetically, by recombinant DNA technology or chemical synthesis, or can be isolated from natural sources such as native tumors or pathogenic organisms. Epitopes may be synthesized individually or joined directly or indirectly in a peptide. Although the peptide will preferably be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides may be synthetically conjugated to be joined to native fragments or particles.

[00213] The peptides of the invention can be prepared in a wide variety of ways. For relatively short sizes, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. (See, for example, Stewart & Young, SOLID PHASE PEPTIDE SYNTHESIS, 2D. ED., Pierce Chemical Co., 1984). Further, individual peptides can be joined using chemical ligation to produce larger peptides that are still within the bounds of the invention.

[00214] Alternatively, recombinant DNA technology can be employed wherein a nucleotide sequence which encodes a peptide inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art, as described generally in Sambrook *et al.*, MOLECULAR CLONING, A LABORATORY MANUAL, Cold Spring Harbor Press, Cold Spring Harbor, New York (1989). Thus, recombinant peptides, which comprise or consist of one or more epitopes of the invention, can be used to present the appropriate T cell epitope.

[00215] Polynucleotides encoding each of the peptides above are also part of the invention. As appreciated by one of ordinary skill in the art, various nucleic acids will encode the same peptide due to the redundancy of the genetic code. Each of these nucleic acids falls within the scope of the present invention. This embodiment of the invention comprises DNA and RNA, and in certain embodiments a combination of DNA and RNA. It is to be appreciated that any polynucleotide that encodes a peptide in accordance with the invention falls within the scope of this invention.

[00216] The polynucleotides encoding peptides contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci, *et al.*, *J. Am. Chem. Soc.* 103:3185 (1981). Polynucleotides encoding peptides comprising or consisting of a variant can be made simply by substituting the appropriate and desired nucleic acid base(s) for those that encode a related (e.g., analogous) epitope.

[00217] The polynucleotide, e.g. minigene (see below), may be produced by assembling oligonucleotides that encode the plus and minus strands of the polynucleotide, e.g. minigene. Overlapping oligonucleotides (15-100 bases long) may be synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides can be joined, for example, using T4 DNA ligase. A polynucleotide, e.g. minigene, encoding the peptide of the invention, can be cloned into a desired vector such as an expression vector. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired peptide such as a fusion protein.

[00218] A large number of such vectors and suitable host systems are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pQE70, pQE60, pQE-9 (Qiagen), pBS, pD10, phagescript, psiX174, pBluescript SK, pbsks, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia); pCR (Invitrogen). Eukaryotic: pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia); p75.6 (valentis); pCEP (Invitrogen); pCEI (Epimmune). However, any other plasmid or vector can be used as long as it is replicable and viable in the host.

[00219] As representative examples of appropriate hosts, there can be mentioned: bacterial cells, such as *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*; fungal cells, such as yeast; insect cells such as *Drosophila* and Sf9; animal cells such as COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines or Bowes melanoma; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

[00220] Thus, the present invention is also directed to vectors, preferably expression vectors useful for the production of the peptides of the present invention, and to host cells comprising such vectors.

[00221] Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which can be, for example, a cloning vector or an expression vector. The vector can be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient

media modified as appropriate for activating promoters, selecting transformants or amplifying the polynucleotides. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

[00222] For expression of the peptides, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired cellular host. For example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts.

[00223] Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), ∇ -factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product.

[00224] Yeast, insect or mammalian cell hosts may also be used, employing suitable vectors and control sequences. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. Such promoters may also be derived from viral sources, such as, *e.g.*, human cytomegalovirus (CMV-IE promoter) or herpes simplex virus type-1 (HSV TK promoter). Nucleic acid sequences

derived from the SV40 splice, and polyadenylation sites can be used to provide the required nontranscribed genetic elements.

[00225] Polynucleotides encoding peptides of the invention may also comprise a ubiquitination signal sequence, and/or a targeting sequence such as an endoplasmic reticulum (ER) signal sequence to facilitate movement of the resulting peptide into the endoplasmic reticulum.

[00226] Polynucleotides of the invention, e.g., minigenes, may be expressed in human cells. A human codon usage table can be used to guide the codon choice for each amino acid. Such polynucleotides preferably comprise spacer amino acid residues between variants, such as those described above, or may comprise naturally-occurring flanking sequences adjacent to the variants (and/or CTL and HTL epitopes).

[00227] The peptides of the invention can also be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. As an example of this approach, vaccinia virus is used as a vector to express nucleotide sequences that encode the peptides of the invention. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the polypeptides of the invention, e.g. adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein. A preferred vector is Modified Vaccinia Ankara (MVA) (e.g., Bavarian Noridic (MVA-BN)).

[00228] Standard regulatory sequences well known to those of skill in the art are preferably included in the vector to ensure expression in the human target cells. Several vector elements are desirable: a promoter with a downstream cloning site for polynucleotide, e.g., minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (e.g. ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, e.g., the human cytomegalovirus (hCMV) promoter. See, e.g., U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences. A preferred promoter is the CMV-IE promoter.

[00229] Polynucleotides, e.g. minigenes, may comprise one or more synthetic or naturally-occurring introns in the transcribed region. The inclusion of mRNA stabilization

sequences and sequences for replication in mammalian cells may also be considered for increasing polynucleotide, e.g. minigene, expression.

[00230] In addition, the polynucleotide, e.g. minigene, may comprise immunostimulatory sequences (ISSs or CpGs). These sequences may be included in the vector, outside the polynucleotide (e.g. minigene) coding sequence to enhance immunogenicity.

[00231] In some embodiments, a bi-cistronic expression vector which allows production of both the polynucleotide- (e.g. minigene-) encoded peptides of the invention and a second protein (e.g., one that modulates immunogenicity) can be used. Examples of proteins or polypeptides that, if co-expressed with peptides of the invention, can enhance an immune response include cytokines (e.g., IL-2, IL-12, GM-CSF), cytokine-inducing molecules (e.g., LeIF), costimulatory molecules, or pan-DR binding proteins (PADRE[®] molecules, Epimmune, San Diego, CA). Helper T cell (HTL) epitopes such as PADRE[®] molecules can be joined to intracellular targeting signals and expressed separately from expressed peptides of the invention. Specifically decreasing the immune response by co-expression of immunosuppressive molecules (e.g. TGF- β) may be beneficial in certain diseases.

[00232] Once an expression vector is selected, the polynucleotide, e.g. minigene, is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate bacterial strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the polynucleotide, e.g. minigene, as well as all other elements included in the vector, are confirmed using restriction mapping, DNA sequence analysis, and/or PCR analysis. Bacterial cells harboring the correct plasmid can be stored as cell banks.

[00233] Therapeutic/prophylactic quantities of DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and are grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA is purified using standard bioseparation technologies such as solid phase anion-exchange resins available, e.g., from QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

[00234] Purified polynucleotides, e.g. minigenes, can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized polynucleotide, e.g. DNA, in sterile phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical

trials. To maximize the immunotherapeutic effects of polynucleotide vaccines, alternative methods of formulating purified plasmid DNA may be used. A variety of such methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, *e.g.*, WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Patent No. 5,279,833; WO 91/06309; and Felgner, *et al.*, *Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) can also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

[00235] Known methods in the art can be used to enhance delivery and uptake of a polynucleotide *in vivo*. For example, the polynucleotide can be complexed to polyvinylpyrrolidone (PVP), to prolong the localized bioavailability of the polynucleotide, thereby enhancing uptake of the polynucleotide by the organism (*see e.g.*, U.S. Patent No. 6,040,295; EP 0 465 529; WO 98/17814). PVP is a polyamide that is known to form complexes with a wide variety of substances, and is chemically and physiologically inert.

[00236] Target cell sensitization can be used as a functional assay of the expression and HLA class I presentation of polynucleotide- (e.g. minigene-) encoded peptides. For example, the polynucleotide, e.g. plasmid DNA, is introduced into a mammalian cell line that is a suitable target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. For example, electroporation can be used for "naked" DNA, whereas cationic lipids or PVP-formulated DNA allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). The transfected cells are then chromium-51 (^{51}Cr) labeled and used as targets for epitope-specific CTLs. Cytolysis of the target cells, detected by ^{51}Cr release, indicates both production and HLA presentation of, polynucleotide-, e.g. minigene-, encoded variants of the invention, or peptides comprising them. Expression of HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.

[00237] *In vivo* immunogenicity is a second approach for functional testing of polynucleotides, e.g. minigenes. Transgenic mice expressing appropriate human HLA proteins are immunized with the polynucleotide, e.g. DNA; product. The dose and route of administration are formulation dependent (*e.g.*, IM for polynucleotide (*e.g.*, naked DNA or PVP-formulated DNA) in PBS, intraperitoneal (IP) for lipid-complexed polynucleotide

(e.g., DNA)). Eleven to twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of polynucleotides encoding each peptide being tested. Thereafter, for peptides comprising or consisting of variants, standard assays are conducted to determine if there is cytolysis of peptide-loaded, ⁵¹Cr-labeled target cells. Once again, lysis of target cells that were exposed to variants corresponding to those encoded by the polynucleotide (e.g. minigene) demonstrates polynucleotide (e.g., DNA) vaccine function and induction of CTLs. Immunogenicity of HTL epitopes is evaluated in transgenic mice in an analogous manner.

[00238] Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles comprised solely of a polynucleotide such as DNA are administered. In a further alternative embodiment for ballistic delivery, polynucleotides such as DNA can be adhered to particles, such as gold particles.

[00239] The use of polynucleotides such as multi-epitope minigenes is described herein and in, e.g. co-pending application U.S.S.N. 09/311,784; Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822, 1996; Whitton, J. L. *et al.*, *J. Virol.* 67:348, 1993; Hanke, R. *et al.*, *Vaccine* 16:426, 1998. For example, a polynucleotide such as a multi-epitope DNA plasmid can be engineered which encodes an epitope derived from multiple regions of a infectious agent (e.g., p53, HER2/nev, MAGE-2/3, or CEA), a pan-DR binding peptide such as the PADRE[®] universal helper T cell epitope, and an endoplasmic reticulum-translocating signal sequence. As described in the sections above, a peptide/polynucleotide may also comprise/encode epitopes that are derived from other infectious agents.

[00240] Thus, the invention includes peptides as described herein, polynucleotides encoding each of said peptides, as well as compositions comprising the peptides and polynucleotides, and includes methods for producing and methods of using the peptides, polynucleotides, and compositions, as further described below.

[00241] **Compositions.** In other embodiments, the invention is directed to a composition comprising one or more peptides and/or polynucleotides of the invention and optionally another component(s).

[00242] In some embodiments, the composition comprises or consists of multiple peptides, e.g., 2, 3, 4, 5, 6, 7, 8, or 9 peptides of the invention. In some embodiments, the composition comprises at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 peptides of the invention. Combinations of peptides include, for example, a peptide

comprising or alternatively consisting of the Gag 545 variant EPLTSLKSLF (SEQ ID NO: 1) and a peptide comprising or alternatively consisting of the Gag 545 variant YPLASLKSLF (SEQ ID NO: 2), or combinations of peptides from different tables in Tables 6-9 and/or Figures 1A-4.

[00243] Compositions of the invention may comprise polynucleotides encoding the above peptides and/or combinations of peptides.

[00244] The composition can comprise at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 peptides and/or polynucleotides selected from those described above or below. At least one of the one or more peptides can be a heteropolymer or a homopolymer. Additionally, the composition can comprise a CTL and/or HTL epitope, which can be derived from a tumor-associated antigen. The additional epitope can also be a PanDR binding molecule, (*e.g.*, a PADRE[®] universal helper T cell epitope).

[00245] Optional components include excipients, diluents, proteins such as peptides comprising a CTL epitope, and/or an HTL epitope such as a pan-DR binding peptide (*e.g.*, a PADRE[®] universal helper T cell epitope), and/or a carrier, polynucleotides encoding such proteins, lipids, or liposomes, as well as other components described herein. There are numerous embodiments of compositions in accordance with the invention, such as a cocktail of one or more peptides and/or polynucleotides (*e.g.*, minigenes); a cocktail of one or more peptides and/or polynucleotides (*e.g.*, minigenes) and one or more CTL and/or HTL epitopes.

[00246] Compositions may comprise one or more peptides (and/or polynucleotides such as minigenes) of the invention, along with one or more other components as described above and herein. "One or more" refers to any whole unit integer from 1-150, *e.g.*, at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 peptides, polynucleotides, or other components.

[00247] Compositions of the invention may be, for example, polynucleotides or polypeptides of the invention combined with or complexed to cationic lipid formulations; lipopeptides (*e.g.*, Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), encapsulated *e.g.*, in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g.*, Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991; Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995); peptide compositions contained in immune stimulating complexes (ISCOMS) (*see, e.g.*, Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*,

Clin Exp Immunol. 113:235-243, 1998); multiple antigen peptide systems (MAPs) (*see e.g.*, Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996); viral, bacterial, or, fungal delivery vectors (Perkus, M. E. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990); particles of viral or synthetic origin (*e.g.*, Kofler, N. *et al.*, *J. Immunol. Methods.* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995); adjuvants (*e.g.*, incomplete Freund's adjuvant) (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993); liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996); or, particle-absorbed cDNA or other polynucleotides of the invention (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993), etc. Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) or attached to a stress protein, *e.g.*, HSP 96 (Stressgen Biotechnologies Corp., Victoria, BC, Canada) can also be used.

[00248] Compositions of the invention comprise polynucleotide-mediated modalities. DNA or RNA encoding one or more of the peptides of the invention can be administered to a patient. This approach is described, for instance, in Wolff *et al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; and, WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers (*e.g.*, PVP, PINC, etc.), peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687). Accordingly, peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as Modified Vaccinia Ankara (MVA) (*e.g.*, Bavarian Noridic), vaccinia or fowlpox. For example, vaccinia virus is used as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into an acutely or chronically infected host or into a non-infected host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune

response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, *e.g.* adeno and adeno-associated virus vectors, alpha virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, are apparent to those skilled in the art from the description herein.

[00249] In certain embodiments, components that induce T cell responses are combined with components that induce antibody responses to the target antigen of interest. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. Alternatively, a composition comprises a class I and/or class II epitope in accordance with the invention, along with a PADRE[®] molecule (Epimmune, San Diego, CA).

[00250] Compositions of the invention can comprise antigen presenting cells, such as dendritic cells. Antigen presenting cells, *e.g.*, dendritic cells, may be transfected, *e.g.*, with a polynucleotide such as a minigene construct in accordance with the invention, in order to elicit immune responses. The peptide can be bound to an HLA molecule on the antigen-presenting cell, whereby when an HLA-restricted cytotoxic T lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HLA molecule and the peptide.

[00251] The compositions of the invention may also comprise antiviral drugs such as interferon- α , or immune adjuvants such as IL-12, GM-CSF, etc.

[00252] Compositions may comprise an HLA heavy chain, β_2 -microglobulin, streptavidin, and/or biotin. The streptavidin may be fluorescently labeled. Compositions may comprise tetramers (*see e.g.*, U.S. Pat. No. 5,635,363; *Science* 274:94-96 (1996)). A tetramer composition comprising an HLA heavy chain, β_2 -microglobulin, streptavidin, and biotin. The streptavidin may be fluorescently labeled. Compositions may also comprise dimers. A dimer composition comprises an MHC molecule and an Ig molecule (*see e.g.*, *PNAS* 95:7568-73 (1998)).

[00253] In some embodiments it may be desirable to include in the compositions of the invention at least one component which primes cytotoxic T lymphocytes. Lipids have been identified as agents capable of priming CTL *in vivo* against viral antigens. For example, palmitic acid residues can be attached to the ϵ - and α - amino groups of a lysine residue and then linked, *e.g.*, via one or more linking residues such as Gly, Gly-Gly-, Ser,

Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be administered either directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, *e.g.*, incomplete Freund's adjuvant. A preferred composition comprises palmitic acid attached to ϵ - and α - amino groups of Lys, which is attached via linkage, *e.g.*, Ser-Ser, to the amino terminus of the peptide.

[00254] As another example of lipid priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinylserine (P₃CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide (*see, e.g.*, Deres, *et al.*, *Nature* 342:561, 1989). Peptides of the invention can be coupled to P₃CSS, for example, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P₃CSS-conjugated epitopes, two such compositions can be combined to more effectively elicit both humoral and cell-mediated responses.

[00255] Another preferred embodiment is a composition comprising one or more peptides of the invention emulsified in IFA.

[00256] Compositions of the invention may also comprise CTL and/or HTL peptides. Such CTL and HTL peptides can be modified by the addition of amino acids to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or naturally or unnaturally occurring amino acid residues, can be introduced at the carboxyl- or amino-terminus of the peptide or oligopeptide, particularly class I peptides. However, it is to be noted that modification at the carboxyl terminus of a CTL epitope may, in some cases, alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-NH₂ acylation, *e.g.*, by alkanoyl (C₁-C₂₀) or thioglycolyl acetylation, terminal-carboxyl amidation, *e.g.*, ammonia, methylamine, *etc.* In some instances these modifications may provide sites for linking to a support or other molecule. CTL and HTL epitopes may comprise additional amino acids, such as those described above including spacers.

[00257] A further embodiment of a composition in accordance with the invention is an antigen presenting cell that comprises one or more peptides in accordance with the invention. The antigen presenting cell can be a "professional" antigen presenting cell,

such as a dendritic cell. The antigen presenting cell can comprise the peptide of the invention by any means known or to be determined in the art. Such means include pulsing of dendritic cells with one or more individual peptides, by nucleic acid administration such as ballistic nucleic acid delivery or by other techniques in the art for administration of nucleic acids, including vector-based, *e.g.* viral vector, delivery of nucleic acids.

[00258] Compositions may comprise carriers. Carriers that can be used with compositions of the invention are well known in the art, and include, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza virus proteins, hepatitis B virus core protein, and the like.

[00259] The compositions (*e.g.* pharmaceutical compositions) can contain a physiologically tolerable diluent such as water, or a saline solution, preferably phosphate buffered saline. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glycerol-cysteinyl-serine (P₃CSS).

[00260] Compositions of the invention may be pharmaceutically acceptable compositions. Pharmaceutical compositions preferably contain an immunologically effective amount of one or more peptides and/or polynucleotides of the invention, and optionally one or more other components which are pharmaceutically acceptable. A preferred composition comprises one or more peptides of the invention and IFA. A more preferred composition of the invention comprises one or more peptides of the invention, one or more peptides, and IFA.

[00261] Upon immunization with a peptide and/or polynucleotide and/or composition in accordance with the invention, via injection (*e.g.*, SC, ID, IM), aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other suitable routes, the immune system of the host responds to the vaccine by an immune response comprising the production of antibodies, CTLs and/or HTLs specific for the desired antigen(s). Consequently, the host becomes at least partially immune to subsequent exposure to the infectious agent(s), or at least partially resistant to further development of infectious agent-bearing cells and thereby derives a prophylactic or therapeutic benefit.

[00262] Furthermore, the peptides, primers, and epitopes of the invention can be used in any desired immunization or administration regimen; *e.g.*, as part of periodic vaccinations such as annual vaccinations as in the veterinary arts or as in periodic vaccinations as in the human medical arts, or as in a prime-boost regime wherein an inventive vector or recombinant is administered either before or after the administration of the same or of a different epitope of interest or recombinant or vector expressing such as a same or

different epitope of interest (including an inventive recombinant or vector expressing such as a same or different epitope of interest), see, e.g., U.S. Pat. Nos. 5,997,878; 6,130,066; 6,180,398; 6,267,965; and 6,348,450. An useful viral vector of the present invention is Modified Vaccinia Ankara (MVA) (e.g., Bavarian Noridic (MVA-BN)).

[00263] Recent studies have indicated that a prime-boost protocol, whereby immunization with a poxvirus recombinant expressing a foreign gene product is followed by a boost using a purified subunit preparation form of that gene product, elicits an enhanced immune response relative to the response elicited with either product alone. Human volunteers immunized with a vaccinia recombinant expressing the HIV-1 envelope glycoprotein and boosted with purified HIV-1 envelope glycoprotein subunit preparation exhibit higher HIV-1 neutralizing antibody titers than individuals immunized with just the vaccinia recombinant or purified envelope glycoprotein alone (Graham *et al.*, *J. Infect. Dis.*, 167:533-537 (1993); Cooney *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:1882-1886 (1993)). Humans immunized with two injections of an ALVAC-HIV-1 env recombinant (vCP125) failed to develop HIV specific antibodies. Boosting with purified rgp160 from a vaccinia virus recombinant resulted in detectable HIV-1 neutralizing antibodies. Furthermore, specific lymphocyte T cell proliferation to rgp160 was clearly increased by the boost with rgp160. Envelope specific cytotoxic lymphocyte activity was also detected with this vaccination regimen (Pialoux *et al.*, *AIDS Res. and Hum. Retroviruses*, 11:272-381 (1995)). Macaques immunized with a vaccinia recombinant expressing the simian immunodeficiency virus (SIV) envelope glycoprotein and boosted with SIV envelope glycoprotein from a baculovirus recombinant are protected against SIV challenge (Hu *et al.*, *AID Res. and Hum. Retroviruses*, 3:615-620 (1991); Hu *et al.*, *Science* 255:456-459 (1992)). In the same fashion, purified HCMVgB protein can be used in prime-boost protocols with NYVAC or ALVAC-gB recombinants.

[00264] In certain embodiments, the polynucleotides are complexed in a liposome preparation. Liposomal preparations for use in the instant invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. However, cationic liposomes are particularly preferred because a tight charge complex can be formed between the cationic liposome and the polyanionic nucleic acid. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner *et al.*, *Proc. Natl. Acad. Sci. USA* 84:7413-7416 (1987), which is herein incorporated by reference); mRNA (Malone *et al.*, *Proc. Natl. Acad. Sci. USA* 86:6077-6081 (1989), which is herein incorporated by reference); and purified transcription factors (Debs *et al.*, *J. Biol.*

Chem. 265:1018910192 (1990), which is herein incorporated by reference), in functional form.

[00265] Cationic liposomes are readily available. For example, N-[12,3-dioleoyloxy)-propyl]-N,N,N-triethylammonium (DOTMA) liposomes are particularly useful and are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, N.Y. (See, also, Felgner *et al.*, *Proc. Natl Acad. Sci. USA* 84:74137416 (1987)). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer).

[00266] Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, e.g. PCT Publication No. WO 90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes. Preparation of DOTMA liposomes is explained in the literature, see, e.g., P. Felgner *et al.*, *Proc. Natl. Acad. Sci. USA* 84:74137417. Similar methods can be used to prepare liposomes from other cationic lipid materials.

[00267] Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, Ala.), or can be easily prepared using readily available materials. Such materials include phosphatidyl, choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

[00268] For example, commercially available dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), and dioleoylphosphatidyl ethanolamine (DOPE) can be used in various combinations to make conventional liposomes, with or without the addition of cholesterol. Thus, for example, DOPG/DOPC vesicles can be prepared by drying 50 mg each of DOPG and DOPC under a stream of nitrogen gas into a sonication vial. The sample is placed under a vacuum pump overnight and is hydrated the following day with deionized water. The sample is then sonicated for 2 hours in a capped vial, using a Heat Systems model 350 sonicator equipped with an inverted cup (bath type) probe at the maximum setting while the bath is circulated at 15EC. Alternatively, negatively charged vesicles can be prepared without sonication to produce multilamellar vesicles or by extrusion through nucleopore membranes to produce unilamellar vesicles of discrete size. Other methods are known and available to those of skill in the art.

[00269] The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs), with SUVs being preferred. The various liposome nucleic acid complexes are prepared using methods well known in the art. See, e.g., Straubinger *et al.*, *Methods of Immunology* 101:512527 (1983). For example, MLVs containing nucleic acid can be prepared by depositing a thin film of phospholipid on the walls of a glass tube and subsequently hydrating with a solution of the material to be encapsulated. SUVs are prepared by extended sonication of MLVs to produce a homogeneous population of unilamellar liposomes. The material to be entrapped is added to a suspension of preformed MLVs and then sonicated. When using liposomes containing cationic lipids, the dried lipid film is resuspended in an appropriate solution such as sterile water or an isotonic buffer solution such as 10 mM Tris/NaCl, sonicated, and then the preformed liposomes are mixed directly with the DNA. The liposome and DNA form a very stable complex due to binding of the positively charged liposomes to the cationic DNA. SUVs find use with small nucleic acid fragments. LUVs are prepared by a number of methods, well known in the art. Commonly used methods include Ca^{2+} -EDTA chelation (Papahadjopoulos *et al.*, *Biochim. Biophys. Acta* 394:483 (1975); Wilson *et al.*, *Cell* 17:77 (1979)); ether injection (Deamer, D. and Bangham, A., *Biochim. Biophys. Acta* 443:629 (1976); Ostro *et al.*, *Biochem. Biophys. Res. Commun.* 76:836 (1977); Fraley *et al.*, *Proc. Natl. Acad. Sci. USA* 76:3348 (1979)); detergent dialysis (Enoch, H. and Strittmatter, P., *Proc. Natl. Acad. Sci. USA* 76:145 (1979)); and reversephase evaporation (REV) (Fraley *et al.*, *J. Biol. Chem.* 255:10431 (1980); Szoka, F. and Papahadjopoulos, D., *Proc. Natl. Acad. Sci. USA* 75:145 (1978); SchaeferRidder *et al.*, *Science* 215:166 (1982)).

[00270] Generally, the ratio of DNA to liposomes will be from about 10:1 to about 1:10. Preferably, the ration will be from about 5:1 to about 1:5. More preferably, the ration will be about 3:1 to about 1:3. Still more preferably, the ratio will be about 1:1.

[00271] U.S. Patent No. 5,676,954 reports on the injection of genetic material, complexed with cationic liposome carriers, into mice. U.S. Patent Nos. 4,897,355, 4,946,787, 5,049,386, 5,459,127, 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication no. WO 94/9469 provide cationic lipids for use in transfecting DNA into cells and mammals. U.S. Patent Nos. 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication no. WO 94/9469 provide methods for delivering DNA-cationic lipid complexes to mammals.

Binding Affinity of Variants for HLA Molecules

[00272] As indicated herein, the large degree of HLA polymorphism is an important factor to be taken into account with the epitope-based approach to developing therapeutics and diagnostics. To address this factor, epitope selection encompassing identification of peptides capable of binding at high or intermediate affinity to multiple HLA molecules is preferably utilized, most preferably these epitopes bind at high or intermediate affinity to two or more allele-specific HLA molecules. However, in some embodiments, it is preferred that all epitopes in a given composition bind to the alleles of a single HLA supertype or a single HLA molecule.

[00273] Variants of the invention preferably include those that have an IC_{50} or binding affinity value for a class I HLA molecule(s) of 500 nM or better (*i.e.*, the value is ≤ 500 nM). In certain embodiments of the invention, peptides of interest have an IC_{50} or binding affinity value for a class I HLA molecule(s) of 200 nM or better. In certain embodiments of the invention, peptides of interest, such as A1 and A24 peptides, have an IC_{50} or binding affinity value for a class I HLA molecule(s) of 100 nM or better. If HTL epitopes are included, they preferably are HTL epitopes that have an IC_{50} or binding affinity value for class II HLA molecules of 1000 nM or better, (*i.e.*, the value is $\leq 1,000$ nM). For example, peptide binding is assessed by testing the capacity of a candidate peptide to bind to a purified HLA molecule *in vitro*. Peptides exhibiting high or intermediate affinity are then considered for further analysis. Selected peptides are generally tested on other members of the supertype family. In preferred embodiments, peptides that exhibit cross-reactive binding are then used in cellular screening analyses or vaccines.

[00274] The relationship between binding affinity for HLA class I molecules and immunogenicity of discrete peptide epitopes on bound antigens was determined for the first time by inventors at Epimmune. As disclosed in greater detail herein, higher HLA binding affinity is correlated with greater immunogenicity.

[00275] Greater immunogenicity can be manifested in several different ways. Immunogenicity corresponds to whether an immune response is elicited at all, and to the vigor of any particular response, as well as to the extent of a population in which a response is elicited. For example, a peptide might elicit an immune response in a diverse array of the population, yet in no instance produce a vigorous response. In accordance with these principles, close to 90% of high binding peptides have been found to elicit a

response and thus be “immunogenic,” as contrasted with about 50% of the peptides that bind with intermediate affinity. (See, e.g., Schaeffer *et al.* PNAS (1988)) High affinity-binding class I peptides generally have an affinity of less than or equal to 100 nM. Moreover, not only did peptides with higher binding affinity have an enhanced probability of generating an immune response, the generated response tended to be more vigorous than the response seen with weaker binding peptides. As a result, less peptide is required to elicit a similar biological effect if a high affinity binding peptide is used rather than a lower affinity one. Thus, in some preferred embodiments of the invention, high affinity binding epitopes are used.

[00276] The correlation between binding affinity and immunogenicity was analyzed by the present inventors by two different experimental approaches (*see, e.g., Sette, et al., J. Immunol.* 153:5586-5592 (1994)). In the first approach, the immunogenicity of potential epitopes ranging in HLA binding affinity over a 10,000-fold range was analyzed in HLA-A*0201 transgenic mice. In the second approach, the antigenicity of approximately 100 different hepatitis B virus (HBV)-derived potential epitopes, all carrying A*0201 binding motifs, was assessed by using PBL from acute hepatitis patients. Pursuant to these approaches, it was determined that an affinity threshold value of approximately 500 nM (preferably 50 nM or less) determines the capacity of a peptide epitope to elicit a CTL response. These data are true for class I binding affinity measurements for naturally processed peptides and for synthesized T cell epitopes. These data also indicate the important role of determinant selection in the shaping of T cell responses (*see, e.g., Schaeffer et al. Proc. Natl. Acad. Sci. USA* 86:4649-4653 (1989)).

[00277] An affinity threshold associated with immunogenicity in the context of HLA class II (*i.e.*, HLA DR) molecules has also been delineated (*see, e.g., Southwood et al. J. Immunology* 160:3363-3373 (1998), and U.S. Patent No. 6,413,527, issued July 2, 2002). In order to define a biologically significant threshold of HLA class II binding affinity, a database of the binding affinities of 32 DR-restricted epitopes for their restricting element (*i.e.*, the HLA molecule that binds the epitope) was compiled. In approximately half of the cases (15 of 32 epitopes), DR restriction was associated with high binding affinities, *i.e.* binding affinity values of 100 nM or less. In the other half of the cases (16 of 32), DR restriction was associated with intermediate affinity (binding affinity values in the 100-1000 nM range). In only one of 32 cases was DR restriction associated with an IC₅₀ of 1000 nM or greater. Thus, 1000 nM is defined as an affinity threshold associated with immunogenicity in the context of DR molecules.

[00278] The binding affinity of peptides for HLA molecules can be determined as described in Example 1, below.

Enhancing Population Coverage of the Vaccine

[00279] The primary anchor residues of the HLA class I peptide epitope supermotifs and motifs are summarized in Tables 1-2. Allele-specific HLA molecules that are comprised by the various HLA class I supertypes are listed in Table 4. In some cases, patterns of amino acid residues are present in both a motif and a supermotif. The relationship of a particular motif and any related supermotif is indicated in the description of the individual motifs.

[00280] By inclusion of one or more epitopes from several motifs or supermotifs in a vaccine composition, enhanced population coverage for major global ethnicities can be obtained.

Assays to Detect T-Cell Responses

[00281] Once HLA binding peptides are identified, they can be tested for the ability to elicit a T-cell response. The preparation and evaluation of motif-bearing peptides are described, *e.g.*, in PCT publications WO 94/20127 and WO 94/03205. Briefly, peptides comprising epitopes from a particular antigen are synthesized and tested for their ability to bind to relevant HLA proteins. These assays may involve evaluation of peptide binding to purified HLA class I molecules in relation to the binding of a radioiodinated reference peptide. Alternatively, cells expressing empty class I molecules (*i.e.* cell surface HLA molecules that lack any bound peptide) may be evaluated for peptide binding by immunofluorescent staining and flow microfluorimetry. Other assays that may be used to evaluate peptide binding include peptide-dependent class I assembly assays and/or the inhibition of CTL recognition by peptide competition. Those peptides that bind to an HLA class I molecule, typically with an affinity of 500 nM or less, are further evaluated for their ability to serve as targets for CTLs derived from infected or immunized individuals, as well as for their capacity to induce primary *in vitro* or *in vivo* CTL responses that can give rise to CTL populations capable of reacting with selected target cells associated with pathology.

- [00282] Analogous assays are used for evaluation of HLA class II binding peptides. HLA class II motif-bearing peptides that are shown to bind, typically at an affinity of 1000 nM or less, are further evaluated for the ability to stimulate HTL responses.
- [00283] Conventional assays utilized to detect T cell responses include proliferation assays, lymphokine secretion assays, direct cytotoxicity assays, and limiting dilution assays. For example, antigen-presenting cells that have been incubated with a peptide can be assayed for the ability to induce CTL responses in responder cell populations. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells or dendritic cells. Alternatively, mutant, non-human mammalian cell lines that have been transfected with a human class I MHC gene, and that are deficient in their ability to load class I molecules with internally processed peptides, are used to evaluate the capacity of the peptide to induce *in vitro* primary CTL responses. Peripheral blood mononuclear cells (PBMCs) can be used as the source of CTL precursors. Antigen presenting cells are incubated with peptide, after which the peptide-loaded antigen-presenting cells are then incubated with the responder cell population under optimized culture conditions. Positive CTL activation can be determined by assaying the culture for the presence of CTLs that lyse radio-labeled target cells, either specific peptide-pulsed targets or target cells that express endogenously processed antigen from which the specific peptide was derived. Alternatively, the presence of epitope-specific CTLs can be determined by IFN γ *in situ* ELISA.
- [00284] In an embodiment of the invention, directed to diagnostics, a method has been devised which allows direct quantification of antigen-specific T cells by staining with fluorescein-labelled HLA tetrameric complexes (Altman, J. D. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:10330, 1993; Altman, J. D. *et al.*, *Science* 274:94, 1996). Other options include staining for intracellular lymphokines, and interferon release assays or ELISPOT assays. Tetramer staining, intracellular lymphokine staining and ELISPOT assays all appear to be at least 10-fold more sensitive than more conventional assays (Lalvani, A. *et al.*, *J. Exp. Med.* 186:859, 1997; Dunbar, P. R. *et al.*, *Curr. Biol.* 8:413, 1998; Murali-Krishna, K. *et al.*, *Immunity* 8:177, 1998). Additionally, DimerX technology can be used as a means of quantitation (*see, e.g.*, *Science* 274:94-99 (1996) and *Proc. Natl. Acad. Sci.* 95:7568-73 (1998)).
- [00285] HTL activation may also be assessed using techniques known to those in the art, such as T cell proliferation or lymphokine secretion (*see, e.g.* Alexander *et al.*, *Immunity* 1:751-761, 1994).

[00286] Alternatively, immunization of HLA transgenic mice can be used to determine immunogenicity of peptide epitopes. Several transgenic mouse strains, *e.g.*, mice with human A2.1, A11 (which can additionally be used to analyze HLA-A3 epitopes), and B7 alleles have been characterized. Other transgenic mice strains (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. Moreover, HLA-DR1 and HLA-DR3 mouse models have been developed. In accordance with principles in the art, additional transgenic mouse models with other HLA alleles are generated as necessary.

[00287] Such mice can be immunized with peptides emulsified in Incomplete Freund's Adjuvant; thereafter any resulting T cells can be tested for their capacity to recognize target cells that have been peptide-pulsed or transfected with genes encoding the peptide of interest. CTL responses can be analyzed using cytotoxicity assays described above. Similarly, HTL responses can be analyzed using, *e.g.*, T cell proliferation or lymphokine secretion assays.

Minigenes

[00288] A number of different approaches are available which allow simultaneous delivery of multiple epitopes. Nucleic acids encoding multiple epitopes are a useful embodiment of the invention; discrete peptide epitopes or polyepitopic peptides can be encoded. The epitopes to be included in a minigene are preferably selected according to the guidelines set forth in the previous section. Examples of amino acid sequences that can be included in a minigene include: HLA class I epitopes, HLA class II epitopes, a ubiquitination signal sequence, and/or a targeting sequence such as an endoplasmic reticulum (ER) signal sequence to facilitate movement of the resulting peptide into the endoplasmic reticulum. Examples of minigene constructs are shown in Tables 23-28.

[00289] The use of multi-epitope minigenes is also described in, *e.g.*, co-pending applications U.S.S.N. 09/311,784, 09/894,018, 60/419,973, 60/415,463; Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822, 1996; Whitton, J. L. *et al.*, *J. Virol.* 67:348, 1993; Hanke, R. *et al.*, *Vaccine* 16:426, 1998. For example, a multi-epitope DNA plasmid encoding nine dominant HLA-A*0201- and A11-restricted CTL epitopes derived from the polymerase, envelope, and core proteins of HBV and human immunodeficiency virus (HIV), a PADRE[®] universal helper T cell (HTL) epitope, and an endoplasmic reticulum-translocating signal sequence has been engineered. Immunization of HLA transgenic mice

with this plasmid construct resulted in strong CTL induction responses against the nine CTL epitopes tested. This CTL response was similar to that observed with a lipopeptide of known immunogenicity in humans, and significantly greater than immunization using peptides in oil-based adjuvants. Moreover, the immunogenicity of DNA-encoded epitopes *in vitro* was also correlated with the *in vitro* responses of specific CTL lines against target cells transfected with the DNA plasmid. These data show that the minigene served: 1.) to generate a CTL response and 2.) to generate CTLs that recognized cells expressing the encoded epitopes. A similar approach can be used to develop minigenes encoding epitopes of an infectious agent.

[00290] For example, to create a DNA sequence encoding the selected epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes may be reverse translated. A human codon usage table can be used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences may be directly adjoined, so that when translated, a continuous peptide sequence is created. However, to optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design such as spacer amino acid residues between epitopes. HLA presentation of CTL and HTL epitopes may be improved by including synthetic (*e.g.* poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL or HTL epitopes; these larger peptides comprising the epitope(s) are within the scope of the invention. In one embodiment, spacer amino acid residues between one or more CTL and/or HTL epitopes are designed so as to minimize junctional epitopes that may result from the juxtaposition of 2 CTL and/or HTL epitopes.

[00291] The minigene sequence may be converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) may be synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides can be joined, for example, using T4 DNA ligase. This synthetic minigene, encoding the epitope peptide, can then be cloned into a desired expression vector.

[00292] Standard regulatory sequences well known to those of skill in the art are preferably included in the vector to ensure expression in the target cells. Several vector elements are desirable: a promoter with a downstream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (*e.g.* ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus

(hCMV) CMV-IE promoter. See, *e.g.*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

[00293] Optimized peptide expression and immunogenicity can be achieved by certain modifications to a minigene construct. For example, in some cases introns facilitate efficient gene expression, thus one or more synthetic or naturally-occurring introns can be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences and sequences for replication in mammalian cells may also be considered for increasing minigene expression.

[00294] Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate bacterial strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping, PCR and/or DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as cell banks.

[00295] In addition, immunostimulatory sequences (ISSs or CpGs) appear to play a role in the immunogenicity of DNA vaccines. These sequences may be included in the vector, outside the minigene coding sequence to enhance immunogenicity.

[00296] In some embodiments, a bi-cistronic expression vector which allows production of both the minigene-encoded epitopes and a second protein (*e.g.*, one that modulates immunogenicity) can be used. Examples of proteins or polypeptides that, if co-expressed with epitopes, can enhance an immune response include cytokines (*e.g.*, IL-2, IL-12, GM-CSF), cytokine-inducing molecules (*e.g.*, LeIF), costimulatory molecules, or pan-DR binding proteins (PADRE[®], Epimmune, San Diego, CA). Helper T cell (HTL) epitopes such as PADRE[®] molecules can be joined to intracellular targeting signals and expressed separately from expressed CTL epitopes. This can be done in order to direct HTL epitopes to a cell compartment different than that of the CTL epitopes, one that provides for more efficient entry of HTL epitopes into the HLA class II pathway, thereby improving HTL induction. In contrast to HTL or CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (*e.g.* TGF- β) may be beneficial in certain diseases.

[00297] Therapeutic quantities of plasmid DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and are grown to saturation in shaker flasks or a

bioreactor according to well known techniques. Plasmid DNA is purified using standard bioseparation technologies such as solid phase anion-exchange resins available, *e.g.*, from QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

[00298] Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize the immunotherapeutic effects of minigene vaccines, alternative methods of formulating purified plasmid DNA may be used. A variety of such methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, *e.g.*, WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Patent No. 5,279,833; WO 91/06309; and Felgner, *et al.*, *Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) can also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

[00299] Known methods in the art can be used to enhance delivery and uptake of a polynucleotide *in vivo*. For example, the polynucleotide can be complexed to polyvinylpyrrolidone (PVP), to prolong the localized bioavailability of the polynucleotide, thereby enhancing uptake of the polynucleotide by the organism (*see e.g.*, U.S. Patent No. 6,040,295; EP 0 465 529; WO 98/17814). PVP is a polyamide that is known to form complexes with a wide variety of substances, and is chemically and physiologically inert.

[00300] Target cell sensitization can be used as a functional assay of the expression and HLA class I presentation of minigene-encoded epitopes. For example, the plasmid DNA is introduced into a mammalian cell line that is a suitable target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation, electroporation can be used for "naked" DNA, whereas cationic lipids or DNA:PVP compositions allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). The transfected cells are then chromium-51 (^{51}Cr) labeled and used as targets for epitope-specific CTLs. Cytolysis of the target cells, detected by ^{51}Cr release, indicates both the production and HLA

presentation of, minigene-encoded CTL epitopes. Expression of HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.

[00301] *In vivo* immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human HLA proteins are immunized with the DNA product. The dose and route of administration are formulation dependent (*e.g.*, IM for DNA in PBS, intraperitoneal (IP) for lipid-complexed DNA). Eleven to twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of peptides encoding each epitope being tested. Thereafter, for CTLs, standard assays are conducted to determine if there is cytolysis of peptide-loaded, ⁵¹Cr-labeled target cells. Once again, lysis of target cells that were exposed to epitopes corresponding to those in the minigene, demonstrates DNA vaccine function and induction of CTLs. Immunogenicity of HTL epitopes is evaluated in transgenic mice in an analogous manner.

[00302] Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles comprised solely of DNA are administered. In a further alternative embodiment for ballistic delivery, DNA can be adhered to particles, such as gold particles.

Vaccine Compositions

[00303] Vaccines that contain an immunologically effective amount of one or more peptides or polynucleotides of the invention are a further embodiment of the invention. The peptides can be delivered by various means or formulations, all collectively referred to as "vaccine" compositions. Such vaccine compositions, and/or modes of administration, can include, for example, naked DNA, DNA formulated with PVP, DNA in cationic lipid formulations; lipopeptides (*e.g.*, Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), DNA or peptides, encapsulated *e.g.*, in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g.*, Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991; Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995); peptide compositions contained in immune stimulating complexes (ISCOMS) (*see, e.g.*, Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998); multiple antigen peptide systems (MAPs) (*see e.g.*, Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996); viral, bacterial, or, fungal delivery vectors (Perkus, M. E. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S.

H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990); particles of viral or synthetic origin (*e.g.*, Kofler, N. *et al.*, *J. Immunol. Methods.* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995); adjuvants (*e.g.*, incomplete freund's adjuvant) (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993); liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996); or, particle-absorbed DNA (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993), etc. Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) or attached to a stress protein, *e.g.*, HSP 96 (Stressgen Biotechnologies Corp., Victoria, BC, Canada) can also be used.

[00304] Vaccines of the invention comprise nucleic acid mediated modalities. DNA or RNA encoding one or more of the peptides of the invention can be administered to a patient. This approach is described, for instance, in Wolff *et al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; and, WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers (*e.g.*, PVP), peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687). Accordingly, peptide vaccines of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. For example, vaccinia virus is used as a vector to express nucleotide sequences that encode the peptides of the invention (*e.g.*, MVA). Upon introduction into an acutely or chronically infected host or into a non-infected host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, *e.g.* adeno and adeno-associated virus

vectors, alpha virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, are apparent to those skilled in the art from the description herein.

[00305] Furthermore, vaccines in accordance with the invention can comprise one or more peptides of the invention. Accordingly, a peptide can be present in a vaccine individually; alternatively, the peptide can exist as a homopolymer comprising multiple copies of the same peptide, or as a heteropolymer of various peptides. Polymers have the advantage of increased probability for immunological reaction and, where different peptide epitopes are used to make up the polymer, the ability to induce antibodies and/or T cells that react with different antigenic determinants of the antigen targeted for an immune response. The composition may be a naturally occurring region of an antigen or can be prepared, *e.g.*, recombinantly or by chemical synthesis.

[00306] Carriers that can be used with vaccines of the invention are well known in the art, and include, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza virus proteins, hepatitis B virus core protein, and the like. The vaccines can contain a physiologically tolerable diluent such as water, or a saline solution, preferably phosphate buffered saline. Generally, the vaccines also include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are examples of materials well known in the art. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glyceryl-cysteinyl-serine (P₃CSS).

[00307] Upon immunization with a peptide composition in accordance with the invention, via injection (*e.g.*, SC, ID, IM), aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other suitable routes, the immune system of the host responds to the vaccine by producing antibodies, CTLs and/or HTLs specific for the desired antigen. Consequently, the host becomes at least partially immune to subsequent exposure to the infectious agent, and thereby derives a prophylactic or therapeutic benefit.

[00308] In certain embodiments, components that induce T cell responses are combined with components that induce antibody responses to the target antigen of interest. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. Alternatively, a composition comprises a class I and/or class II epitope in accordance with the invention, along with a PADRE[®] molecule (Epimmune, San Diego, CA).

[00309] Vaccines of the invention can comprise antigen presenting cells, such as dendritic cells, as a vehicle to present peptides of the invention. For example, dendritic cells are transfected, *e.g.*, with a minigene construct in accordance with the invention, in order to elicit immune responses. Minigenes are discussed in greater detail in a following section. Vaccine compositions can be created *in vitro*, following dendritic cell mobilization and harvesting, whereby loading of dendritic cells occurs *in vitro*.

[00310] The vaccine compositions of the invention may also be used in combination with antiviral drugs such as interferon- α , or immune adjuvants such as IL-12, GM-CSF, etc.

[00311] Preferably, the following principles are utilized when selecting epitope(s) and/or analogs for inclusion in a vaccine, either peptide-based or nucleic acid-based formulations. Exemplary variants that may be utilized in a vaccine to treat or prevent infectious agent-mediated disease are set out in Tables 6-9 and Figures 1A-4. Each of the following principles can be balanced in order to make the selection. When multiple epitopes are to be used in a vaccine, the epitopes may be, but need not be, contiguous in sequence in the native antigen from which the epitopes are derived. Such multiple epitopes can refer to the order of epitopes within a peptide, or to the selection of epitopes that come from the same region, for use in either individual peptides or in a multi-epitopic peptide.

1.) Variants are selected which, upon administration, mimic immune responses that have been observed to be correlated with prevention or clearance of infectious disease. For HLA Class I, this generally includes 3-7 variants from at least one infectious agent or antigen thereof.

2.) Variants are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an IC_{50} of 500 nM or less, or for Class II an IC_{50} of 1000 nM or less. For HLA Class I it is presently preferred to select a peptide having an IC_{50} of 200 nM or less, as this is believed to better correlate not only to induction of an immune response, but to *in vitro* tumor cell killing as well. For HLA A1 and A24, it is especially preferred to select a peptide having an IC_{50} of 100 nM or less.

3.) Supermotif bearing-variants, or a sufficient array of allele-specific motif-bearing variants, are selected to give broad population coverage. In general, it is preferable to have at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess the breadth of population coverage.

4.) Of particular relevance are "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. For example, a nested epitope can be a fragment of an antigen from a region that contains multiple epitopes that are overleapping, or one epitope that is completely encompassed by another, *e.g.*, A2 peptides MAGE3.159 and MAGE3.160 are nested epitopes. A peptide comprising "transcendent nested epitopes" is a

peptide that has both HLA class I and HLA class II epitopes in it. When providing nested epitopes, it is preferable to provide a sequence that has the greatest number of epitopes per provided sequence. Preferably, one avoids providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a sequence comprising nested epitopes, it is important to evaluate the sequence in order to insure that it does not have pathological or other deleterious biological properties; this is particularly relevant for vaccines directed to infectious organisms.

5.) If a protein with multiple epitopes or a polynucleotide (e.g., minigene) is created, an objective is to generate the smallest peptide that encompasses the epitopes of interest. This principle is similar, if not the same as that employed when selecting a peptide comprising nested epitopes. However, with an artificial peptide comprising multiple epitopes, the size minimization objective is balanced against the need to integrate any spacer sequences between epitopes in the polyepitopic protein. Spacer amino acid residues can be introduced to avoid junctional epitopes (an epitope recognized by the immune system, not present in the target antigen, and only created by the man-made juxtaposition of epitopes), or to facilitate cleavage between epitopes and thereby enhance epitope presentation. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that non-native epitope. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

[00312] The principles are the same, except junctional epitopes applies to the sequences surrounding the epitope. One must also take care with other sequences in construct to avoid immune response.

T CELL PRIMING MATERIALS

[00313] In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes cytotoxic T lymphocytes. Lipids have been identified as agents capable of facilitating the priming *in vitro* CTL response against viral antigens. For example, palmitic acid residues can be attached to the ϵ - and α - amino groups of a lysine residue and then linked to an immunogenic peptide. One or more linking moieties can be used such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like. The lipidated peptide can then be administered directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, e.g., incomplete Freund's adjuvant. A preferred immunogenic composition comprises palmitic

acid attached to ϵ - and α - amino groups of Lys via a linking moiety, *e.g.*, Ser-Ser, added to the amino terminus of an immunogenic peptide.

- [00314] In another embodiment of lipid-facilitated priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glyceryl-cysteinyl-seryl-serine (P₃CSS) can be used to prime CTL when covalently attached to an appropriate peptide. (*See, e.g.*, Deres, *et al.*, *Nature* 342:561, 1989). Thus, peptides of the invention can be coupled to P₃CSS, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P₃CSS-conjugated epitopes, two such compositions can be combined to elicit both humoral and cell-mediated responses.

DENDRITIC CELLS PULSED WITH CTL AND/OR HTL PEPTIDES

- [00315] An embodiment of a vaccine composition in accordance with the invention comprises *ex vivo* administration of a cocktail of epitope-bearing peptides to PBMC, or isolated DC therefrom, from the patient's blood. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoiectin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides. In this embodiment, a vaccine comprises peptide-pulsed DCs which present the pulsed peptide epitopes in HLA molecules on their surfaces.
- [00316] The DC can be pulsed *ex vivo* with a cocktail of peptides, some of which stimulate CTL responses to one or more antigens of interest, *e.g.*, antigens from infectious agents such as HIV env, HIV pol, HIV gag, HIV vpu, HBV and/or the antigens in Tables 11-22, or otherwise described herein or known in the art. Optionally, a helper T cell (HTL) peptide such as PADRE®, can be included to facilitate the CTL response. Thus, a vaccine in accordance with the invention comprising epitopes from an infectious agent is used to treat or prevent disease mediated by these agents in patients. A vaccine can be used prior to, during, or following other therapies including, for example, antibiotic therapy, antiviral therapy (*e.g.*, highly active antiretroviral therapy (HAART) in the case of HIV-AIDS), antibody therapy, cancer therapy, and adjunct therapy, whereupon the vaccine provides decreased morbidity, increased disease free survival and overall survival in recipients.

DIAGNOSTIC AND PROGNOSTIC USES

- [00317] In one embodiment of the invention, HLA class I and class II binding peptides can be used as reagents to evaluate an immune response. Preferably, the following principles are utilized when selecting a variant(s) for diagnostic, prognostic and similar uses. Potential principles include having the binding affinities described earlier, and/or matching the HLA-motif/supermotif of a peptide with the HLA-type of a patient.
- [00318] The evaluated immune response can be induced by any immunogen. For example, the immunogen may result in the production of antigen-specific CTLs or HTLs that recognize the peptide epitope(s) employed as the reagent. Thus, a peptide of the invention may or may not be used as the immunogen. Assay systems that can be used for such analyses include tetramer-based protocols (*e.g.*, DimerX technology (*see, e.g., Science* 274:94-99 (1996) and *Proc. Natl. Acad. Sci.* 95:7568-73 (1998)), staining for intracellular lymphokines, interferon release assays, or ELISPOT assays.
- [00319] For example, following exposure to a putative immunogen, a peptide of the invention can be used in a tetramer staining assay to assess peripheral blood mononuclear cells for the presence of any antigen-specific CTLs. The HLA-tetrameric complex is used to directly visualize antigen-specific CTLs and thereby determine the frequency of such antigen-specific CTLs in a sample of peripheral blood mononuclear cells (*see, e.g., Ogg et al., Science* 279:2103-2106, 1998; and Altman *et al., Science* 174:94-96, 1996).
- [00320] A tetramer reagent comprising a peptide of the invention is generated as follows: A peptide that binds to an HLA molecule is refolded in the presence of the corresponding HLA heavy chain and β_2 -microglobulin to generate a trimolecular complex. The complex is biotinylated at the carboxyl terminal end of the HLA heavy chain, at a site that was previously engineered into the protein. Tetramer formation is then induced by adding streptavidin. When fluorescently labeled streptavidin is used, the tetrameric complex is used to stain antigen-specific cells. The labeled cells are then readily identified, *e.g.*, by flow cytometry. Such procedures are used for diagnostic or prognostic purposes; the cells identified by the procedure can be used for therapeutic purposes.
- [00321] Peptides of the invention are also used as reagents to evaluate immune recall responses. (*see, e.g., Bertoni et al., J. Clin. Invest.* 100:503-513, 1997 and Penna *et al., J. Exp. Med.* 174:1565-1570, 1991.) For example, a PBMC sample from an individual expressing a disease-associated antigen (*e.g.* an antigen from an infectious agent) can be analyzed for the presence of antigen-specific CTLs or HTLs using specific peptides. A

blood sample containing mononuclear cells may be evaluated by cultivating the PBMCs and stimulating the cells with a peptide of the invention. After an appropriate cultivation period, the expanded cell population may be analyzed, for example, for CTL or for HTL activity.

[00322] Thus, the peptides can be used to evaluate the efficacy of a vaccine. PBMCs obtained from a patient vaccinated with an immunogen may be analyzed by methods such as those described herein. The patient is HLA typed, and peptide epitopes that are bound by the HLA molecule(s) present in that patient are selected for analysis. The immunogenicity of the vaccine is indicated by the presence of CTLs and/or HTLs directed to epitopes present in the vaccine.

[00323] The peptides of the invention may also be used to make antibodies, using techniques well known in the art (see, *e.g.* *CURRENT PROTOCOLS IN IMMUNOLOGY*, Wiley/Greene, NY; and *Antibodies A Laboratory Manual* Harlow, Harlow and Lane, Cold Spring Harbor Laboratory Press, 1989). Such antibodies are useful as reagents to determine the presence of disease-associated antigens. Antibodies in this category include those that recognize a peptide when bound by an HLA molecule, *i.e.*, antibodies that bind to a peptide-MHC complex.

ADMINISTRATION FOR THERAPEUTIC OR PROPHYLACTIC PURPOSES

[00324] The peptides and polynucleotides of the present invention, including cells and compositions comprising them, are useful for administration to mammals, particularly humans, to treat and/or prevent infection by an infectious agent such as HIV, HBV, HCV, HPV, *Plasmodium falciparum* and other agents described herein or known in the art. Vaccine compositions containing the peptides of the invention are administered to a patient infected with a particular infectious agent or to an individual susceptible to, or otherwise at risk for, infection with such an agent to elicit an immune response against antigens of that agent and thus enhance the patient's own immune response capabilities. Where susceptible individuals are identified prior to infection, the composition can be targeted to them, thus minimizing the need for administration to a larger population.

[00325] In therapeutic applications, peptide and/or nucleic acid compositions are administered to a patient in an amount sufficient to elicit an effective immune response to the infectious agent antigen and to thereby cure, arrest or slow symptoms and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use

will depend on, *e.g.*, the particular composition administered, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician.

[00326] The vaccine compositions of the invention can be used purely as prophylactic agents. Generally the dosage for an initial prophylactic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1000 μg of peptide and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg of peptide. Dosage values for a human typically range from about 500 μg to about 50,000 μg of peptide per 70 kilogram patient. This is followed by boosting dosages of between about 1.0 μg to about 50,000 μg of peptide, administered at defined intervals from about four weeks to six months after the initial administration of vaccine. The immunogenicity of the vaccine may be assessed by measuring the specific activity of CTL and HTL obtained from a sample of the patient's blood.

[00327] As noted above, peptides comprising CTL and/or HTL epitopes of the invention induce immune responses when presented by HLA molecules and contacted with a CTL or HTL specific for an epitope comprised by the peptide. The manner in which the peptide is contacted with the CTL or HTL is not critical to the invention. For instance, the peptide can be contacted with the CTL or HTL either *in vitro* or *in vivo*. If the contacting occurs *in vivo*, peptide can be administered directly, or in other forms/vehicles, *e.g.*, DNA vectors encoding one or more peptides, viral vectors encoding the peptide(s), liposomes, antigen presenting cells such as dendritic cells, and the like.

[00328] Accordingly, for pharmaceutical compositions of the invention in the form of peptides or polypeptides, the peptides or polypeptides can be administered directly. Alternatively, the peptide/polypeptides can be administered indirectly presented on APCs, or as DNA encoding them. Furthermore, the peptides or DNA encoding them can be administered individually or as fusions of one or more peptide sequences.

[00329] For therapeutic use, administration should generally begin at the first diagnosis of infectious agent-related disease. This is followed by boosting doses at least until symptoms are substantially abated and for a period thereafter. In chronic disease states, loading doses followed by boosting doses may be required.

[00330] The dosage for an initial therapeutic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1,000 μg of peptide and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg of peptide. Dosage values for a human typically range from about 500 μg to about 50,000 μg of peptide per 70 kilogram patient. Boosting dosages of between about 1.0 μg to about 50,000 μg of peptide, administered pursuant to a boosting regimen over weeks to months, can be administered depending upon the patient's response and condition. Patient response can be determined by measuring the specific activity of CTL and HTL obtained from the patient's blood.

[00331] In certain embodiments, peptides and compositions of the present invention are used in serious disease states. In such cases, as a result of the minimal amounts of extraneous substances and the relative nontoxic nature of the peptides, it is possible and may be desirable to administer substantial excesses of these peptide compositions relative to these stated dosage amounts.

[00332] For treatment of chronic disease, a representative dose is in the range disclosed above, namely where the lower value is about 1, 5, 50, 500, or 1,000 µg of peptide and the higher value is about 10,000; 20,000; 30,000; or 50,000 µg of peptide, preferably from about 500 µg to about 50,000 µg of peptide per 70 kilogram patient. Initial doses followed by boosting doses at established intervals, *e.g.*, from four weeks to six months, may be required, possibly for a prolonged period of time to effectively immunize an individual. In the case of chronic disease, administration should continue until at least clinical symptoms or laboratory tests indicate that the disease has been eliminated or substantially abated, and for a follow-up period thereafter. The dosages, routes of administration, and dose schedules are adjusted in accordance with methodologies known in the art.

[00333] The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral, intrathecal, or local administration. Preferably, the pharmaceutical compositions are administered parentally, *e.g.*, intravenously, subcutaneously, intradermally, or intramuscularly.

[00334] Thus, in a preferred embodiment the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, *e.g.*, water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances or pharmaceutical excipients as may be required to approximate physiological conditions, such as pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, *etc.*

[00335] The concentration of peptides of the invention in the pharmaceutical formulations can vary widely, *i.e.*, from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, *etc.*, in accordance with the particular mode of administration selected.

[00336] A human unit dose form of the peptide composition is typically included in a pharmaceutical composition that also comprises a human unit dose of an acceptable carrier, preferably an aqueous carrier, and is administered in a volume of fluid that is known by those of skill in the art to be used for administration of such compositions to humans (*see, e.g.*,

Remington's Pharmaceutical Sciences, 17th Edition, A. Gennaro, Editor, Mack Publishing Co., Easton, Pennsylvania, 1985).

[00337] The peptides of the invention can also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or to target selectively to infected cells, as well as to increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations, the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to a receptor prevalent among lymphoid cells (such as monoclonal antibodies which bind to the CD45 antigen) or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the peptide compositions. Liposomes for use in accordance with the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, *e.g.*, liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, *e.g.*, Szoka, *et al.*, *Ann. Rev. Biophys. Bioeng.* 9:467 (1980), and U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369.

[00338] For targeting compositions of the invention to cells of the immune system, a ligand can be incorporated into the liposome, *e.g.*, antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, *etc.* in a dose which varies according to, *inter alia*, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

[00339] For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, often at a concentration of 25%-75%.

[00340] For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form, along with a surfactant and propellant. Typical percentages of peptides are 0.01%-20% by weight, often 1%-10%. The surfactant must, of course, be pharmaceutically acceptable, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol

or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant, although an atomizer may be used in which no propellant is necessary and other percentages are adjusted accordingly. A carrier can also be included, *e.g.*, lecithin for intranasal delivery.

[00341] Antigenic peptides of the invention have been used to elicit a CTL and/or HTL response *ex vivo*, as well. The resulting CTLs or HTLs can be used to treat chronic infections, or tumors in patients that do not respond to other conventional forms of therapy, or who do not respond to a therapeutic peptide or nucleic acid vaccine in accordance with the invention. *Ex vivo* CTL or HTL responses to a particular antigen (infectious or tumor-associated) are induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of antigen-presenting cells (APC), such as dendritic cells, and the appropriate immunogenic peptide. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy (CTL) or facilitate destruction (HTL) of their specific target cell (an infected cell or a tumor cell).

KITS

[00342] The peptide and nucleic acid compositions of this invention can be provided in kit form together with instructions for vaccine administration. Typically the kit would include desired composition(s) of the invention in a container, preferably in unit dosage form and instructions for administration. For example, a kit would include an APC, such as a dendritic cell, previously exposed to and now presenting peptides of the invention in a container, preferably in unit dosage form together with instructions for administration. An alternative kit would include a minigene construct with desired nucleic acids of the invention in a container, preferably in unit dosage form together with instructions for administration. Lymphokines such as IL-2 or IL-12 may also be included in the kit. Other kit components that may also be desirable include, for example, a sterile syringe, booster dosages, and other desired excipients.

[00343] The invention will be described in greater detail by way of specific examples. The following examples are offered for illustrative purposes, and are not intended to limit the invention in any manner. Those of skill in the art will readily recognize a variety of non-critical parameters that can be changed or modified to yield alternative embodiments in accordance with the invention.

EXAMPLES

EXAMPLE 1. HLA CLASS I AND CLASS II BINDING ASSAYS

- [00344] The following example of peptide binding to HLA molecules demonstrates quantification of binding affinities of HLA class I and class II peptides. Binding assays can be performed with peptides that are either motif-bearing or not motif-bearing.
- [00345] Cell lysates were prepared and HLA molecules purified in accordance with disclosed protocols (Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al.*, *J. Immunol.* 154:247 (1995); Sette, *et al.*, *Mol. Immunol.* 31:813 (1994)). The cell lines used as sources of HLA molecules and the antibodies used for the extraction of the HLA molecules from the cell lysates are also described in these publications and are well known in the art.
- [00346] Epstein-Barr virus (EBV)-transformed homozygous cell lines, fibroblasts, CIR, or 721.221-transfectants were used as sources of HLA class I molecules. These cells were cultured in RPMI 1640 medium supplemented with 2mM L-glutamine (GIBCO, Grand Island, NY), 50µM 2-ME, 100µg/ml of streptomycin, 100U/ml of penicillin (Irvine Scientific) and 10% heat-inactivated FCS (Irvine Scientific, Santa Ana, CA).
- [00347] Cell lysates were prepared as follows. Briefly, cells were lysed at a concentration of 10^8 cells/ml in 50 mM Tris-HCl, pH 8.5, containing 1% Nonidet P-40 (Fluka Biochemika, Buchs, Switzerland), 150 mM NaCl, 5 mM EDTA, and 2 mM PMSF. Lysates were cleared of debris and nuclei by centrifugation at 15,000 x g for 30min.
- [00348] HLA molecules were purified from lysates by affinity chromatography. Lysates were passed twice through two pre-columns of inactivated Sepharose CL4-B and protein A-Sepharose. Next, the lysate was passed over a column of Sepharose CL-4B beads coupled to an appropriate antibody. The anti-HLA column was then washed with 10-column volumes of 10mM Tris-HCL, pH 8.0, in 1% NP-40, PBS, 2-column volumes of PBS, and 2-column volumes of PBS containing 0.4% n-octylglucoside. Finally, MHC molecules were eluted with 50mM diethylamine in 0.15M NaCl containing 0.4% n-octylglucoside, pH 11.5. A 1/25 volume of 2.0M Tris, pH 6.8, was added to the eluate to reduce the pH to ~8.0. Eluates were then concentrated by centrifugation in Centriprep 30 concentrators at 2000 rpm (Amicon, Beverly, MA). Protein content was evaluated by a BCA protein assay (Pierce Chemical Co., Rockford, IL) and confirmed by SDS-PAGE.

[00349] A detailed description of the protocol utilized to measure the binding of peptides to Class I and Class II MHC has been published (Sette *et al.*, *Mol. Immunol.* 31:813, 1994; Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998). Briefly, purified MHC molecules (5 to 500nM) were incubated with various unlabeled peptide inhibitors and 1-10nM ¹²⁵I-radiolabeled probe peptides for 48h in PBS containing 0.05% Nonidet P-40 (NP40) (or 20% w/v digitonin for H-2 IA assays) in the presence of a protease inhibitor cocktail. The final concentrations of protease inhibitors (each from CalBioChem, La Jolla, CA) were 1 mM PMSF, 1.3 nM 1.10 phenanthroline, 73 μM pepstatin A, 8mM EDTA, 6mM N-ethylmaleimide (for Class II assays), and 200 μM N alpha-p-tosyl-L-lysine chloromethyl ketone (TLCK). All assays were performed at pH 7.0 with the exception of DRB1*0301, which was performed at pH 4.5, and DRB1*1601 (DR2w21β₁) and DRB4*0101 (DRw53), which were performed at pH 5.0. pH was adjusted as described elsewhere (*see* Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998).

[00350] Following incubation, MHC-peptide complexes were separated from free peptide by gel filtration on 7.8 mm x 15 cm TSK200 columns (TosoHaas 16215, Montgomeryville, PA), eluted at 1.2 mls/min with PBS pH 6.5 containing 0.5% NP40 and 0.1% NaN₃. Because the large size of the radiolabeled peptide used for the DRB1*1501 (DR2w2β₁) assay makes separation of bound from unbound peaks more difficult under these conditions, all DRB1*1501 (DR2w2β₁) assays were performed using a 7.8mm x 30cm TSK2000 column eluted at 0.6 mls/min. The eluate from the TSK columns was passed through a Beckman 170 radioisotope detector, and radioactivity was plotted and integrated using a Hewlett-Packard 3396A integrator, and the fraction of peptide bound was determined.

[00351] Radiolabeled peptides were iodinated using the chloramine-T method. Representative radiolabeled probe peptides utilized in each assay, and its assay specific IC₅₀ nM, are known in the art. Typically, in preliminary experiments, each MHC preparation was titrated in the presence of fixed amounts of radiolabeled peptides to determine the concentration of HLA molecules necessary to bind 10-20% of the total radioactivity. All subsequent inhibition and direct binding assays were performed using these HLA concentrations.

[00352] Since under these conditions [label]<[HLA] and IC₅₀≥[HLA], the measured IC₅₀ values are reasonable approximations of the true K_D values. Peptide inhibitors are

typically tested at concentrations ranging from 120 µg/ml to 1.2 ng/ml, and are tested in two to four completely independent experiments. To allow comparison of the data obtained in different experiments, a relative binding figure is calculated for each peptide by dividing the IC₅₀ of a positive control for inhibition by the IC₅₀ for each tested peptide (typically unlabeled versions of the radiolabeled probe peptide). For inter-experiment comparisons, relative binding values are compiled. These values can subsequently be converted back into IC₅₀ nM values by dividing the IC₅₀ nM of the positive controls for inhibition by the relative binding of the peptide of interest. This method of data compilation has proven to be the most accurate and consistent for comparing peptides that have been tested on different days, or with different lots of purified MHC.

[00353] Because the antibody used for HLA-DR purification (LB3.1) is α-chain specific, β₁ molecules are not separated from β₃ (and/or β₄ and β₅) molecules. The β₁ specificity of the binding assay is obvious in the cases of DRB1*0101 (DR1), DRB1*0802 (DR8w2), and DRB1*0803 (DR8w3), where no β₃ is expressed. It has also been demonstrated for DRB1*0301 (DR3) and DRB3*0101 (DR52a), DRB1*0401 (DR4w4), DRB1*0404 (DR4w14), DRB1*0405 (DR4w15), DRB1*1101 (DR5), DRB1*1201 (DR5w12), DRB1*1302 (DR6w19) and DRB1*0701 (DR7). The problem of β chain specificity for DRB1*1501 (DR2w2β₁), DRB5*0101 (DR2w2β₂), DRB1*1601 (DR2w21β₁), DRB5*0201 (DR51Dw21), and DRB4*0101 (DRw53) assays is circumvented by the use of fibroblasts. Development and validation of assays with regard to DRβ molecule specificity have been described previously (*see, e.g., Southwood et al., J. Immunol.* 160:3363-3373, 1998).

[00354] Binding assays as outlined above may be used to analyze supermotif and/or motif-bearing epitopes.

EXAMPLE 2. RECOGNITION OF VARIANT PEPTIDES BY CTL DERIVED FROM DNA IMMUNIZATION

[00355] Variants corresponding to five HLA-A2 and –A3 restricted epitopes from 167 HIV variant were identified and synthesized. These represented all the complete sequences in the Los Alamos database at the time (116 strains), as well as 51 complete clade C sequences from Botswana, and included 22 subtype B and 62 subtype C sequences. These

peptides were then characterized with regard to MHC binding, variant distribution, and immunogenicity. To measure immunogenicity, HLA-A2/K^b or HLA-A11/K^b transgenic mice were immunized with the epitopes encoded in a DNA based format (). Eleven days after immunization, splenocytes were restimulated with either the epitope corresponding to the epitope encoded by the DNA (parent) or each of the variant peptides. After 6 days in culture, IFN- γ secretion was measured in response to the peptide used to stimulate each culture.

[00356] The data for these epitopes are shown in Figure 1. The HLA-A2-restricted epitope corresponding to the Env 134 epitope (KLTPLCVTL, SEQ ID NO: 9; Figure 1A) used as the immunogen was the form observed most often (134/167). All single anchor variants were recognized to approximately the same extent as the parent peptide. Many of the single non-anchor variants (9/13) were also recognized within 10-fold of the parent peptide. Conservative substitutions (R and Q for K; see Table 4) at position 1 (P1) were tolerated, while the non-conservative substitution (E for K; see Table 4) lowered binding and eliminated recognition. Three P4 variants were observed. Two of these (F or S for P) were recognized within 10-fold of the recognition of the parent peptide, while one substitution (Q for P) completely eliminated recognition. The binding for these peptides was not significantly different from the parent peptide, indicating that this residue may be involved in TCR recognition. Both the conservative (F for L) and non-conservative (R for L) substitutions seen at P5 completely abrogated recognition, indicating that this residue is important in TCR recognition. Finally, one substitution at P8 (I for V), and four substitutions at P9 show little effect on recognition. None of the variants with multiple substitutions were recognized, although this may be due to the poor binding of these peptides.

[00357] The Gag 386 sequence utilized as the immunogen was the second most common form (VLAEAMSQV, SEQ ID NO: 10), present in 54 strains (Figure 1B). The most prevalent variant, differing by a single tolerated C terminal anchor residue (V to A; 67 strains), was recognized equally to the parent epitope by CTL raised against the parent, as were the remaining single-anchor variants. Single substitutions were also tolerated at the non-anchor positions, P1 (I for V) and P8 (R, K, or H for Q). Only the P7 variant (G for S), probably a TCR contact residue, was not recognized.

[00358] Many of the multiple variants for Gag 386 were also recognized by CTL raised against the parent peptide. All the variants with multiple changes combined a change of V to A or T at the C terminus with 1-3 additional substitutions. Two variants with N terminal

changes (V to A or I) were observed. The non-conservative A substitution was not recognized, while the conservative I substitution was. A double variant with a conservative substitution at P3 (A to G) was not recognized, implicating P3 in TCR recognition. Double variants with conservative changes at position 8 (Q to R, K, or H) were not well recognized, although the variants with single changes at the same positions were recognized. The variant combining a non-conservative A residue at position 8 with A at the C terminus was recognized as well as the parent. Equally surprising was the observation that all the variants with 3 or 4 substitutions were recognized within 10-fold of the parent peptide.

[00359] The parent form of the HLA-A2-restricted epitope, Vpr 62 (RILQQLLFI, SEQ ID NO: 11; Figure 1C) was the most common form observed (86/167). Seven well-tolerated single anchor substitutions, 4 P2 and 3 C terminal, were also observed, accounting for most of the remaining variants (47/167). Single substitutions were, in general, also well tolerated. The single exception was the non-conservative substitution (P for L) at P6, while an M for L substitution at the same site was well tolerated. Binding was not affected for either variant, indicating that the reduction in activity is due to a change in a contact residue. Most variants with multiple changes also showed recognition to approximately the same extent as the parent. Several variants however did show reduced recognition. The variant with changes at both anchors (I to T at P2 and I to T at P9) had reduced binding (IC_{50} of 9700), and recognition of the peptide was reduced, although not lost completely. Two variants with Q to H changes at P5, in combination with anchor residue changes (I to M at P2 and I to A at P9), exhibited greatly reduced recognition although binding was not affected. Other changes at P5 (Q to R or L at P5) reduced recognition only slightly.

[00360] The HLA-A3/11-restricted epitope, Pol 98 (Figure 1D), represented the most diverse epitope in terms of the number of variant epitopes identified. The peptide encoded in the DNA was represented in only 18 out of 167 strains. Approximately a third of the peptides identified at that position (49 out of 167) did not have recognizable A3/A11 motifs. The most common variant (30 strains) differed from the parent peptide at 3 residues (VSIKVGQIK, SEQ ID NO: 12), but was recognized within 10-fold of the parent peptide. Two variants with conservative changes at anchor residues were both recognized, although the T to A substitution at P2 resulted in a 10-fold reduction in recognition of the variant peptide. All peptides with single changes in non-anchor positions were also recognized, although the P5 variant (G to E) exhibited a decrease in

recognition. As the binding was not affected, this probably indicates involvement in T cell recognition.

[00361] Peptides with two changes showed mixed results. In general, peptides with a V substitution at position 3, in combination with another substitution were recognized to the same extent as the corresponding single substitution, indicating the V substitution was tolerated well and is not a TCR contact residue. Combinations including the P2 anchor residue (T to A or N) were not recognized, although the binding of these peptides was also low. Variants with 3 substitutions were generally not recognized well. Two exceptions with very conservative substitutions were noted (Figure 1D). CTL were unable to recognize peptides with four or more substitutions.

[00362] The HLA-A3/11- restricted Env 47 epitope (Figure 1E; VTVYYGVPVWK, SEQ ID NO: 13) was highly conserved, with only 9 variants identified. The most common form observed was the parent peptide (99 strains), while the second most common form, a single anchor substitution observed in 40 strains, was recognized to the same extent as the parent. All the variants were recognized within 10-fold of the parent epitope.

[00363] Taken together, these data show trends towards promiscuous recognition of variant peptides by CTL generated from immunization with a single peptide. In general, changes that disrupted binding also decreased recognition. Recognition was also affected by the position of the change, with potential TCR contact residues (P3-7) exerting a greater effect on recognition than other residues. In general, conservative residue changes were more widely tolerated than were non-conservative changes. Recognition was also dependent on the number of changes, with progressively lower recognition with a greater number of changes.

[00364] **Recognition after multiple restimulations** The observed recognition of variant peptides by CTL raised against the parent peptide might be due to either promiscuous recognition at the level of a single TCR or simply a mixture of TCRs against the immunizing peptide which are each able to recognize subtly different peptides. To distinguish between these two possibilities, Env 134- or Gag 386-specific T cell lines were generated by stimulating five times with the immunizing peptide, and then tested for recognition of a partial panel of variant peptides. These T cell lines were also characterized for V β TCR usage against a panel of antibodies predicted to react with the TCR of the mouse strains utilized for these experiments.

[00365] The data for these peptide-specific lines are shown in Table 5. Because the SU is a measure of the number of cells needed to secrete a defined amount of IFN- γ , a higher SU value would correspond to an enrichment of IFN- γ producing cells. A comparison of one and five peptide stimulations indeed shows an enrichment of CTL specific for the immunizing peptide for both of the peptide lines generated (Table 5A and 5B, first line). The Gag 386 line (Table 5A) also demonstrated increased recognition of all the variant peptides measured except one peptide (ILAEAMSKA, SEQ ID NO: 14) that was never recognized. The Env 134 line also demonstrated enrichment for CTL able to recognize several of the variant peptides (Table 5B).

[00366] To further characterize these lines, we examined them for V β usage, utilizing a panel of commercially available antibodies available for mouse TCR V β 2-14. To determine background levels for the various TCR V β molecules, primary splenocytes from mice that had been immunized with EP HIV-1090 were also examined. The results for the Gag 386 line are shown in Figure 2A. After a single stimulation with the parent peptide, the Gag 386 line showed a mixture of TCR positive populations, including V β 3, 5, and 14. After 5 stimulations, those populations had been reduced to background levels, and approximately 50% of the CD8⁺ cells expressed the V β 6 TCR. The Env 134 line showed a similar pattern of multiple TCR positive populations after a single round of stimulation with reduction to background levels after 5 stimulations (data not shown). However, no single V β usage significantly above background could be demonstrated, probably due to lack of the relevant TCR V β antibody.

[00367] Both lines were also characterized with regard to the affinity of certain of the variant peptides by titrating the variant peptides examined above (Table 5A and 5B). The data for both the Gag 386 and Env 134 lines are shown in Figure 2B. For the Gag 386 line, the parent peptide along with two single anchor variants (VLAEAMSQI, SEQ ID NO: 15, and VLAEAMSQA, SEQ ID NO: 16) showed the highest affinity. Four other peptides demonstrated lower affinity, but still produced IFN- γ in response to higher peptide concentrations. A single peptide (ILAEAMSKA, SEQ ID NO: 14) was not recognized.

[00368] As expected, the parent peptide, which was used to generate the Env 134 line, showed the highest affinity for the TCR. The other 2 variant peptides, KITPLCVTL (SEQ ID NO: 18) and QLTPLCVTL (SEQ ID NO: 19), also demonstrated higher affinity, but reduced from the parent peptide by approximately 10-fold and 100-fold, respectively. It was notable that only at the highest peptide concentration examined (1 μ g/ml) was any IFN- γ secretion detected for five of the peptides (QITPLCVTL, SEQ ID NO: 20,

ELTPLCVTL, SEQ ID NO: 21, KLTPFCVTL, SEQ ID NO: 22, KLTPLCVIL, SEQ ID NO: 23, and KLTPLCVPL, SEQ ID NO: 24). These five peptides showed little or no enrichment of CTL able to recognize them, and exhibited the lowest activity as measured by SU after five restimulations (see Table 5B).

[00369] In summary, these cell lines seem to consist of a narrow, possibly single, TCR population. This TCR population recognizes the parent peptide with the highest affinity, but is also able to recognize a number of other variant peptides with equal or lesser affinity.

[00370] **Recognition of variant peptides by CTL derived from an HIV infected patient.**

[00371] To determine if the same immunological conservation was observed in natural infections, we identified an HIV-infected individual expressing the HLA-A3 allele. The HIV strain and subtype with which this patient was infected is unknown. We had previously shown that T cells from this individual responded to the HLA-A3 restricted epitopes Pol 98 and Env 47. PBL from this patient were examined in an ELISPOT assay to determine if they also showed the capacity for broad cross-reactivity. The data are shown in Figure 3. Although the actual peptide represented in the HIV strain with which this individual is infected is unknown, we observed recognition of a large number of the variant peptides for both Pol 98 (Figure 3A) and Env 47 (Figure 3B). The recognition patterns were remarkably similar for the mouse and patient data (compare Figure 1 and Figure 3), although the mouse expressed a transgene for HLA-A11 and the patient was HLA-A3.

[00372] **Prediction of Immunological Conservation.** We had observed that the variant peptides that were recognized by CTL raised against the parent epitope had amino acid substitutions that followed previous observations. For example, the anchor residue changes that were tolerated in the variant peptides were also described as anchors that to define the respective HLA supertypes (). In general, conservative substitutions were tolerated at non-anchor residues, while non-conservative substitutions were less well tolerated. These followed closely the prediction model used to identify heteroclitic analogs (Tangri et al).

[00373] Based on these observations, we designed a computer program to predict immunological conservation. For anchor positions, this program utilized the conserved anchor residues described for the A2, A3, and B7 supertypes. For non-anchor positions only conservative substitutions, as defined in Tangri et.al. (), were allowed. All

substitutions at non-anchor positions were analyzed independently and all conservative substitutions were allowed regardless of the number of substitutions. Finally, the position of the substitution was not factored into analysis. Each variant was compared with the parent epitope, and its ability to be recognized was predicted as either positive or negative.

[00374] The first sets of epitopes to be evaluated by this program were the five HIV epitopes and variants previously described. For the Env 134 epitope, the program predicted that 13 of the variant peptides should be immunologically conserved, while 6 should not be recognized. Comparison of the observed immunological data with the prediction showed that the program predicted correctly for 14 of the peptides and incorrectly for 5. Of the incorrect predictions, in two cases the program predicted negative results for peptides that were recognized, while in 3 cases the program predicted positive results for peptides that were not recognized. A similar analysis was performed for all five peptides. Of 101 total variant peptides, 68 were correctly identified (67%). The discordant data were fairly evenly split between peptides incorrectly predicted negative (15) and those incorrectly predicted positive (18).

[00375] As noted previously, the more substitutions present in a variant peptide, the lower the likelihood of its immunogenicity. Since the prediction program treated all substitutions independently, and did not take into account the number of substitutions, we hypothesized that prediction of single substitutions would be more accurate. Indeed, the immunogenicity of 38 of 47 single substitution variants (80%) was correctly predicted.

[00376] With the limitations of the program in mind, it is useful to predict the recognition of the variants for a package of HLA-A2, -A3, and -B7 supertype epitopes. These epitopes had been identified as being well conserved in Clade B variants. When comparing the conservation of this group of epitopes based on sequence identity versus immunological conservation, it is interesting to note that the predicted recognition gains taking into account immunological conservation are significant (Table 6).

[00377] This particular group of 21 epitopes was selected based on their identity conservation in Clade B HIV sequences, with conservation across HIV clades as a secondary consideration. Because of this criteria, the form of epitope chosen as the parent peptide was not the most common variant (e.g. Gag 386, Gag 271, Pol 98). In some cases (e.g., see Gag 386 data), the “parent” epitope and the most common variant were recognized to the same extent. However, in some cases the selection of epitope to include as the “parent” epitope was predicted to make a difference in the immunological conservation. An example of this was the Gag 271 epitope (Figure 4). The variant most

commonly seen in clade B sequences was the MTNNPPIPV form (SEQ ID NO: 25), while the most common form of the epitope was MTSNPPIPV (SEQ ID NO: 26). Not all amino acids are considered equal to each other in their ability to substitute (Tangri). For example, asparagine (N) is considered a conservative substitution for serine (S), while the opposite substitution is only considered semi-conserved. When the program calculated immunological conservation using the MTNNPPIPV peptide (SEQ ID NO: 25) as the parent peptide, only two variants were predicted to be immunogenic. However, when the immunological conservation was predicted using the MTSNPPIPV peptide (SEQ ID NO: 26), most of the variants were predicted to be recognized (Figure 4). This prediction was tested using HLA-A2 transgenic mice. The results show that if the MTSNPPIPV form (SEQ ID NO: 26) of the peptide was utilized in vaccines, approximately 152 of 167 variants would be recognized, while if the MTNNPPIPV form (SEQ ID NO: 25) of the epitope was utilized, only 39 of 167 variants would be recognized. This has important implications in epitope selection for vaccine development, and epitope performance can be predicted.

EXAMPLE 3. A PADRE® MOLECULE AS A HELPER EPITOPE FOR ENHANCEMENT OF CTL INDUCTION

[00378] There is increasing evidence that HTL activity is critical for the induction of long-lasting CTL responses (Livingston *et al. J. Immunol* 162:3088-3095 (1999); Walter *et al., New Engl. J. Med.* 333:1038-1044 (1995); Hu *et al., J. Exp. Med.* 177:1681-1690 (1993)). Therefore, one or more peptides that bind to HLA class II molecules and stimulate HTLs can be used in accordance with the invention. Accordingly, a preferred embodiment of a vaccine includes a molecule from the PADRE® family of universal T helper cell epitopes (HTL) that target most DR molecules in a manner designed to stimulate helper T cells. For instance, a pan-DR-binding epitope peptide having the formula: aKXVAAZTLKAAa, where "X" is either cyclohexylalanine, phenylalanine, or tyrosine; "Z" is either tryptophan, tyrosine, histidine or asparagine; and "a" is either D-alanine or L-alanine (SEQ ID NO:29), has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type.

[00379] A particularly preferred PADRE® molecule is a synthetic peptide, aKXVAAWTLKAAa SEQ ID NO: 28 (a = D-alanine, X = cyclohexylalanine), containing

non-natural amino acids, specifically engineered to maximize both HLA-DR binding capacity and induction of T cell immune responses.

[00380] Alternative preferred PADRE[®] molecules are the peptides, aKFVAAWTLKAAa (SEQ ID NO: 29), aKYVAAWTLKAAa (SEQ ID NO: 30), aKFVAAWTLKAAa (SEQ ID NO: 31), aKXVAAWTLKAAa (SEQ ID NO: 32), aKYVAAWTLKAAa (SEQ ID NO: 33), aKFVAAHTLKAAa (SEQ ID NO: 34), aKXVAAHTLKAAa (SEQ ID NO: 35), aKYVAAHTLKAAa (SEQ ID NO: 36), aKFVAAANTLKAAa (SEQ ID NO: 37), aKXVAAANTLKAAa (SEQ ID NO: 38), aKYVAAANTLKAAa (SEQ ID NO: 39), AKXVAAWTLKAAA (SEQ ID NO: 40), AKFVAAWTLKAAA (SEQ ID NO: 41), AKYVAAWTLKAAA (SEQ ID NO: 42), AKFVAAWTLKAAA (SEQ ID NO: 43), AKXVAAWTLKAAA (SEQ ID NO: 44), AKYVAAWTLKAAA (SEQ ID NO: 45), AKFVAAHTLKAAA (SEQ ID NO: 46), AKXVAAHTLKAAA (SEQ ID NO: 47), AKYVAAHTLKAAA (SEQ ID NO: 48), AKFVAAANTLKAAA (SEQ ID NO: 49), AKXVAAANTLKAAA (SEQ ID NO: 50), AKYVAAANTLKAAA (SEQ ID NO: 51) (a = D-alanine, X = cyclohexylalanine).

[00381] In a preferred embodiment, the PADRE[®] peptide is amidated. For example, a particularly preferred amidated embodiment of a PADRE[®] molecule is conventionally written aKXVAAWTLKAAa-NH₂.

[00382] Competitive inhibition assays with purified HLA-DR molecules demonstrated that the PADRE[®] molecule aKXVAAWTLKAAa-NH₂ binds with high or intermediate affinity (IC₅₀ ≤ 1,000 nM) to 15 out of 16 of the most prevalent HLA-DR molecules ((Kawashima *et al.*, *Human Immunology* 59:1-14 (1998); Alexander *et al.*, *Immunity* 1:751-761 (1994)). A comparison of the DR binding capacity of PADRE[®] and tetanus toxoid (TT) peptide 830-843, a "universal" epitope has been published (Panina-Bordignon *et al.*, *Eur. J. Immunology* 19:2237-2242 (1989)). The TT 830-843 peptide bound to only seven of 16 DR molecules tested, while PADRE[®] bound 15 of 16. At least 1 of the 15 DR molecules that bind PADRE[®] is predicted to be present in >95% of all humans. Therefore, this PADRE[®] molecule is anticipated to induce an HTL response in virtually all patients, despite the extensive polymorphism of HLA-DR molecules in the human population.

[00383] PADRE[®] has been specifically engineered for optimal immunogenicity for human T cells. Representative data from *in vitro* primary immunizations of normal human T cells with TT 830-843 antigen and the PADRE[®] molecule aKXVAAWTLKAAa-NH₂ are

shown in Figure 1. Peripheral blood mononuclear cells (PBMC) from three normal donors were stimulated with the peptides *in vitro*. Following the third round of stimulation, it was observed that PADRE[®] generated significant primary T cell responses for all three donors as measured in a standard T cell proliferation assay. With the PADRE[®] peptide, the 10,000 cpm proliferation level was generally reached with 10 to 100 ng/ml of antigen. In contrast, TT 830-843 antigen generated responses for only 2 out of 3 of the individuals tested. Responses approaching the 10,000 cpm range were reached with about 10,000 ng/ml of antigen. In this respect, it was noted that PADRE[®] was, on a molar basis, about 100-fold more potent than TT 830-843 antigen for activation of T cell responses.

[00384] Early data from a phase I/II investigator-sponsored trial, conducted at the University of Leiden (C.J.M. Melief), support the principle that the PADRE[®] molecule aKXVAAWTLKAAa (SEQ ID NO: 28), possibly the amidated aKXVAAWTLKAAa - NH₂, is highly immunogenic in humans (Ressing *et al.*, J. Immunother. 23(2):255-66 (2000)). In this trial, a PADRE[®] molecule was co-emulsified with various human papilloma virus (HPV)-derived CTL epitopes and was injected into patients with recurrent or residual cervical carcinoma. However, because of the late stage of carcinoma with the study patients, it was expected that these patients were immunocompromised. The patients' immunocompromised status was demonstrated by their low frequency of influenza virus-specific CTL, reduced levels of CD3 expression, and low incidence of proliferative recall responses after *in vitro* stimulation with conventional antigens. Thus, no efficacy was anticipated in the University of Leiden trial, rather the goal of that trial was essentially to evaluate safety. Safety was, in fact, demonstrated. In addition to a favorable safety profile, PADRE[®] T cell reactivity was detected in four of 12 patients (Figure 2) in spite of the reduced immune competence of these patients.

[00385] Thus, the PADRE[®] peptide component(s) of the vaccine bind with broad specificity to multiple allelic forms of HLA-DR molecules. Moreover, PADRE[®] peptide component(s) bind with high affinity ($IC_{50} \leq 1000$ nM), i.e., at a level of affinity correlated with being immunogenic for HLA Class II restricted T cells. The *in vivo* administration of PADRE[®] peptide(s) stimulates the proliferation of HTL in normal humans as well as patient populations.

[00386] One or more PADRE[®] peptide(s) may be included in a composition, e.g., a vaccine, comprising one or more peptides, either as an individual peptide(s), fused to one or more variant peptides, or both.

EXAMPLE 4. CTL RECOGNITION OF ENDOGENOUS PROCESSED ANTIGENS AFTER PRIMING

- [00387] This example determines that CTL induced by native or analoged peptide epitopes recognize endogenously synthesized, *i.e.*, native antigens.
- [00388] Effector cells isolated from transgenic mice that are immunized with peptide epitopes are re-stimulated *in vitro* using peptide-coated stimulator cells. Six days later, effector cells are assayed for cytotoxicity and the cell lines that contain peptide-specific cytotoxic activity are further re-stimulated. An additional six days later, these cell lines are tested for cytotoxic activity on ^{51}Cr labeled Jurkat-A2.1/K^b target cells in the absence or presence of peptide, and also tested on ^{51}Cr labeled target cells bearing the endogenously synthesized antigen, *i.e.* cells that are stably transfected with HIV expression vectors.
- [00389] The result will demonstrate that CTL lines obtained from animals primed with peptide epitope recognize endogenously synthesized HIV antigen. The choice of transgenic mouse model to be used for such an analysis depends upon the epitope(s) that is being evaluated. In addition to HLA-A*0201/K^b transgenic mice, several other transgenic mouse models including mice with human A11, which may also be used to evaluate A3 epitopes, and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed, which may be used to evaluate HTL epitopes.

EXAMPLE 5. ACTIVITY OF CTL-HTL CONJUGATED EPITOPES IN TRANSGENIC MICE

- [00390] This example illustrates the induction of CTLs and HTLs in transgenic mice by use of a HIV CTL/HTL peptide conjugate whereby the vaccine composition comprises peptides administered to an HIV-infected patient or an individual at risk for HIV. The peptide composition can comprise multiple CTL and/or HTL epitopes. This analysis demonstrates enhanced immunogenicity that can be achieved by inclusion of one or more HTL epitopes in a vaccine composition. Such a peptide composition can comprise an HTL epitope conjugated to a preferred CTL epitope containing, for example, at least one CTL epitope, or an analog of that epitope. The peptides may be lipidated, if desired.

- [00391] Immunization procedures: Immunization of transgenic mice is performed as described (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997). For example, A2/K^b mice, which are transgenic for the human HLA A2.1 allele and are useful for the assessment of the immunogenicity of HLA-A*0201 motif- or HLA-A2 supermotif-bearing epitopes, are primed subcutaneously (base of the tail) with a 0.1 ml of peptide in Incomplete Freund's Adjuvant, or if the peptide composition is a lipidated CTL/HTL conjugate, in DMSO/saline or if the peptide composition is a polypeptide, in PBS or Incomplete Freund's Adjuvant. Seven days after priming, splenocytes obtained from these animals are restimulated with syngenic irradiated LPS-activated lymphoblasts coated with peptide.
- [00392] Cell lines: Target cells for peptide-specific cytotoxicity assays are Jurkat cells transfected with the HLA-A2.1/K^b chimeric gene (*e.g.*, Vitiello *et al.*, *J. Exp. Med.* 173:1007, 1991).
- [00393] *In vitro* CTL activation: One week after priming, spleen cells (30×10^6 cells/flask) are co-cultured at 37°C with syngeneic, irradiated (3000 rads), peptide coated lymphoblasts (10×10^6 cells/flask) in 10 ml of culture medium/T25 flask. After six days, effector cells are harvested and assayed for cytotoxic activity.
- [00394] Assay for cytotoxic activity: Target cells (1.0 to 1.5×10^6) are incubated at 37°C in the presence of 200 μ l of ^{51}Cr . After 60 minutes, cells are washed three times and resuspended in R10 medium. Peptide is added where required at a concentration of 1 $\mu\text{g/ml}$. For the assay, 10^4 ^{51}Cr -labeled target cells are added to different concentrations of effector cells (final volume of 200 μ l) in U-bottom 96-well plates. After a 6 hour incubation period at 37°C, a 0.1 ml aliquot of supernatant is removed from each well and radioactivity is determined in a Micromedic automatic gamma counter. The percent specific lysis is determined by the formula: percent specific release = $100 \times (\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})$. To facilitate comparison between separate CTL assays run under the same conditions, % ^{51}Cr release data is expressed as lytic units/ 10^6 cells. One lytic unit is arbitrarily defined as the number of effector cells required to achieve 30% lysis of 10,000 target cells in a 6 hour ^{51}Cr release assay. To obtain specific lytic units/ 10^6 , the lytic units/ 10^6 obtained in the absence of peptide is subtracted from the lytic units/ 10^6 obtained in the presence of peptide. For example, if 30% ^{51}Cr release is obtained at the effector (E): target (T) ratio of 50:1 (*i.e.*, 5×10^5 effector cells for 10,000 targets) in the absence of peptide and 5:1 (*i.e.*, 5×10^4

effector cells for 10,000 targets) in the presence of peptide, the specific lytic units would be: $[(1/50,000)-(1/500,000)] \times 10^6 = 18 \text{ LU}$.

[00395] The results are analyzed to assess the magnitude of the CTL responses of animals injected with the immunogenic CTL/HTL conjugate vaccine preparation and are compared to the magnitude of the CTL response achieved using the CTL epitope as outlined in above. Analyses similar to this may be performed to evaluate the immunogenicity of peptide conjugates containing multiple CTL epitopes and/or multiple HTL epitopes. In accordance with these procedures it is found that a CTL response is induced, and concomitantly that an HTL response is induced upon administration of such compositions.

EXAMPLE 6. SELECTION OF CTL AND HTL EPITOPES FOR INCLUSION IN AN HIV-SPECIFIC VACCINE.

[00396] This example illustrates the procedure for the selection of peptide epitopes for vaccine compositions of the invention. The peptides in the composition can be in the form of a nucleic acid sequence, either single or one or more sequences (*i.e.*, minigene) that encodes peptide(s), or can be single and/or polypeptidic peptides.

[00397] The following principles are utilized when selecting an array of epitopes for inclusion in a vaccine composition. Each of the following principles is balanced in order to make the selection.

[00398] Epitopes are selected which, upon administration, mimic immune responses that correlate with virus clearance. For example, if it has been observed that patients who clear HIV generate an immune response to at least 3 epitopes on at least one HIV antigen, then 3-4 epitopes should be included for HLA class I. A similar rationale is used to determine HLA class II epitopes.

[00399] When selecting an array of HIV epitopes, it is preferred that at least some of the epitopes are derived from early and late proteins. The early proteins of HIV are expressed when the virus is replicating, either following acute or dormant infection. Therefore, it is particularly preferred to use epitopes from early stage proteins to alleviate disease manifestations at the earliest stage possible.

[00400] Epitopes are often selected that have a binding affinity of an IC_{50} of 500 nM or less for an HLA class I molecule, or for class II, an IC_{50} of 1000 nM or less.

- [00401] Sufficient supermotif bearing peptides, or a sufficient array of allele-specific motif bearing peptides, are selected to give broad population coverage. For example, epitopes are selected to provide at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess breadth, or redundancy, of population coverage.
- [00402] When creating a polyepitopic compositions, *e.g.* a minigene, it is typically desirable to generate the smallest peptide possible that encompasses the epitopes of interest. The principles employed are similar, if not the same, as those employed when selecting a peptide comprising nested epitopes.
- [00403] In cases where the sequences of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide be conserved in a designated percentage of the sequences evaluated for a specific protein antigen.
- [00404] Peptide epitopes for inclusion in vaccine compositions are, for example, selected from those listed in Tables 6-9 or Figures 1A-4. A vaccine composition comprised of selected peptides, when administered, is safe, efficacious, and elicits an immune response similar in magnitude of an immune response that clears an acute HIV infection.

EXAMPLE 7. CONSTRUCTION OF MINIGENE MULTI-EPITOPE DNA PLASMIDS

- [00405] This example provides general guidance for the construction of a minigene expression plasmid. Minigene plasmids may, of course, contain various configurations of CTL and/or HTL epitopes or epitope analogs as described herein. Expression plasmids have been constructed and evaluated as described, for example, in co-pending U.S.S.N. 09/311,784 filed 5/13/99 and in Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999. An example of such a plasmid for the expression of HIV epitopes is shown in Figure 2, which illustrates the orientation of HIV peptide epitopes in a minigene construct.
- [00406] A minigene expression plasmid typically includes multiple CTL and HTL peptide epitopes. In the present example, HLA-A2, -A3, -B7 supermotif-bearing peptide epitopes and HLA-A1 and -A24 motif-bearing peptide epitopes are used in conjunction with DR supermotif-bearing epitopes and/or DR3 epitopes (Figure 2). Preferred epitopes are identified, for example, in Tables 6-9 and Figures 1A-4. HLA class I supermotif or motif-

bearing peptide epitopes derived from multiple HIV antigens, are selected such that multiple supermotifs/motifs are represented to ensure broad population coverage. Similarly, HLA class II epitopes are selected from multiple HIV antigens to provide broad population coverage, *i.e.* both HLA DR-1-4-7 supermotif-bearing epitopes and HLA DR-3 motif-bearing epitopes are selected for inclusion in the minigene construct. The selected CTL and HTL epitopes are then incorporated into a minigene for expression in an expression vector.

[00407] Such a construct may additionally include sequences that direct the HTL epitopes to the endoplasmic reticulum. For example, the Ii protein may be fused to one or more HTL epitopes as described in co-pending application U.S.S.N. 09/311,784 filed 5/13/99, wherein the CLIP sequence of the Ii protein is removed and replaced with an HLA class II epitope sequence so that HLA class II epitope is directed to the endoplasmic reticulum, where the epitope binds to an HLA class II molecules.

[00408] This example illustrates the methods to be used for construction of a minigene-bearing expression plasmid. Other expression vectors that may be used for minigene compositions are available and known to those of skill in the art.

[00409] The minigene DNA plasmid contains a consensus Kozak sequence and a consensus murine kappa Ig-light chain signal sequence followed by CTL and/or HTL epitopes selected in accordance with principles disclosed herein. The construct can also include, for example, The sequence encodes an open reading frame fused to the Myc and His antibody epitope tag coded for by the pcDNA 3.1 Myc-His vector.

[00410] Overlapping oligonucleotides, for example eight oligonucleotides, averaging approximately 70 nucleotides in length with 15 nucleotide overlaps, are synthesized and HPLC-purified. The oligonucleotides encode the selected peptide epitopes as well as appropriate linker nucleotides, Kozak sequence, and signal sequence. The final multi-epitope minigene is assembled by extending the overlapping oligonucleotides in three sets of reactions using PCR. A Perkin/Elmer 9600 PCR machine is used and a total of 30 cycles are performed using the following conditions: 95°C for 15 sec, annealing temperature (5° below the lowest calculated T_m of each primer pair) for 30 sec, and 72°C for 1 min.

[00411] For the first PCR reaction, 5 µg of each of two oligonucleotides are annealed and extended: Oligonucleotides 1+2, 3+4, 5+6, and 7+8 are combined in 100 µl reactions containing *Pfu* polymerase buffer (1x= 10 mM KCL, 10 mM (NH₄)₂SO₄, 20 mM Tris-chloride, pH 8.75, 2 mM MgSO₄, 0.1% Triton X-100, 100 µg/ml BSA), 0.25 mM each

dNTP, and 2.5 U of *Pfu* polymerase. The full-length dimer products are gel-purified, and two reactions containing the product of 1+2 and 3+4, and the product of 5+6 and 7+8 are mixed, annealed, and extended for 10 cycles. Half of the two reactions are then mixed, and 5 cycles of annealing and extension carried out before flanking primers are added to amplify the full length product for 25 additional cycles. The full-length product is gel-purified and cloned into pCR-blunt (Invitrogen) and individual clones are screened by sequencing.

EXAMPLE 8. THE PLASMID CONSTRUCT AND THE DEGREE TO WHICH IT INDUCES IMMUNOGENICITY.

[00412] The degree to which a plasmid construct, for example a plasmid constructed in accordance as above is able to induce immunogenicity can be evaluated *in vitro* by testing for epitope presentation by APC following transduction or transfection of the APC with an epitope-expressing nucleic acid construct. Such a study determines “antigenicity” and allows the use of human APC. The assay determines the ability of the epitope to be presented by the APC in a context that is recognized by a T cell by quantifying the density of epitope-HLA class I complexes on the cell surface. Quantitation can be performed by directly measuring the amount of peptide eluted from the APC (*see, e.g.,* Sijts *et al.*, *J. Immunol.* 156:683-692, 1996; Demotz *et al.*, *Nature* 342:682-684, 1989); or the number of peptide-HLA class I complexes can be estimated by measuring the amount of lysis or lymphokine release induced by infected or transfected target cells, and then determining the concentration of peptide necessary to obtained equivalent levels of lysis or lymphokine release (*see, e.g.,* Kageyama *et al.*, *J. Immunol.* 154:567-576, 1995).

[00413] Alternatively, immunogenicity can be evaluated through *in vivo* injections into mice and subsequent *in vitro* assessment of CTL and HTL activity, which are analysed using cytotoxicity and proliferation assays, respectively, as detailed *e.g.,* in copending U.S.S.N. 09/311,784 filed 5/13/99 and Alexander *et al.*, *Immunity* 1:751-761, 1994.

[00414] For example, to assess the capacity of a DNA minigene construct (*e.g.,* a pMin minigene construct generated as described in U.S.S.N. 09/311,784) containing at least one HLA-A2 supermotif peptide to induce CTLs *in vivo*, HLA-A2.1/K^b transgenic mice, for example, are immunized intramuscularly with 100 µg of naked cDNA. As a means of comparing the level of CTLs induced by cDNA immunization, a control group of animals

is also immunized with an actual peptide composition that comprises multiple epitopes synthesized as a single polypeptide as they would be encoded by the minigene.

[00415] Splenocytes from immunized animals are stimulated twice with each of the respective compositions (peptide epitopes encoded in the minigene or the polyepitopic peptide), then assayed for peptide-specific cytotoxic activity in a ^{51}Cr release assay. The results indicate the magnitude of the CTL response directed against the A2-restricted epitope, thus indicating the *in vivo* immunogenicity of the minigene vaccine and polyepitopic vaccine. It is, therefore, found that the minigene elicits immune responses directed toward the HLA-A2 supermotif peptide epitopes as does the polyepitopic peptide vaccine. A similar analysis is also performed using other HLA-A3 and HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 and HLA-B7 motif or supermotif epitopes.

[00416] To assess the capacity of a class II epitope encoding minigene to induce HTLs *in vivo*, DR transgenic mice, or for those epitope that cross react with the appropriate mouse MHC molecule, I-A^b-restricted mice, for example, are immunized intramuscularly with 100 µg of plasmid DNA. As a means of comparing the level of HTLs induced by DNA immunization, a group of control animals is also immunized with an actual peptide composition emulsified in complete Freund's adjuvant. CD4⁺ T cells, *i.e.* HTLs, are purified from splenocytes of immunized animals and stimulated with each of the respective compositions (peptides encoded in the minigene). The HTL response is measured using a ^3H -thymidine incorporation proliferation assay, (*see, e.g.*, Alexander et al. *Immunity* 1:751-761, 1994). The results indicate the magnitude of the HTL response, thus demonstrating the *in vivo* immunogenicity of the minigene.

[00417] DNA minigenes, constructed as described above or below, may also be evaluated as a vaccine in combination with a boosting agent using a prime boost protocol. The boosting agent can consist of recombinant protein (*e.g.*, Barnett *et al.*, *Aids Res. and Human Retroviruses* 14, Supplement 3:S299-S309, 1998) or recombinant vaccinia, for example, expressing a minigene or DNA encoding the complete protein of interest (*see, e.g.*, Hanke *et al.*, *Vaccine* 16:439-445, 1998; Sedegah *et al.*, *Proc. Natl. Acad. Sci USA* 95:7648-53, 1998; Hanke and McMichael, *Immunol. Letters* 66:177-181, 1999; and Robinson *et al.*, *Nature Med.* 5:526-34, 1999).

[00418] For example, the efficacy of the DNA minigene used in a prime boost protocol is initially evaluated in transgenic mice. In this example, A2.1/K^b transgenic mice are

immunized IM with 100 µg of a DNA minigene encoding the immunogenic peptides including at least one HLA-A2 supermotif-bearing peptide. After an incubation period (ranging from 3-9 weeks), the mice are boosted IP with 10^7 pfu/mouse of a recombinant vaccinia virus expressing the same sequence encoded by the DNA minigene. Control mice are immunized with 100 µg of DNA or recombinant vaccinia without the minigene sequence, or with DNA encoding the minigene, but without the vaccinia boost. After an additional incubation period of two weeks, splenocytes from the mice are immediately assayed for peptide-specific activity in an ELISPOT assay. Additionally, splenocytes are stimulated *in vitro* with the A2-restricted peptide epitopes encoded in the minigene and recombinant vaccinia, then assayed for peptide-specific activity in an IFN-γ ELISA.

[00419] It is found that the minigene utilized in a prime-boost protocol elicits greater immune responses toward the HLA-A2 supermotif peptides than with DNA alone. Such an analysis can also be performed using HLA-A11 or HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 or HLA-B7 motif or supermotif epitopes.

[00420] The use of prime boost protocols in humans is described in below.

EXAMPLE 9. PEPTIDE COMPOSITION FOR PROPHYLACTIC USES

[00421] Vaccine compositions of the present invention can be used to prevent HIV infection in persons who are at risk for such infection. For example, a polypeptidic peptide epitope composition (or a nucleic acid comprising the same) containing multiple CTL and HTL epitopes, which are also selected to target greater than 80% of the population, is administered to individuals at risk for HIV infection.

[00422] For example, a peptide-based composition can be provided as a single polypeptide that encompasses multiple epitopes. The vaccine is typically administered in a physiological solution that comprises an adjuvant, such as Incomplete Freund's Adjuvant. The dose of peptide for the initial immunization is from about 1 to about 50,000 µg, generally 100-5,000 µg, for a 70 kg patient. The initial administration of vaccine is followed by booster dosages at 4 weeks followed by evaluation of the magnitude of the immune response in the patient, by techniques that determine the presence of epitope-specific CTL populations in a PBMC sample. Additional booster doses are administered as required. The composition is found to be both safe and efficacious as a prophylaxis against HIV infection.

[00423] Alternatively, a composition typically comprising transfecting agents can be used for the administration of a nucleic acid-based vaccine in accordance with methodologies known in the art and disclosed herein.

EXAMPLE 10. POLYEPITOPIC VACCINE COMPOSITIONS DERIVED FROM NATIVE HIV SEQUENCES

[00424] A native HIV polyprotein sequence is screened, preferably using computer algorithms defined for each class I and/or class II supermotif or motif, to identify “relatively short” regions of the polyprotein that comprise multiple epitopes and is preferably less in length than an entire native antigen. This relatively short sequence that contains multiple distinct, even overlapping, epitopes is selected and used to generate a minigene construct. The construct is engineered to express the peptide, which corresponds to the native protein sequence. The “relatively short” peptide is generally less than 250 amino acids in length, often less than 100 amino acids in length, preferably less than 75 amino acids in length, and more preferably less than 50 amino acids in length. The protein sequence of the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. As noted herein, epitope motifs may be nested or overlapping, for example, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Such a vaccine composition is administered for therapeutic or prophylactic purposes.

[00425] The vaccine composition will preferably include, for example, three CTL epitopes and at least one HTL epitope from HIV. This polyepitopic native sequence is administered either as a peptide or as a nucleic acid sequence which encodes the peptide. Alternatively, an analog can be made of this native sequence, whereby one or more of the epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity properties of the polyepitopic peptide.

[00426] The embodiment of this example provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune response-inducing vaccine compositions. Additionally such an embodiment provides for the possibility of motif-bearing epitopes for an HLA makeup that is presently unknown. Furthermore, this embodiment (absent analogs) directs the immune response to multiple

peptide sequences that are actually present in native HIV antigens thus avoiding the need to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing nucleic acid vaccine compositions.

[00427] Related to this embodiment, computer programs can be derived in accordance with principles in the art, which identify in a target sequence, the greatest number of epitopes per sequence length.

EXAMPLE 11. POLYEPITOPIC VACCINE COMPOSITIONS DIRECTED TO MULTIPLE DISEASES

[00428] The HIV peptide epitopes of the present invention are used in conjunction with peptide epitopes from target antigens related to one or more other diseases, to create a vaccine composition that is useful for the prevention or treatment of HIV as well as the one or more other disease(s). Examples of the other diseases include, but are not limited to, HCV and HBV.

[00429] For example, a polyepitopic peptide composition comprising multiple CTL and HTL epitopes that target greater than 98% of the population may be created for administration to individuals at risk for both HBV and HIV infection. The composition can be provided as a single polypeptide that incorporates the multiple epitopes from the various disease-associated sources, or can be administered as a composition comprising one or more discrete epitopes.

EXAMPLE 12. USE OF PEPTIDES TO EVALUATE AN IMMUNE RESPONSE

[00430] Peptides of the invention may be used to analyze an immune response for the presence of specific CTL or HTL populations directed to HIV. Such an analysis may be performed in a manner as that described by Ogg *et al.*, *Science* 279:2103-2106, 1998. In the following example, peptides in accordance with the invention are used as a reagent for diagnostic or prognostic purposes, not as an immunogen.

[00431] In this example highly sensitive human leukocyte antigen tetrameric complexes ("tetramers") are used for a cross-sectional analysis of, for example, HIV HLA-A*0201-specific CTL frequencies from HLA A*0201-positive individuals at different stages of infection or following immunization using an HIV peptide containing an A*0201 motif.

Tetrameric complexes are synthesized as described (Musey *et al.*, *N. Engl. J. Med.* 337:1267, 1997). Briefly, purified HLA heavy chain (A*0201 in this example) and β 2-microglobulin are synthesized by means of a prokaryotic expression system. The heavy chain is modified by deletion of the transmembrane-cytosolic tail and COOH-terminal addition of a sequence containing a BirA enzymatic biotinylation site. The heavy chain, β 2-microglobulin, and peptide are refolded by dilution. The 45-kD refolded product is isolated by fast protein liquid chromatography and then biotinylated by BirA in the presence of biotin (Sigma, St. Louis, Missouri), adenosine 5'triphosphate and magnesium. Streptavidin-phycoerythrin conjugate is added in a 1:4 molar ratio, and the tetrameric product is concentrated to 1 mg/ml. The resulting product is referred to as tetramer-phycoerythrin.

[00432] For the analysis of patient blood samples, approximately one million PBMCs are centrifuged at 300 x g for 5 minutes and resuspended in 50 μ l of cold phosphate-buffered saline. Tri-color analysis is performed with the tetramer-phycoerythrin, along with anti-CD8-Tricolor, and anti-CD38. The PBMCs are incubated with tetramer and antibodies on ice for 30 to 60 min and then washed twice before formaldehyde fixation. Gates are applied to contain >99.98% of control samples. Controls for the tetramers include both A*0201-negative individuals and A*0201-positive uninfected donors. The percentage of cells stained with the tetramer is then determined by flow cytometry. The results indicate the number of cells in the PBMC sample that contain epitope-restricted CTLs, thereby readily indicating the extent of immune response to the HIV epitope, and thus the stage of infection with HIV, the status of exposure to HIV, or exposure to a vaccine that elicits a protective or therapeutic response.

EXAMPLE 13. USE OF PEPTIDE EPITOPES TO EVALUATE RECALL RESPONSES

[00433] The peptide epitopes of the invention are used as reagents to evaluate T cell responses, such as acute or recall responses, in patients. Such an analysis may be performed on patients who have recovered from infection, who are chronically infected with HIV, or who have been vaccinated with an HIV vaccine.

[00434] For example, the class I restricted CTL response of persons who have been vaccinated may be analyzed. The vaccine may be any HIV vaccine. PBMC are collected from vaccinated individuals and HLA typed. Appropriate peptide epitopes of the

invention that, optimally, bear supermotifs to provide cross-reactivity with multiple HLA supertype family members, are then used for analysis of samples derived from individuals who bear that HLA type.

[00435] PBMC from vaccinated individuals are separated on Ficoll-Histopaque density gradients (Sigma Chemical Co., St. Louis, MO), washed three times in HBSS (GIBCO Laboratories), resuspended in RPMI-1640 (GIBCO Laboratories) supplemented with L-glutamine (2mM), penicillin (50U/ml), streptomycin (50 µg/ml), and Hepes (10mM) containing 10% heat-inactivated human AB serum (complete RPMI) and plated using microculture formats. A synthetic peptide comprising an epitope of the invention is added at 10 µg/ml to each well and HBV core 128-140 epitope is added at 1 µg/ml to each well as a source of T cell help during the first week of stimulation.

[00436] In the microculture format, 4×10^5 PBMC are stimulated with peptide in 8 replicate cultures in 96-well round bottom plate in 100 µl/well of complete RPMI. On days 3 and 10, 100 ml of complete RPMI and 20 U/ml final concentration of rIL-2 are added to each well. On day 7 the cultures are transferred into a 96-well flat-bottom plate and restimulated with peptide, rIL-2 and 10^5 irradiated (3,000 rad) autologous feeder cells. The cultures are tested for cytotoxic activity on day 14. A positive CTL response requires two or more of the eight replicate cultures to display greater than 10% specific ^{51}Cr release, based on comparison with uninfected control subjects as previously described (Rehermann, *et al.*, *Nature Med.* 2:1104,1108, 1996; Rehermann *et al.*, *J. Clin. Invest.* 97:1655-1665, 1996; and Rehermann *et al.* *J. Clin. Invest.* 98:1432-1440, 1996).

[00437] Target cell lines are autologous and allogeneic EBV-transformed B-LCL that are either purchased from the American Society for Histocompatibility and Immunogenetics (ASHI, Boston, MA) or established from the pool of patients as described (Guilhot, *et al.* *J. Virol.* 66:2670-2678, 1992).

[00438] Cytotoxicity assays are performed in the following manner. Target cells consist of either allogeneic HLA-matched or autologous EBV-transformed B lymphoblastoid cell line that are incubated overnight with the synthetic peptide epitope of the invention at 10 µM, and labeled with 100 µCi of ^{51}Cr (Amersham Corp., Arlington Heights, IL) for 1 hour after which they are washed four times with HBSS.

[00439] Cytolytic activity is determined in a standard 4-h, split well ^{51}Cr release assay using U-bottomed 96 well plates containing 3,000 targets/well. Stimulated PBMC are tested at effector/target (E/T) ratios of 20-50:1 on day 14. Percent cytotoxicity is determined from the formula: $100 \times [(\text{experimental release} - \text{spontaneous$

release)/maximum release-spontaneous release)]. Maximum release is determined by lysis of targets by detergent (2% Triton X-100; Sigma Chemical Co., St. Louis, MO). Spontaneous release is <25% of maximum release for all experiments.

[00440] The results of such an analysis indicate the extent to which HLA-restricted CTL populations have been stimulated by previous exposure to HIV or an HIV vaccine.

[00441] The class II restricted HTL responses may also be analyzed. Purified PBMC are cultured in a 96-well flat bottom plate at a density of 1.5×10^5 cells/well and are stimulated with 10 µg/ml synthetic peptide, whole antigen, or PHA. Cells are routinely plated in replicates of 4-6 wells for each condition. After seven days of culture, the medium is removed and replaced with fresh medium containing 10U/ml IL-2. Two days later, 1 µCi ^3H -thymidine is added to each well and incubation is continued for an additional 18 hours. Cellular DNA is then harvested on glass fiber mats and analyzed for ^3H -thymidine incorporation. Antigen-specific T cell proliferation is calculated as the ratio of ^3H -thymidine incorporation in the presence of antigen divided by the ^3H -thymidine incorporation in the absence of antigen.

EXAMPLE 14. INDUCTION OF SPECIFIC CTL RESPONSE IN HUMANS

[00442] A human clinical trial for an immunogenic composition comprising CTL and HTL epitopes of the invention is set up as an IND Phase I, dose escalation study and carried out as a randomized, double-blind, placebo-controlled trial. Such a trial is designed, for example, as follows:

[00443] A total of about 27 subjects are enrolled and divided into 3 groups:

Group I: 3 subjects are injected with placebo and 6 subjects are injected with 5 µg of peptide composition;

Group II: 3 subjects are injected with placebo and 6 subjects are injected with 50 µg peptide composition;

Group III: 3 subjects are injected with placebo and 6 subjects are injected with 500 µg of peptide composition.

[00444] After 4 weeks following the first injection, all subjects receive a booster inoculation at the same dosage.

[00445] The endpoints measured in this study relate to the safety and tolerability of the peptide composition as well as its immunogenicity. Cellular immune responses to the

peptide composition are an index of the intrinsic activity of this the peptide composition, and can therefore be viewed as a measure of biological efficacy. The following summarize the clinical and laboratory data that relate to safety and efficacy endpoints.

[00446] Safety: The incidence of adverse events is monitored in the placebo and drug treatment group and assessed in terms of degree and reversibility.

[00447] Evaluation of Vaccine Efficacy: For evaluation of vaccine efficacy, subjects are bled before and after injection. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

[00448] The vaccine is found to be both safe and efficacious.

EXAMPLE 15. PHASE II TRIALS IN PATIENTS INFECTED WITH HIV

[00449] Phase II trials are performed to study the effect of administering the CTL-HTL peptide compositions to HIV-infected patients. The main objectives of the trials are to determine an effective dose and regimen for inducing CTLs in chronically infected HIV patients, to establish the safety of inducing a CTL and HTL response in these patients, and to see to what extent activation of CTLs improves the clinical picture of chronically infected HIV patients, as manifested by a reduction in viral load and an increase in CD4⁺ cells counts. Such a study is designed, for example, as follows:

[00450] The studies are performed in multiple centers. The trial design is an open-label, uncontrolled, dose escalation protocol wherein the peptide composition is administered as a single dose followed six weeks later by a single booster shot of the same dose. The dosages are 50, 500 and 5,000 micrograms per injection. Drug-associated adverse effects (severity and reversibility) are recorded.

[00451] There are three patient groupings. The first group is injected with 50 micrograms of the peptide composition and the second and third groups with 500 and 5,000 micrograms of peptide composition, respectively. The patients within each group range in age from 21-65, include both males and females, and represent diverse ethnic backgrounds. All of them are infected with HIV for over five years and are HCV, HBV and delta hepatitis virus (HDV) negative, but have positive levels of HIV antigen.

[00452] The viral load and CD4⁺ levels are monitored to assess the effects of administering the peptide compositions. The vaccine composition is found to be both safe and efficacious in the treatment of HIV infection.

EXAMPLE 16. INDUCTION OF CTL RESPONSES USING A PRIME BOOST PROTOCOL

[00453] A prime boost protocol can also be used for the administration of the vaccine to humans. Such a vaccine regimen can include an initial administration of, for example, naked DNA followed by a boost using recombinant virus encoding the vaccine, or recombinant protein/polypeptide or a peptide mixture administered in an adjuvant.

[00454] For example, the initial immunization is performed using an expression vector, such as that constructed above, in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 µg) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster is, for example, recombinant fowlpox virus administered at a dose of $5 \cdot 10^7$ to $5 \cdot 10^9$ pfu. An alternative recombinant virus, such as an MVA, canarypox, adenovirus, or adeno-associated virus, can also be used for the booster, or the polyepitopic protein or a mixture of the peptides can be administered. For evaluation of vaccine efficacy, patient blood samples are obtained before immunization as well as at intervals following administration of the initial vaccine and booster doses of the vaccine. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

[00455] Analysis of the results indicates that a magnitude of sufficient response to achieve protective immunity against HIV is generated.

EXAMPLE 17. ADMINISTRATION OF VACCINE COMPOSITIONS USING DENDRITIC CELLS

[00456] Vaccines comprising peptide epitopes of the invention can be administered using APCs, or “professional” APCs such as DC. In this example, the peptide-pulsed DC are administered to a patient to stimulate a CTL response *in vivo*. In this method, dendritic

cells are isolated, expanded, and pulsed with a vaccine comprising peptide CTL and HTL epitopes of the invention. The dendritic cells are infused back into the patient to elicit CTL and HTL responses *in vivo*. The induced CTL and HTL then destroy or facilitate destruction of the specific target cells that bear the proteins from which the epitopes in the vaccine are derived.

[00457] For example, a cocktail of epitope-bearing peptides is administered *ex vivo* to PBMC, or isolated DC therefrom. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoiectin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides.

[00458] As appreciated clinically, and readily determined by one of skill based on clinical outcomes, the number of DC reinfused into the patient can vary (*see, e.g., Nature Med.* 4:328, 1998; *Nature Med.* 2:52, 1996 and *Prostate* 32:272, 1997). Although $2-50 \times 10^6$ DC per patient are typically administered, larger number of DC, such as 10^7 or 10^8 can also be provided. Such cell populations typically contain between 50-90% DC.

[00459] In some embodiments, peptide-loaded PBMC are injected into patients without purification of the DC. For example, PBMC containing DC generated after treatment with an agent such as Progenipoiectin™ are injected into patients without purification of the DC. The total number of PBMC that are administered often ranges from 10^8 to 10^{10} . Generally, the cell doses injected into patients is based on the percentage of DC in the blood of each patient, as determined, for example, by immunofluorescence analysis with specific anti-DC antibodies. Thus, for example, if Progenipoiectin™ mobilizes 2% DC in the peripheral blood of a given patient, and that patient is to receive 5×10^6 DC, then the patient will be injected with a total of 2.5×10^8 peptide-loaded PBMC. The percent DC mobilized by an agent such as Progenipoiectin™ is typically estimated to be between 2-10%, but can vary as appreciated by one of skill in the art.

Ex vivo activation of CTL/HTL responses

[00460] Alternatively, *ex vivo* CTL or HTL responses to HIV antigens can be induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of APC, such as DC, and the appropriate immunogenic peptides. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back

into the patient, where they will destroy or facilitate destruction of their specific target cells.

[00461] It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, patent applications and sequence listings cited herein are hereby incorporated by reference in their entirety for all purposes.

TABLE 1

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	T, I, L, V, M, S		F, W, Y
A2	L, I, V, M, A, T, Q		I, V, M, A, T, L
A3	V, S, M, A, T, L, I		R, K
A24	Y, F, W, I, V, L, M, T		F, I, Y, W, L, M
B7	P		V, I, L, F, M, W, Y, A
B27	R, H, K		F, Y, L, W, M, I, V, A
B44	E, D		F, W, L, I, M, V, A
B58	A, T, S		F, W, Y, L, I, V, M, A
B62	Q, L, I, V, M, P		F, W, Y, M, I, V, L, A
MOTIFS			
A1	T, S, M		Y
A1		D, E, A, S	Y
A2.1	L, M, V, Q, I, A, T		V, L, I, M, A, T
A3	L, M, V, I, S, A, T, F, C, G, D		K, Y, R, H, F, A
A11	V, T, M, L, I, S, A, G, N, C, D, F		K, R, Y, H
A24	Y, F, W, M		F, L, I, W
A*3101	M, V, T, A, L, I, S		R, K
A*3301	M, V, A, L, F, I, S, T		R, K
A*6801	A, V, T, M, S, L, I		R, K
B*0702	P		L, M, F, W, Y, A, I, V
B*3501	P		L, M, F, W, Y, I, V, A
B51	P		L, I, V, F, W, Y, A, M
B*5301	P		I, M, F, W, Y, A, L, V
B*5401	P		A, T, I, V, L, M, F, W, Y

Bolded residues are preferred, italicized residues are tolerated: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE 2

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	T, I, L, V, M, S		F, W, Y
A2	V, Q, A, T		I, V, L, M, A, T
A3	V, S, M, A, T, L, I		R, K
A24	Y, F, W, I, V, L, M, T		F, I, Y, W, L, M
B7	P		V, I, L, F, M, W, Y, A
B27	R, H, K		F, Y, L, W, M, I, V, A
B58	A, T, S		F, W, Y, L, I, V, M, A
B62	Q, L, I, V, M, P		F, W, Y, M, I, V, L, A
MOTIFS			
A1	T, S, M		Y
A1		D, E, A, S	Y
A2.1	<i>V, Q, A, T*</i>		V, L, I, M, A, T
A3.2	L, M, V, I, S, A, T, F, C, G, D		K, Y, R, H, F, A
A11	V, T, M, L, I, S, A, G, N, C, D, F		K, R, H, Y
A24	Y, F, W		F, L, I, W

*If 2 is V, or Q, the C-term is not L

Bolded residues are preferred, italicized residues are tolerated: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

Table 4

HLA-supertype	Allele-specific HLA-supertype members	
	Verified ^a	Predicted ^b
A1	A*0101, A*2501, A*2601, A*2602, A*3201	A*0102, A*2604, A*3601, A*4301, A*8001
A2	A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, A*6901	A*0208, A*0210, A*0211, A*0212, A*0213
A3	A*0301, A*1101, A*3101, A*3301, A*6801	A*0302, A*1102, A*2603, A*3302, A*3303, A*3401, A*3402, A*6601, A*6602, A*7401
A24	A*2301, A*2402, A*3001	A*2403, A*2404, A*3002, A*3003
B7	B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, B*7801	B*1511, B*4201, B*5901
B27	B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, B*7301	B*2701, B*2707, B*2708, B*3802, B*3903, B*3904, B*3905, B*4801, B*4802, B*1510, B*1518, B*1503
B44	B*1801, B*1802, B*3701, B*4402, B*4403, B*4404, B*4001, B*4002, B*4006	B*4101, B*4501, B*4701, B*4901, B*5001
B58	B*5701, B*5702, B*5801, B*5802, B*1516, B*1517	
B62	B*1501, B*1502, B*1513, B*5201	B*1301, B*1302, B*1504, B*1505, B*1506, B*1507, B*1515, B*1520, B*1521, B*1512, B*1514, B*1510

- a. Verified alleles include alleles whose specificity has been determined by pool sequencing analysis, peptide binding assays, or by analysis of the sequences of CTL epitopes.
- b. Predicted alleles are alleles whose specificity is predicted on the basis of B and F pocket structure to overlap with the supertype specificity.

Table 5. Compiled rankings and similarity assignments.

A	C	D	E	F	G	H	I	K	L
A 1.0	C 1.0	D 1.0	E 1.0	F 1.0	G 1.0	H 1.0	I 1.0	K 1.0	L 1.0
S 4.5	V 5.5	N 3.5	Q 3.3	L 3.8	S 2.8	Q 2.0	L 2.5	R 2.7	I 3.3
T 4.8	T 6.5	E 4.0	N 4.2	Y 4.3	A 4.2	E 5.8	M 4.5	Q 6.0	M 4.0
P 5.3	A 6.7	Q 6.2	D 4.7	I 4.8	T 4.7	N 6.2	F 5.2	H 6.8	F 4.5
G 5.7	S 7.3	T 7.2	H 5.3	M 6.2	D 6.3	R 8.2	V 5.2	N 7.2	V 5.5
C 9.3	P 8.0	S 7.7	T 8.3	V 6.7	P 7.0	K 8.7	Y 8.8	E 7.5	Y 8.2
V 9.5	I 9.0	H 7.8	K 8.7	W 7.2	N 7.3	P 9.0	T 10.3	D 8.5	H 9.7
D 10.0	Y 10.2	G 8.8	P 9.0	H 10.2	E 8.3	D 9.2	H 11.3	M 9.2	Q 10.5
M 10.0	N 10.7	P 9.2	R 10.5	C 11.2	Q 9.3	S 10.5	A 11.5	T 10.5	W 11.0
N 10.2	F 11.0	A 9.3	S 10.5	T 11.5	H 9.8	T 10.5	C 11.7	S 11.3	T 11.3
E 11.3	G 11.0	K 9.5	V 11.0	R 11.8	C 11.5	Y 11.0	K 12.0	P 11.5	A 11.8
Q 11.3	M 11.0	R 11.5	G 12.0	A 13.0	V 12.0	M 11.2	P 12.0	I 12.2	K 12.2
H 12.3	H 11.3	C 12.0	A 12.2	K 13.3	M 13.5	V 12.2	Q 12.2	L 12.7	P 12.2
Y 13.0	D 12.0	V 13.3	M 12.3	P 13.3	K 13.8	L 13.3	R 13.0	Y 12.8	R 13.2
		M 14.3	T 15.0	S 13.8	Y 14.2	T 13.7	S 13.2	V 13.7	C 13.7
		V 15.3	C 15.2	Q 14.0	R 15.5	A 13.8	E 14.0	A 14.3	E 14.2
		I 16.0	L 15.3	N 14.2	I 16.3	G 13.3	N 14.3	C 14.3	N 14.5
		L 16.7	Y 15.7	E 15.3	L 16.8	F 15.3	W 14.7	F 14.8	S 15.3
		W 16.0	F 17.8	G 16.3	W 17.3	C 17.2	D 15.7	W 15.5	G 16.8
		F 16.3	W 18.0	D 18.0	F 18.2	W 17.5	G 17.0	C 17.5	D 17.2

Conserved (1-7)

Semi-conserved (7.1-13)

Non-conserved (13.1-20)

Table 5 (continued)

M	N	P	Q	R	S	T	V	W	Y
M 1.0	N 1.0	P 1.0	Q 1.0	R 1.0	S 1.0	T 1.0	V 1.0	W 1.0	Y 1.0
L 3.8	D 3.2	T 3.5	E 3.2	K 2.0	T 4.0	P 4.7	L 5.3	F 4.2	F 6.2
I 5.0	E 4.5	S 6.0	H 3.3	H 5.8	G 4.2	S 5.0	I 5.5	Y 4.5	W 6.3
V 5.2	Q 5.8	A 6.3	N 6.0	Q 6.7	A 4.7	A 5.7	M 5.5	L 6.3	H 7.3
F 7.0	H 6.8	H 7.2	K 7.0	E 8.7	P 5.3	N 6.5	P 7.8	M 6.5	M 8.0
K 9.7	T 7.2	Q 7.2	D 7.2	N 8.7	N 6.5	D 7.8	T 8.2	R 8.7	L 9.7
Q 10.3	S 7.7	N 7.8	R 8.3	M 9.2	D 8.0	E 8.3	F 8.5	I 9.2	T 10.0
R 10.5	K 8.5	D 9.2	P 8.5	D 10.0	C 9.3	G 8.8	A 10.0	H 10.2	I 10.3
Y 10.8	P 8.7	E 9.5	M 10.5	P 10.2	E 9.3	H 10.5	C 10.7	V 10.3	C 10.7
H 11.0	R 10.5	G 10.2	T 10.8	W 10.3	H 10.2	Q 10.5	H 11.0	K 10.5	V 11.0
A 11.2	A 10.7	V 11.2	V 11.3	S 11.3	Q 10.5	V 10.5	Q 11.0	Q 12.3	P 11.5
T 11.3	G 11.8	C 11.8	S 12.3	T 12.0	K 12.3	C 12.2	E 11.3	S 12.3	A 11.7
P 11.8	V 12.8	M 12.2	A 13.0	I 12.5	V 13.5	K 12.2	N 12.3	A 12.5	N 11.7
W 12.7	C 13.0	R 13.2	G 13.3	L 13.0	R 13.7	M 12.3	S 12.7	P 12.7	Q 12.0
C 13.0	M 13.8	K 13.5	L 13.8	Y 13.0	M 14.5	I 13.7	G 13.2	T 12.7	S 12.2
I 14.0	S 14.2	Y 13.8	I 14.2	V 13.7	Y 14.7	Y 14.3	Y 14.0	N 13.2	K 12.7
N 14.2	I 14.0	I 14.0	Y 15.0	F 14.3	I 16.0	R 15.5	D 14.8	C 13.5	R 13.0
E 14.5	E 14.3	E 14.3	C 16.3	A 15.2	W 16.5	W 16.3	K 15.2	E 13.7	E 14.2
K 14.5	A 14.7	W 16.2	F 17.3	G 15.2	L 17.3	L 16.5	W 15.7	C 16.7	C 14.7
D 14.8	E 14.8	F 17.3	W 17.5	C 17.3	F 18.3	F 17.7	R 16.3	D 17.3	D 16.0

Conserved (1-7)

Semi-conserved (7.1-13)

Non-conserved (13.1-20)

Table 6. Recognition of variant peptides by CTL generated after one and five stimulations with the parent peptide.

A. Gag 386 (VLAEAMSQV)			
Peptide Sequence	Binding IC50 (nM)	1 Stimulation (SU)	5 Stimulations (SU)
VLAEAMSQV	49.9	31.6	222.0
VLAEAMSQA	23.8	17.0	133.5
VLAEAMSQI	70.9	21.2	246.1
VLAEAMSKV	230.5	10.8	130.9
VLAEAMSKA	69.4	NT	36.6
ILAEAMSQA	29.3	4.0	49.7
ILAEAMSKA	72.4	--	--
VLAEAMAAA	17	16.3	90.3
B. Env 134 (KLTPLCVTL)			
KLTPLCVTL	77.0	278.4	683.6
KITPLCVTL	461	231.8	700.8
QLTPLCVTL	63.6	166.2	361.5
QITPLCVTL	975	105.0	166.9
ELTPLCVTL	7190	91.7	100.0
KLTPFCVTL	87.3	36.1	75.4
KLTPLCVIL	356	77.2	29.1
KLTPLCVPL	14.6	9.6	14.8

Table 7. Conservation of EP HIV-1090 epitopes across clades, calculated as identity or immunological conservation

Protein	Sequence	<u>Total</u>		<u>Clade B</u>		<u>Clade C</u>	
		Identity	Imm. Cons.	Identity	Imm. Cons.	Identity	Imm. Cons.
Pol 498	ILKEPVHGV	62%	87%	77%	86%	74%	95%
Gag 386	VLAEAMSQV	32%	93%	68%	91%	5%	94%
Pol 448	KLVGKLNWA	95%	96%	95%	95%	95%	98%
Env 134	KLTPLCVTL	80%	93%	90%	95%	89%	98%
Vpr 62	RILQQLLFI	51%	93%	68%	91%	61%	95%
Nef 221	LTFGWCFKL	49%	74%	77%	91%	47%	81%
Gag 271	MTNNPPIPV	20%	25%	91%	95%	8%	19%
Env 47	VTVYYGVPVWK	59%	87%	95%	100%	61%	92%
Pol 929	QMAVFIHNFK	84%	98%	100%	100%	94%	97%
Pol 98	VTIKIGGQLK	11%	71%	59%	91%	2%	89%
Pol 971	KIQNFRVYYR	80%	86%	91%	95%	79%	89%
Pol 347	AIFQSSMTK	53%	75%	77%	82%	44%	79%
Pol 722	KVYLAWVPAHK	14%	97%	82%	95%	3%	97%
Env 61	TTLFCASDAK	72%	89%	90%	100%	69%	92%
Nef 94	FPVRPQVPL	81%	93%	77%	95%	82%	94%
Gag 545	YPLASLRSLF	7%	29%	45%	95%	0%	0%
Rev 75	VPLQLPPL	44%	78%	68%	77%	27%	79%
Env 259	IPIHYCAPA	74%	95%	45%	95%	79%	97%
Gag 237	HPVHAGPIA	27%	54%	68%	95%	44%	94%
Pol 893	IPYNPQSQGVV	92%	96%	82%	95%	240%	97%
Env 250	CPKVSFEPI	45%	91%	77%	100%	45%	97%
Mean		54%	81%	77%	93%	59%	84%
n=		167		22		62	

Table 8. HIV Peptides predicted to be immunologically conserved

Protein	Sequence	Conserved Epitopes*	SEQ ID NO	Sequence Distribution					
				All	Subtype				
					A	B	C	D	G
Pol 498	ILKEPVHGV	ILKEPVHGV	69	104	1	17	46	2	2
		ILREPVHGV	91	12			5		1
		ILKEPVHGA	92	10			2	1	
		ILKDPVHGV	93	8	5				
		KLKEPVHGV	94	3					
		ILKDPVHGA	95	2	2				
		ILKNPVHGV	96	2					
Gag 386	VLAEAMSQV	VLAEAMSQA	16	67	2	1	36	3	3
		VLAEAMSQV	10	54	7	15	3	1	
		VLAEAMSQT	99	11			9		
		VLAEAMSHA	100	6			4		
		ILAEAMSQV	101	5		3			
		ILAEAMSQA	58	3			2		
		VLAEAMSHV	103	2					
Pol 448	KLVGKLNWA	KLVGKLNWA	72	158	9	21	59	3	3
		KLIGKLNWA	105	1					
Env 134	KLTPLCVTL	KLTPLCVTL	9	134	8	19	55		
		QLTPLCVTL	19	5	2	1			
		KLTPLCVAL	108	3					
		RLTPLCVTL	109	3			3		
		KITPLCVTL	18	2					
Vpr 62	RILQQLLFI	RILQQLLFI	11	86	1	15	28	4	3
		RILQQLLFV	112	21	2		2		
		RTLQQLLFI	113	10		2	4		
		RTLQQLLFV	114	10			1		
		RILQQLLFT	115	6			2		
		RMLQQLLFI	116	4		1	3		
		RVLQQLLFI	117	3			3		
Nef 221	LTFGWCFKL	LTFGWCFKL	74	82	8	17	29		3
		LTFGWCYKL	119	31	1	2	17		
		LTLGWCFKL	120	4			1		

Gag 271	MTNNPPIPV	MTSNPPIPV	26	60	3		24	4	1
		MTNNPPIPV	25	33		20	5		
		MTSNPPVPV	123	26	1		15		1
		MTGNPPIPV	124	15	5		1		
		MTGNPPVPV	125	9			5		
		MTNNPPVPV	126	6			6		
		MTANPPVPV	127	3			2		
Env 47	VTVYYGVPVWK	VTVYYGVPVWK	13	99	6	21	30	3	
		VTVYYGVPVWR	129	40	1		18		
		VTIYYGVPVWK	130	2					
Pol 929	QMAVFIHNFK	QMAVFIHNFK	77	153	10	22	58	4	3
		QMAVFVHNFK	132	3			1		
		QMAVFVHNYK	133	2					
Pol 98	VTIKIGGQLK	VSIKVGGOIK	12	30			30		
		VTIKIGGQLK	78	18		13	1		
		VTVKIGGQLK	136	11	1	1		1	
		VTVRIGGQLK	137	6	3				
		VSIKVGGOIR	138	6			6		
		VSIRVGGOIK	139	4			4		
		VTIRIGGQLK	140	3		2			
		VTVKIGGQLR	141	3	1				
		VTVKVGGOIK	142	3					
Pol 971	KIQNFRVYYR	KIQNFRVYYR	79	133	6	20	49	4	3
Pol 347	AIFQSSMTK	AIFQSSMTK	80	88	5	17	27	3	2
		AIFQCSMTK	145	19		2	5		
		AIFQSSMTR	146	13		1	11		1
		AIFQASMTK	147	9	1		1		
		SIFQSSMTK	148	9	3		6		
		AIFQYSMTK	149	4					
		AIFQSTMTK	150	2			1		
Pol 722	KVYLAWVPAHK	KVYLSWVPAHK	151	56	8		12	1	3
		RVYLSWVPAHK	152	55			41		
		KVYLAWVPAHK	81	23	1	18		3	
		KVYLTWVPAHK	154	5		2			

		KIYLSWVPAHK	155	5			3		
		RIYLSWVPAHK	156	5			4		
		KIYLAWVPAHK	157	2		1			
		QVYLTWVPAHK	158	2					
Env 61	TTLFCASDAK	TTLFCASDAK	82	121	9	19	41	4	1
		ATLFCASDAK	160	7			7		
		TILFCASDAK	161	6					
		PTLFCASDAK	162	2			1		
		TTLFCASDAR	163	2		2			
		TTLFCASEAK	164	2		1			
		ATLFCASDAR	165	2			2		
Nef 94	FPVRPQVPL	FPVRPQVPL	83	135	8	17	51	4	3
		FPVKPQVPL	167	9	1	3	2		
		FPVRPQVPV	168	4			2		
Gag 545	YPLASLRSLF	EPLTSLKSLF*	1	22			21		
		YPLASLKSLF*	2	13		5		2	
*These two would not be predicted to XR. Would choose both to get maximal population coverage.									
		YPLASLRSLF	84	11		10			
		YPLTSLKSLF	172	10		1		2	1
		YPPLASLKSL	173	10					
		YPLTSLRSLF	174	6		4			
		YPPLTSLKSL	175	6					
Rev 75	VPLQLPPL	VPLQLPPL	85	64	5	15	7	4	2
		VPLQLPPI	177	34	2	1	19		
		VPFQLPPI	178	26			23		
		VPFQLPPL	179	3		1			1
Env 259	IPIHYCAPA	IPIHYCAPA	86	124	8	10	49	3	2
		IPIHYCTPA	181	25	1	8	8		
		IPIHFCAPA	182	3		1	1	1	
Gag 237	HPVHAGPIA	HPVHAGPIA	87	39		15	21	1	
		HPVHAGPVA	184	34	1	3	27	2	
		HPVQAGPVA	185	12		3	6	1	
		HPIHAGPIA	186	2			2		

Pol 893	IPYNPQSQGVV	IPYNPQSQGVV	88	153	9	18	60	4	3
		IPYNPQSQGVI	188	5		3			
		IPYNPQSQGAV	189	2			1		
Env 250	CPKVSFEPI	CPKVSFEPI	89	50	5	17	3	2	0
		CPKVSFDPI	191	42			33		
		CPKVTFDPI	192	16			13		1
		CPKVTFEPI	193	13	3		1		1
		CPKISFDPI	194	9			5		
		CPKISFEPI	195	7		4		1	
		CPKVSWDPI	196	6					
		CPKVSFQPI	197	4		1			

* The preferred epitopes are shown in bold

Table 9. Predicted immunological conservation for a panel of HLA-A2 restriction peptides.

Source	Parent Sequence	HPV Strain	Variant Sequences	SEQ ID NO	Predicted Immunogenicity	Measured Immunogenicity (SU) *
HPV16.E7.86	TLGIVCPI	16	TLGIVCPI	198	+	103.7
		18	TLSFVCPW	199	-	
		31	SFGIVCPN	200	-	
		33	TVNIVCPT	201	-	
		45	TLSFVCPW	199	-	
		52	TLQVVC PG	203	-	
		56	ALTVTCPL	204	-	
		58	TCTIVCPS	205	-	
HPV31.E6.11	KLHELSSAL	16	KLPQLCTEL	206	-	
		18	KLPDLCTEL	207	-	
		31	KLHELSSAL	208	+	26.3
		33	TLHDL CQAL	209	-	
		45	KLPDLCTEL	207	-	
		52	TLHELCEVL	211	-	
		56	SLHHLSEVL	212	-	
		58	TLHDL CQAL	209	-	
HPV18/45.E6.13	KLPDLCTEL	16	KLPQLCTEL	206	+	15.7
		18	KLPDLCTEL	210	+	212.7
		31	KLHELSSAL	208	-	
		33	TLHDL CQAL	209	-	
		45	KLPDLCTEL	207	+	205.1
		52	TLHELCEVL	211	-	
		56	SLHHLSEVL	212	-	
		58	TLHDL CQAL	209	-	
HPV52.E6.18	VLEESVHEI	16	ELQTTIHDI	222	-	
		18	ELNTSLQDI	223	-	
		31	ALEIPYDEL	224	-	
		33	ALETTIHNI	225	-	
		45	ELNTSLQDV	226	-	
		52	VLEESVHEI	227	+	64.1
		56	VLEIPLIDL	228	-	
		58	ALETSVHEI	229	-	
HPV18.E6.47	FAFKDLFVV	16	FAFRDLCIV	230	-	
		18	FAFKDLFVV	231	+	350.6
		31	FAFTDLTIV	232	-	
		33	FAFADLTIV	233	-	31.4
		45	FAFKDLCIV	234	-	176.9
		52	FLFTDLRIV	235	-	
		56	FACTELKLV	236	-	

		58	FVFADLRIV	237	-	7.7
HPV31.E6.45	FAFTDLTIV	16	FAFRDLCIV	230	-	
		18	FAFKDLFVV	231	-	
		31	FAFTDLTIV	232	+	20.7
		33	FAFADLTVV	233	+	11.6
		45	FAFKDLCIV	234	-	
		52	FLFTDLRIV	235	-	
		56	FACTELKLV	236	-	
		58	FVFADLRIV	237	-	
HPV52.E6.45	FLFTDLRIV	16	FAFRDLCIV	230	-	
		18	FAFKDLFVV	231	-	
		31	FAFTDLTIV	232	-	
		33	FAFADLTVV	233	-	
		45	FAFKDLCIV	234	-	
		52	FLFTDLRIV	235	+	421.4
		56	FACTELKLV	236	-	57.5
		58	FVFADLRIV	237	+	94.1
HPV58.E6.45	FVFADLRIV	16	FAFRDLCIV	230	-	
		18	FAFKDLFVV	231	-	
		31	FAFTDLTIV	232	-	
		33	FAFADLTVV	233	-	
		45	FAFKDLCIV	234	-	
		52	FLFTDLRIV	235	+	13.3
		56	FACTELKLV	236	-	21.0
		58	FVFADLRIV	237	+	62.8
HPV18.E7.7	TLQDIVLHL	16	TLHEYMLDL	262	-	
		18	TLQDIVLHL	263	+	99.0
		31	TLQDYVLDL	264	-	
		33	TLKEYVLDL	265	-	
		45	TLQEIVLHL	266	+	
		52	TIKDYILD	267	-	
		56	TLQDVVLEL	268	+	38.0
		58	TLREYILD	269	-	
HPV16.E7.82	LLMGTLGIV	16	LLMGTLGIV	270	+	518.5
		18	LFLNTLSFV	271	-	
		31	LLMGSGFIV	272	+	90.1
		33	LLMGTVNIV	273	-	
		45	LFLSTLSFV	274	+	
		52	MLLGTQV	275	-	
		56	LLMGALTVT	276	+	
		58	LLMGCTIV	277	-	
HPV33.E7.81	LLMGTVNIV	16	LLMGTLGIV	270	-	

		18	LFLNTLSFV	271	-	
		31	LLMGSFGIV	272	-	
		33	LLMGTVNIV	273	+	179.4
		45	LFLSTLSFV	274	-	
		52	MLLGTLQVV	275	+	
		56	LLMGALTVT	276	-	20.8
		58	LLMGCTIV	277	-	
HPV52.E7.84	MLLGTLQVV	16	LLMGTLGIV	270	-	
		18	LFLNTLSFV	271	-	
		31	LLMGSFGIV	272	-	
		33	LLMGTVNIV	273	+	
		45	LFLSTLSFV	274	-	
		52	MLLGTLQVV	275	+	99.8
		56	LLMGALTVT	276	-	
		58	LLMGCTIV	277	-	
HPV56.E7.89	LLMGALTVT	16	LLMGTLGIV	270	-	
		18	LFLNTLSFV	271	-	
		31	LLMGSFGIV	272	-	
		33	LLMGTVNIV	273	+	
		45	LFLSTLSFV	274	-	
		52	MLLGTLQVV	275	-	
		56	LLMGALTVT	276	+	263.5
		58	LLMGCTIV	277	-	43.6
* Immunogenicity was measured for all variants. Only the positive responses are shown in the table. All other responses were negative.						

Table 10. 167 HIV-1 Variants

Sequence Designation	Name	Accession Number	SubType	Country
A.UG.92UG037_U51190	92UG037	U51190	A	UG
A.BY.97BL006_AF1932	97BL006	AF193275	A	BY
A.KE.Q23_AF004885	Q23	AF004885	A	KE
A.SE.SE6594_AF06967	SE6594	AF069672	A	SE
A.SE.SE7253_AF06967	SE7253	AF069670	A	SE
A.SE.SE7535_AF06967	SE7535	AF069671	A	SE
A.SE.SE8538_AF06966	SE8538	AF069669	A	SE
A.SE.SE8891_AF06967	SE8891	AF069673	A	SE
A.UG.U455_M62320	U455	M62320	A	UG
A.SE.UGSE8131_AF107	UGSE8131	AF107771	A	SE
A2.CY.94CY017.41_AF	94CY017.41	AF286237	A2	CY
A2.CD.97CDKTB48_AF2	97CDKTB48	AF286238	A2	CD
A2D.-.97KR004_AF286	97KR004	AF286239	A2D	KR
A2G.CD.97CDKP58_AF3	97CDKP58	AF316544	A2G	CD
AC.IN.21301_AF06715	21301	AF067156	AC	IN
AC.RW.92RW009_U8882	92RW009	U88823	AC	RW
AC.SE.SE9488_AF0714	SE9488	AF071474	AC	SE
ACD.SE.SE8603_AF075	SE8603	AF075702	ACD	SE
ACG.BE.VI1035_AJ276	VI1035	AJ276595	ACG	BE
AD.SE.SE6954_AF0757	SE6954	AF075701	AD	SE
AD.SE.SE7108_AF0714	SE7108	AF071473	AD	SE
ADHK.NO.97NOGIL3_AJ	97NOGIL3	AJ237565	ADHK	NO
ADK.CD.MAL_X04415	MAL	X04415	ADK	CD
AG.NG.92NG003_U8882	92NG003	U88825	AG	NG
AG.BE.VI1197_AJ2765	VI1197	AJ276596	AG	BE
AGHU.GA.VI354_AF076	VI354	AF076474	AGHU	GA
AGU.CD.Z321_U76035	Z321	U76035	AGU	CD
AJ.BW.BW2117_AF1921	BW2117	AF192135	AJ	BW
B.NL.3202A21_U34604	3202A21	U34604	B	NL
B.US.BC_L02317	BC	L02317	B	US
B.GB.CAM1_D10112	CAM1	D10112	B	GB
B.DE.D31_U43096	D31	U43096	B	DE
B.US.DH123_AF069140	DH123	AF069140	B	US
B.GB.GB8.C1_Y13716	GB8	AJ271445	B	GB
B.DE.HAN_U43141	HAN	U43141	B	DE
B.FR.HXB2_K03455	HXB2	K03455	B	FR
B.US.JRCSF_M38429	JRCSF	M38429	B	US
B.GB.MANC_U23487	MANC	U23487	B	GB
B.US.MNCG_M17449	MNCG	M17449	B	US
B.GA.OYI,_M26727	OYI	M26727	B	GA
B.US.P896_U39362	P896	M96155	B	US
B.US.RF_M17451	RF	M17451	B	US
B.CN.RL42_U71182	RL42	U71182	B	CN
B.US.SF2_K02007	SF2	K02007	B	US
B.TW.TWCYS_AF086817	TWCYS	AF086817	B	TW
B.AU.VH_AF146728	VH	AF146728	B	AU
B.US.WEAU160_U21135	WEAU160	U21135	B	US
B.KR.WK_AF224507	WK	AF224507	B	KR
B.US.WR27_U26546	WR27	U26546	B	US

B.US.YU2_M93258	YU2	M93258	B	US
BF1.BR.93BR029.4_AF	93BR029.4	AF005495	BF1	BR
C.BR.92BR025_U52953	92BR025	U52953	C	BR
C.IN.93IN101_AB0238	93IN101	AB023804	C	IN
C.IN.93IN904_AF0671	93IN904	AF067157	C	IN
C.IN.93IN999_AF0671	93IN999	AF067154	C	IN
C.IN.94IN11246_AF06	94IN11246	AF067159	C	IN
C.IN.95IN21068_AF06	95IN21068	AF067155	C	IN
C.BW.96BW0402_AF110	96BW0402	AF110962	C	BW
C.BW.96BW1210_AF110	96BW1210	AF110972	C	BW
C.BW.96BW15B03_AF11	96BW15B03	AF110973	C	BW
C.ET.ETH2220_U46016	ETH2220	U46016	C	ET
C.BW.96BW11B01_AF11	96BW11	AF110969	C	BW
C.BW.00BW0762.1_AF44	00BW0762.1	AF443088	C	BW
C.BW.00BW0768.20_AF44	00BW0768.20	AF443089	C	BW
C.BW.00BW0874.21_AF44	00BW0874.21	AF443090	C	BW
C.BW.00BW1471.27_AF44	00BW1471.27	AF443091	C	BW
C.BW.00BW1616.2_AF44	00BW1616.2	AF443092	C	BW
C.BW.00BW1686.8_AF44	00BW1686.8	AF443093	C	BW
C.BW.00BW1759.3_AF44	00BW1759.3	AF443094	C	BW
C.BW.00BW1773.2_AF44	00BW1773.2	AF443095	C	BW
C.BW.00BW1783.5_AF44	00BW1783.5	AF443096	C	BW
C.BW.00BW1795.6_AF44	00BW1795.6	AF443097	C	BW
C.BW.00BW1811.3_AF44	00BW1811.3	AF443098	C	BW
C.BW.00BW1859.5_AF44	00BW1859.5	AF443099	C	BW
C.BW.00BW1880.2_AF44	00BW1880.2	AF443100	C	BW
C.BW.00BW1921.13_AF44	00BW1921.13	AF443101	C	BW
C.BW.00BW2036.1_AF44	00BW2036.1	AF443102	C	BW
C.BW.00BW2063.6_AF44	00BW2063.6	AF443103	C	BW
C.BW.00BW2087.2_AF44	00BW2087.2	AF443104	C	BW
C.BW.00BW2127.214_AF44	00BW2127.214	AF443105	C	BW
C.BW.00BW2128.3_AF44	00BW2128.3	AF443106	C	BW
C.BW.00BW2276.7_AF44	00BW2276.7	AF443107	C	BW
C.BW.00BW3819.3_AF44	00BW3819.3	AF443108	C	BW
C.BW.00BW3842.8_AF44	00BW3842.8	AF443109	C	BW
C.BW.00BW3871.3_AF44	00BW3871.3	AF443110	C	BW
C.BW.00BW3876.9_AF44	00BW3876.9	AF443111	C	BW
C.BW.00BW3886.8_AF44	00BW3886.8	AF443112	C	BW
C.BW.00BW3891.6_AF44	00BW3891.6	AF443113	C	BW
C.BW.00BW3970.2_AF44	00BW3970.2	AF443114	C	BW
C.BW.00BW5031.1_AF44	00BW5031.1	AF443115	C	BW
C.BW.96BW01B21_AF11	96BW01B21	AF110960	C	BW
C.BW.96BW0407_AF11	96BW0407	AF110963	C	BW
C.BW.96BW0502_AF11	96BW0502	AF110967	C	BW
C.BW.96BW06.J4_AF29	96BW06.J4	AF290028	C	BW
C.BW.96BW11.06_AF11	96BW11.06	AF110970	C	BW
C.BW.96BW1210_AF11	96BW1210	AF110972	C	BW
C.BW.96BW15B03_AF11	96BW15B03	AF110973	C	BW
C.BW.96BW16.26_AF11	96BW16.26	AF110978	C	BW
C.BW.96BW17A09_AF11	96BW17A09	AF110979	C	BW
C.BW.96BWMO1.5_AF44	96BWMO1.5	AF443074	C	BW
C.BW.96BWMO3.2_AF44	96BWMO3.2	AF443075	C	BW
C.BW.98BWMC12.2_AF44	98BWMC12.2	AF443076	C	BW
C.BW.98BWMC13.4_AF44	98BWMC13.4	AF443077	C	BW
C.BW.98BWMC14.a3_AF44	98BWMC14.a3	AF443078	C	BW

C.BW.98BWMO14.10_AF44	98BWMO14.10	AF443079	C	BW
C.BW.98BWMO18.d5_AF44	98BWMO18.d5	AF443080	C	BW
C.BW.98BWMO36.a5_AF44	98BWMO36.a5	AF443081	C	BW
C.BW.98BWMO37.d5_AF44	98BWMO37.d5	AF443082	C	BW
C.BW.99BW3932.12_AF44	99BW3932.12	AF443083	C	BW
C.BW.99BW4642.4_AF44	99BW4642.4	AF443084	C	BW
C.BW.99BW4745.8_AF44	99BW4745.8	AF443085	C	BW
C.BW.99BW4754.7_AF44	99BW4754.7	AF443086	C	BW
C.BW.99BWMC16.8_AF44	99BWMC16.8	AF443087	C	BW
CRF01_AE.CF.90CF11697_	90CF11697	AF197340	CRF01_AE	CF
CRF01_AE.CF.90CF402_U5	90CF402	U51188	CRF01_AE	CF
CRF01_AE.CF.90CF4071_A	90CF4071	AF197341	CRF01_AE	CF
CRF01_AE.TH.93TH057_AF	93TH057	AF197338	CRF01_AE	TH
CRF01_AE.TH.93TH065_AF	93TH065	AF197339	CRF01_AE	TH
CRF01_AE.TH.93TH253_U5	93TH253	U51189	CRF01_AE	TH
CRF01_AE.TH.95TNIH047_	95TNIH047	AB032741	CRF01_AE	TH
CRF01_AE.TH.CM240_U547	CM240	U54771	CRF01_AE	TH
CRF01_AE.TH.TH022_AB03	TH022	AB032740	CRF01_AE	TH
CRF02_AG.SN.98SEMP1211	98SEMP1211	AJ251056	CRF02_AG	SN
CRF02_AG.FR.DJ263_AF06	DJ263	AF063223	CRF02_AG	FR
CRF02_AG.FR.DJ264_AF06	DJ264	AF063224	CRF02_AG	FR
CRF02_AG.GH.G829_AF184	G829	AF184155	CRF02_AG	GH
CRF02_AG.NG.IBNG_L3910	IBNG	L39106	CRF02_AG	NG
CRF02_AG.SE.SE7812_AF1	SE7812	AF107770	CRF02_AG	SE
CRF03_AB.RU.KAL153-2_A	KAL153-2	AF193276	CRF03_AB	RU
CRF03_AB.RU.RU98001_AF	RU98001	AF193277	CRF03_AB	RU
CRF04_cpx.CY.94CY032-3	94CY032-3	AF049337	CRF04_cpx	CY
CRF04_cpx.GR.97PVCH_AF	97PVCH	AF119820	CRF04_cpx	GR
CRF04_cpx.GR.97PVMY_AF	97PVMY	AF119819	CRF04_cpx	GR
CRF05_DF.BE.VI1310_AF1	VI1310	AF193253	CRF05_DF	BE
CRF05_DF.BE.VI961_AF07	VI961	AF076998	CRF05_DF	BE
CRF06_cpx.ML.95ML127_A	95ML127	AJ288982	CRF06_cpx	ML
CRF06_cpx.ML.95ML84_AJ	95ML84	AJ245481	CRF06_cpx	ML
CRF06_cpx.SN.97SE1078_	97SE1078	AJ288981	CRF06_cpx	SN
CRF06_cpx.AU.BFP90_AF0	BFP90	AF064699	CRF06_cpx	AU
CRF11_cpx.CM.97CM-MP81	97CM-MP818	AJ291718	CRF11_cpx	CM
CRF11_cpx.GR.GR17_AF17	GR17	AF179368	CRF11_cpx	GR
D.CD.84ZR085_U88822	84ZR085	U88822	D	CD
D.UG.94UG1141_U8882	94UG1141	U88824	D	UG
D.CD.ELI_K03454	ELI	K03454	D	CD
D.CD.NDK_M27323	NDK	M27323	D	CD
F1.BR.93BR020.1_AF0	93BR020.1	AF005494	F1	BR
F1.FI.FIN9363_AF075	FIN9363	AF075703	F1	FI
F1.FR.MP411_AJ24923	MP411	AJ249238	F1	FR
F1.BE.VI850_AF07733	VI850	AF077336	F1	BE
F2.CM.MP257_AJ24923	MP257	AJ249237	F2	CM
F2KU.BE.VI1126_AF07	VI1126	AF076475	F2KU	BE
G.NG.92NG083_U88826	92NG083	U88826	G	NG
G.BE.DRCBL_AF084936	DRCBL	AF084936	G	BE
G.SE.SE6165_AF06164	SE6165	AF061642	G	SE
H.CF.90CF056_AF0054	90CF056	AF005496	H	CF
H.BE.VI991_AF190127	VI991	AF190127	H	BE
H.BE.VI997_AF190128	VI997	AF190128	H	BE
J.SE.SE7022_AF08239	SE7022	AF082395	J	SE
J.SE.SE7887_AF08239	SE7887	AF082394	J	SE

K.CD.EQTB11C_AJ2492	EQTB11C	AJ249235	K	CD
K.CM.MP535_AJ249239	MP535	AJ249239	K	CM
N.CM.YBF30_AJ006022	YBF30	AJ006022	N	CM
O.SN.99SE-MP1299_ZX	SEMP1299	AJ302646	O	SN
O.SN.99SE-MP1300_ZX	SEMP1300	AJ302647	O	SN
O.CM.ANT70_L20587	ANT70	L20587	O	CM
O.CM.MVP5180_L20571	MVP5180	L20571	O	CM
U.CD.-.83CD0031	83CD0031	AF286236	U	CD

Table 11. HIV Gag Sequence Alignment

GCG Multiple Sequence File.

Written by Omega 1.1

Name: 00BW0762_1	SEQ	ID NO: 302	Len: 556	Check: 2513	Weight: 1.00
Name: 00BW0768_2	SEQ	ID NO: 303	Len: 556	Check: 8965	Weight: 1.00
Name: 00BW0874_2	SEQ	ID NO: 304	Len: 556	Check: 9574	Weight: 1.00
Name: 00BW1471_2	SEQ	ID NO: 305	Len: 556	Check: 5395	Weight: 1.00
Name: 00BW1616_2	SEQ	ID NO: 306	Len: 556	Check: 4692	Weight: 1.00
Name: 00BW1686_8	SEQ	ID NO: 307	Len: 556	Check: 7822	Weight: 1.00
Name: 00BW1759_3	SEQ	ID NO: 308	Len: 556	Check: 7777	Weight: 1.00
Name: 00BW1773_2	SEQ	ID NO: 309	Len: 556	Check: 9727	Weight: 1.00
Name: 00BW1783_5	SEQ	ID NO: 310	Len: 556	Check: 9681	Weight: 1.00
Name: 00BW1795_6	SEQ	ID NO: 311	Len: 556	Check: 9667	Weight: 1.00
Name: 00BW1811_3	SEQ	ID NO: 312	Len: 556	Check: 4422	Weight: 1.00
Name: 00BW1859_5	SEQ	ID NO: 313	Len: 556	Check: 7320	Weight: 1.00
Name: 00BW1880_2	SEQ	ID NO: 314	Len: 556	Check: 1603	Weight: 1.00
Name: 00BW1921_1	SEQ	ID NO: 315	Len: 556	Check: 883	Weight: 1.00
Name: 00BW2036_1	SEQ	ID NO: 316	Len: 556	Check: 2591	Weight: 1.00
Name: 00BW2063_6	SEQ	ID NO: 317	Len: 556	Check: 5152	Weight: 1.00
Name: 00BW2087_2	SEQ	ID NO: 318	Len: 556	Check: 5183	Weight: 1.00
Name: 00BW2127_2	SEQ	ID NO: 319	Len: 556	Check: 5469	Weight: 1.00
Name: 00BW2128_3	SEQ	ID NO: 320	Len: 556	Check: 9621	Weight: 1.00
Name: 00BW2276_7	SEQ	ID NO: 321	Len: 556	Check: 4153	Weight: 1.00
Name: 00BW3819_3	SEQ	ID NO: 322	Len: 556	Check: 4227	Weight: 1.00
Name: 00BW3842_8	SEQ	ID NO: 323	Len: 556	Check: 9312	Weight: 1.00
Name: 00BW3871_3	SEQ	ID NO: 324	Len: 556	Check: 501	Weight: 1.00
Name: 00BW3876_9	SEQ	ID NO: 325	Len: 556	Check: 773	Weight: 1.00
Name: 00BW3886_8	SEQ	ID NO: 326	Len: 556	Check: 2351	Weight: 1.00
Name: 00BW3891_6	SEQ	ID NO: 327	Len: 556	Check: 129	Weight: 1.00
Name: 00BW3970_2	SEQ	ID NO: 328	Len: 556	Check: 8768	Weight: 1.00
Name: 00BW5031_1	SEQ	ID NO: 329	Len: 556	Check: 3966	Weight: 1.00
Name: 96BW01B21	SEQ	ID NO: 330	Len: 556	Check: 602	Weight: 1.00
Name: 96BW0407	SEQ	ID NO: 331	Len: 556	Check: 9836	Weight: 1.00
Name: 96BW0502	SEQ	ID NO: 332	Len: 556	Check: 6402	Weight: 1.00
Name: 96BW06_J4	SEQ	ID NO: 333	Len: 556	Check: 254	Weight: 1.00
Name: 96BW11_06	SEQ	ID NO: 334	Len: 556	Check: 6801	Weight: 1.00
Name: 96BW1210	SEQ	ID NO: 335	Len: 556	Check: 6016	Weight: 1.00
Name: 96BW15B03	SEQ	ID NO: 336	Len: 556	Check: 6072	Weight: 1.00
Name: 96BW16_26	SEQ	ID NO: 337	Len: 556	Check: 9409	Weight: 1.00
Name: 96BW17A09	SEQ	ID NO: 338	Len: 556	Check: 2723	Weight: 1.00
Name: 96BWM01_5	SEQ	ID NO: 339	Len: 556	Check: 5051	Weight: 1.00
Name: 96BWM03_2	SEQ	ID NO: 340	Len: 556	Check: 496	Weight: 1.00
Name: 98BWMC12_2	SEQ	ID NO: 341	Len: 556	Check: 1164	Weight: 1.00
Name: 98BWMC13_4	SEQ	ID NO: 342	Len: 556	Check: 4961	Weight: 1.00
Name: 98BWMC14_a	SEQ	ID NO: 343	Len: 556	Check: 7351	Weight: 1.00
Name: 98BWM014_1	SEQ	ID NO: 344	Len: 556	Check: 288	Weight: 1.00
Name: 98BWM018_d	SEQ	ID NO: 345	Len: 556	Check: 6836	Weight: 1.00
Name: 98BWM036_a	SEQ	ID NO: 346	Len: 556	Check: 4386	Weight: 1.00
Name: 98BWM037_d	SEQ	ID NO: 347	Len: 556	Check: 6900	Weight: 1.00
Name: 99BW3932_1	SEQ	ID NO: 348	Len: 556	Check: 292	Weight: 1.00
Name: 99BW4642_4	SEQ	ID NO: 349	Len: 556	Check: 1347	Weight: 1.00
Name: 99BW4745_8	SEQ	ID NO: 350	Len: 556	Check: 7980	Weight: 1.00
Name: 99BW4754_7	SEQ	ID NO: 351	Len: 556	Check: 9892	Weight: 1.00
Name: 99BWMC16_8	SEQ	ID NO: 352	Len: 556	Check: 4279	Weight: 1.00
Name: A2_CD_97CD	SEQ	ID NO: 353	Len: 556	Check: 9920	Weight: 1.00
Name: A2_CY_94CY	SEQ	ID NO: 354	Len: 556	Check: 3070	Weight: 1.00
Name: A2D___97KR	SEQ	ID NO: 355	Len: 556	Check: 6350	Weight: 1.00
Name: A2G_CD_97C	SEQ	ID NO: 356	Len: 556	Check: 856	Weight: 1.00
Name: A_BY_97BL0	SEQ	ID NO: 357	Len: 556	Check: 9315	Weight: 1.00
Name: A_KE_Q23_A	SEQ	ID NO: 358	Len: 556	Check: 2442	Weight: 1.00

Name: A_SE_SE659	SEQ	ID NO: 359	Len: 556	Check: 8612	Weight: 1.00
Name: A_SE_SE725	SEQ	ID NO: 360	Len: 556	Check: 8315	Weight: 1.00
Name: A_SE_SE753	SEQ	ID NO: 361	Len: 556	Check: 2915	Weight: 1.00
Name: A_SE_SE853	SEQ	ID NO: 362	Len: 556	Check: 9112	Weight: 1.00
Name: A_SE_SE889	SEQ	ID NO: 363	Len: 556	Check: 8732	Weight: 1.00
Name: A_SE_UGSE8	SEQ	ID NO: 364	Len: 556	Check: 8696	Weight: 1.00
Name: A_UG_92UG0	SEQ	ID NO: 365	Len: 556	Check: 6290	Weight: 1.00
Name: A_UG_U455_	SEQ	ID NO: 366	Len: 556	Check: 164	Weight: 1.00
Name: AC_IN_2130	SEQ	ID NO: 367	Len: 556	Check: 8482	Weight: 1.00
Name: AC_RW_92RW	SEQ	ID NO: 368	Len: 556	Check: 977	Weight: 1.00
Name: AC_SE_SE94	SEQ	ID NO: 369	Len: 556	Check: 8752	Weight: 1.00
Name: ACD_SE_SE8	SEQ	ID NO: 370	Len: 556	Check: 9655	Weight: 1.00
Name: ACG_BE_VI1	SEQ	ID NO: 371	Len: 556	Check: 3777	Weight: 1.00
Name: AD_SE_SE69	SEQ	ID NO: 372	Len: 556	Check: 732	Weight: 1.00
Name: AD_SE_SE71	SEQ	ID NO: 373	Len: 556	Check: 8506	Weight: 1.00
Name: ADHK_NO_97	SEQ	ID NO: 374	Len: 556	Check: 5257	Weight: 1.00
Name: ADK_CD_MAL	SEQ	ID NO: 375	Len: 556	Check: 5301	Weight: 1.00
Name: AG_BE_VI11	SEQ	ID NO: 376	Len: 556	Check: 1610	Weight: 1.00
Name: AG_NG_92NG	SEQ	ID NO: 377	Len: 556	Check: 4188	Weight: 1.00
Name: AGHU_GA_VI	SEQ	ID NO: 378	Len: 556	Check: 8242	Weight: 1.00
Name: AGU_CD_Z32	SEQ	ID NO: 379	Len: 556	Check: 2601	Weight: 1.00
Name: AJ_BW_BW21	SEQ	ID NO: 380	Len: 556	Check: 8389	Weight: 1.00
Name: B_AU_VH_AF	SEQ	ID NO: 381	Len: 556	Check: 9166	Weight: 1.00
Name: B_CN_RL42_	SEQ	ID NO: 382	Len: 556	Check: 3865	Weight: 1.00
Name: B_DE_D31_U	SEQ	ID NO: 383	Len: 556	Check: 9464	Weight: 1.00
Name: B_DE_HAN_U	SEQ	ID NO: 384	Len: 556	Check: 6999	Weight: 1.00
Name: B_FR_HXB2_	SEQ	ID NO: 385	Len: 556	Check: 141	Weight: 1.00
Name: B_GA_OYI_	SEQ	ID NO: 386	Len: 556	Check: 7578	Weight: 1.00
Name: B_GB_CAM1_	SEQ	ID NO: 387	Len: 556	Check: 8023	Weight: 1.00
Name: B_GB_GB8_A	SEQ	ID NO: 388	Len: 556	Check: 2675	Weight: 1.00
Name: B_GB_MANC_	SEQ	ID NO: 389	Len: 556	Check: 8961	Weight: 1.00
Name: B_KR_WK_AF	SEQ	ID NO: 390	Len: 556	Check: 7372	Weight: 1.00
Name: B_NL_3202A	SEQ	ID NO: 391	Len: 556	Check: 7117	Weight: 1.00
Name: B_TW_TWCYS	SEQ	ID NO: 392	Len: 556	Check: 8767	Weight: 1.00
Name: B_US_BC_L0	SEQ	ID NO: 393	Len: 556	Check: 7091	Weight: 1.00
Name: B_US_DH123	SEQ	ID NO: 394	Len: 556	Check: 5049	Weight: 1.00
Name: B_US_JRCSF	SEQ	ID NO: 395	Len: 556	Check: 975	Weight: 1.00
Name: B_US_MNCG_	SEQ	ID NO: 396	Len: 556	Check: 688	Weight: 1.00
Name: B_US_P896_	SEQ	ID NO: 397	Len: 556	Check: 8809	Weight: 1.00
Name: B_US_RF_M1	SEQ	ID NO: 398	Len: 556	Check: 9306	Weight: 1.00
Name: B_US_SF2_K	SEQ	ID NO: 399	Len: 556	Check: 9799	Weight: 1.00
Name: B_US_WEAU1	SEQ	ID NO: 400	Len: 556	Check: 9636	Weight: 1.00
Name: B_US_WR27_	SEQ	ID NO: 401	Len: 556	Check: 3349	Weight: 1.00
Name: B_US_YU2_M	SEQ	ID NO: 402	Len: 556	Check: 8828	Weight: 1.00
Name: BF1_BR_93B	SEQ	ID NO: 403	Len: 556	Check: 7935	Weight: 1.00
Name: C_BR_92BR0	SEQ	ID NO: 404	Len: 556	Check: 4429	Weight: 1.00
Name: C_BW_96BW0	SEQ	ID NO: 405	Len: 556	Check: 1550	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 406	Len: 556	Check: 7158	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 407	Len: 556	Check: 6016	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 408	Len: 556	Check: 6072	Weight: 1.00
Name: C_ET_ETH22	SEQ	ID NO: 409	Len: 556	Check: 4314	Weight: 1.00
Name: C_IN_93IN1	SEQ	ID NO: 410	Len: 556	Check: 6959	Weight: 1.00
Name: C_IN_93IN9	SEQ	ID NO: 411	Len: 556	Check: 9362	Weight: 1.00
Name: C_IN_93IN9	SEQ	ID NO: 412	Len: 556	Check: 3298	Weight: 1.00
Name: C_IN_94IN1	SEQ	ID NO: 413	Len: 556	Check: 6744	Weight: 1.00
Name: C_IN_95IN2	SEQ	ID NO: 414	Len: 556	Check: 8559	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 415	Len: 556	Check: 4763	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 416	Len: 556	Check: 4315	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 417	Len: 556	Check: 3920	Weight: 1.00
Name: CRF01_AE_T	SEQ	ID NO: 418	Len: 556	Check: 5074	Weight: 1.00
Name: CRF01_AE_T	SEQ	ID NO: 419	Len: 556	Check: 4026	Weight: 1.00

Name:	CRF01_AE_T	SEQ	ID NO:	420	Len:	556	Check:	2981	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	421	Len:	556	Check:	6648	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	422	Len:	556	Check:	6948	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	423	Len:	556	Check:	6129	Weight:	1.00
Name:	CRF02_AG_F	SEQ	ID NO:	424	Len:	556	Check:	8134	Weight:	1.00
Name:	CRF02_AG_F	SEQ	ID NO:	425	Len:	556	Check:	8925	Weight:	1.00
Name:	CRF02_AG_G	SEQ	ID NO:	426	Len:	556	Check:	9991	Weight:	1.00
Name:	CRF02_AG_N	SEQ	ID NO:	427	Len:	556	Check:	9388	Weight:	1.00
Name:	CRF02_AG_S	SEQ	ID NO:	428	Len:	556	Check:	9371	Weight:	1.00
Name:	CRF02_AG_S	SEQ	ID NO:	429	Len:	556	Check:	3289	Weight:	1.00
Name:	CRF03_AB_R	SEQ	ID NO:	430	Len:	556	Check:	5554	Weight:	1.00
Name:	CRF03_AB_R	SEQ	ID NO:	431	Len:	556	Check:	5307	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	432	Len:	556	Check:	5488	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	433	Len:	556	Check:	6046	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	434	Len:	556	Check:	3807	Weight:	1.00
Name:	CRF05_DF_B	SEQ	ID NO:	435	Len:	556	Check:	6702	Weight:	1.00
Name:	CRF05_DF_B	SEQ	ID NO:	436	Len:	556	Check:	5563	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	437	Len:	556	Check:	8164	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	438	Len:	556	Check:	1975	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	439	Len:	556	Check:	1486	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	440	Len:	556	Check:	4050	Weight:	1.00
Name:	CRF11_cpx	SEQ	ID NO:	441	Len:	556	Check:	1515	Weight:	1.00
Name:	CRF11_cpx	SEQ	ID NO:	442	Len:	556	Check:	9474	Weight:	1.00
Name:	D_CD_84ZR0	SEQ	ID NO:	443	Len:	556	Check:	4739	Weight:	1.00
Name:	D_CD_ELI_K	SEQ	ID NO:	444	Len:	556	Check:	8533	Weight:	1.00
Name:	D_CD_NDK_M	SEQ	ID NO:	445	Len:	556	Check:	6100	Weight:	1.00
Name:	D_UG_94UG1	SEQ	ID NO:	446	Len:	556	Check:	7681	Weight:	1.00
Name:	F1_BE_VI85	SEQ	ID NO:	447	Len:	556	Check:	8540	Weight:	1.00
Name:	F1_BR_93BR	SEQ	ID NO:	448	Len:	556	Check:	241	Weight:	1.00
Name:	F1_FI_FIN9	SEQ	ID NO:	449	Len:	556	Check:	7510	Weight:	1.00
Name:	F1_FR_MP41	SEQ	ID NO:	450	Len:	556	Check:	9846	Weight:	1.00
Name:	F2_CM_MP25	SEQ	ID NO:	451	Len:	556	Check:	1247	Weight:	1.00
Name:	F2KU_BE_VI	SEQ	ID NO:	452	Len:	556	Check:	2186	Weight:	1.00
Name:	G_BE_DRCBL	SEQ	ID NO:	453	Len:	556	Check:	8049	Weight:	1.00
Name:	G_NG_92NG0	SEQ	ID NO:	454	Len:	556	Check:	254	Weight:	1.00
Name:	G_SE_SE616	SEQ	ID NO:	455	Len:	556	Check:	6407	Weight:	1.00
Name:	H_BE_VI991	SEQ	ID NO:	456	Len:	556	Check:	808	Weight:	1.00
Name:	H_BE_VI997	SEQ	ID NO:	457	Len:	556	Check:	4749	Weight:	1.00
Name:	H_CF_90CF0	SEQ	ID NO:	458	Len:	556	Check:	4718	Weight:	1.00
Name:	J_SE_SE702	SEQ	ID NO:	459	Len:	556	Check:	2564	Weight:	1.00
Name:	J_SE_SE788	SEQ	ID NO:	460	Len:	556	Check:	2692	Weight:	1.00
Name:	K_CD_EQTB1	SEQ	ID NO:	461	Len:	556	Check:	6586	Weight:	1.00
Name:	K_CM_MP535	SEQ	ID NO:	462	Len:	556	Check:	3803	Weight:	1.00
Name:	N_CM_YBF30	SEQ	ID NO:	463	Len:	556	Check:	8603	Weight:	1.00
Name:	O_CM_ANT70	SEQ	ID NO:	464	Len:	556	Check:	365	Weight:	1.00
Name:	O_CM_MVP51	SEQ	ID NO:	465	Len:	556	Check:	9160	Weight:	1.00
Name:	O_SN_99SE	SEQ	ID NO:	466	Len:	556	Check:	9380	Weight:	1.00
Name:	O_SN_99SE	SEQ	ID NO:	467	Len:	556	Check:	8796	Weight:	1.00
Name:	U_CD_83C	SEQ	ID NO:	468	Len:	556	Check:	4633	Weight:	1.00

//

SEQ	ID	NO		1					50
302	00BW0762_1		MGARASILRG	.EKLDKWEKI	RLRPGGRKHY	MIKHIVWASR	ELERFALNPG		
303	00BW0768_2		MGARASVLRG	.EKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG		
304	00BW0874_2		MGARASILRG	.GKLDTWEEKI	RLRPGGKKQY	MIKHLVWASR	ELERFALNPG		
305	00BW1471_2		MGARASILRG	.GKLDTWEEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG		
306	00BW1616_2		MGARASILRG	.GKLDEWEKI	RLRPGGKKRY	MMKHLVWASR	ELERFALNPG		
307	00BW1686_8		MGARASILRG	.GKLDTWEEKI	RLRPGGKKHY	MIKHLVWASR	ELERFALNPG		
308	00BW1759_3		MGARASILRG	.GKLDKWERI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG		
309	00BW1773_2		MGASASILRG	.GKLDKWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNSG		

310	00BW1783_5	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MMKHLVWASR	ELERFALNPG
311	00BW1795_6	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MMKHLVWASR	ELERFALNPG
312	00BW1811_3	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
313	00BW1859_5	MGARASVLKG	.EKLDWEKI	RLRPGEKKGY	MLKHLVWASR	ELERFALNPG
314	00BW1880_2	MGARASILRG	.GKLDKWERI	RLRPGGKKQY	MIKHLVWASR	ELERFALNPG
315	00BW1921_1	MGARASILRG	.GKLDTWEKI	RLRPGGKKRY	MLKHLIWTSR	ELERFALNPD
316	00BW2036_1	MGARASILRG	.EKLDTWERI	KLRPGGKKHY	MLKHLVWASR	ELERFALNPG
317	00BW2063_6	MGARASILRG	.GKLDKWEKI	RLRPGGKKQY	MIKHLVWASR	ELERFALNPG
318	00BW2087_2	MGARASILRG	.GKLDTWEKI	KLRPGGKKSY	KLKHLVWASR	ELERFALNPS
319	00BW2127_2	MGARASILRG	XEKLDWEKI	RLRPGGRKKY	RLKHLVWASR	ELENFALNPG
320	00BW2128_3	MGARASILRG	.GQLDKWEKI	RLRPGGKKHY	MLKHLVWASG	ELEKFALNPG
321	00BW2276_7	MGARASVLKG	.DKLDAWEKI	KLRPGGKKHY	MLKHLVWASR	ELERFALNPG
322	00BW3819_3	MGARASILRG	.GKLDAWERT	RLRPGGKKHY	RLKHLVWASR	ELERFALNPG
323	00BW3842_8	MGARASVLRG	.EKLDTWERI	KLRPGGKKHY	MLKHIVWASR	ELERFALNPG
324	00BW3871_3	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
325	00BW3876_9	MGARASILKG	.GKLDTWEKI	RLRPGGKKHY	MVKHLVWASR	ELERFALNPG
326	00BW3886_8	MGARASILRG	.GKLDKWEKI	RLRPGGKKCY	MIKHIIWASR	ELERFALNPG
327	00BW3891_6	MGARASILRG	.GKLDKWEKI	RLRPGGKKKY	MLKHLVWASR	ELERFALNSG
328	00BW3970_2	MGARASILRG	.GKLDAWERI	KLRPGGKKHY	MLKHLVWASR	ELERFALNPS
329	00BW5031_1	MGARASILRG	.GKLDRWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
330	96BW01B21	MGARASILRG	.GKLDQWEKI	RLRPGGKKCY	MLKHLVWASR	ELERFALNPG
331	96BW0407	MGARASILRG	.GKLDAWERI	RLRPGGKKCY	MMKHLVWASR	ELEKFALNPG
332	96BW0502	MGARASILRG	.EKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELEGFALNPG
333	96BW06_J4	MGARASILRG	.GNLDTWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
334	96BW11_06	MGARASILRG	.GKLDKWEKI	RLRPGGKKRY	MIKHLVWASR	ELERFALNPG
335	96BW1210	MGARASILRG	.EKLDTWEKI	RLRPGGKKRY	MMKHLVWASR	ELENFALNPA
336	96BW15B03	MGARASISRG	.EKLDTWEKI	RSRPGGKKCY	MLKHIVWASR	ELERFALNPG
337	96BW16_26	MGARASILRG	.GKLDKWEKI	RLRPGGKKRY	MLKHLVWASR	ELERFALNPG
338	96BW17A09	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
339	96BWM01_5	MGARASILRR	.GKLDKWEKI	RLRPGGKKRY	MIKHLVWASR	ELERYALNPG
340	96BWM03_2	MGARASILRG	.EKLDKWEKI	RLRPGGKKHY	MLKHIVWASR	ELEKFALNPG
341	98BWMC12_2	MGARASILRG	.EKLDTWEKI	RLRPGGKKQY	RIKHLVWASR	ELDRFALNSG
342	98BWMC13_4	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MMKHLVWASR	ELGRFALNPG
343	98BWMC14_a	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
344	98BWM014_1	MGARASILRG	.GKLDKWERI	RLRPGGKKQY	RLKHLVWASR	ELERFALNPG
345	98BWM018_d	MGARASILRG	.GKLDTWERI	KLRPGGKKHY	MMKHLVWASR	ELERFALNPS
346	98BWM036_a	MGARASILRG	.GKLDTWEKI	RLRPGGKKPY	MLKHLVWASR	ELERFALNPG
347	98BWM037_d	MGARASILRG	.GKLDWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
348	99BW3932_1	MGARASILRG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPE
349	99BW4642_4	MGARASVLKG	.EKLDTWEKI	RLRPGGRKKY	MLKHLVWASR	ELERFALNPG
350	99BW4745_8	MGARASILRG	.GKLGWERI	KLRPGGRKTY	MLKHLVWASR	ELERFALNPS
351	99BW4754_7	MGARASILRG	.EKLDWEKI	WLRPGGKNHY	MLKHLVWASR	ELERFALNPA
352	99BWMC16_8	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MIKHLVWASR	ELERFALNPG
353	A2_CD_97CD	MGARASVLSG	.GKLEAWEKI	RLRPGGKKKY	RLKHLVWASR	ELEKFSINPS
354	A2_CY_94CY	MGARASILSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELEKFSINPG
355	A2D___97KR	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
356	A2G_CD_97C	..ARASILSG	.GKLEAWEKI	RLRPGGKKKY	RLKHLVWASR	ELEKFSINPG
357	A_BY_97BL0	XGARASVLSG	.GKLDA_EKI	RLRPXGKKKY	RIKHLVWASR	ELERFALNPG
358	A_KE_Q23_A	MGARASVLSG	.GKFDAWEKI	RLRPGGKKKY	RMKHLIWASR	ELDRFALNPS
359	A_SE_SE659	...RASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
360	A_SE_SE725	...RASVLSG	.GKLDWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFALNPS
361	A_SE_SE753	MGARASVLSG	.GKLDWEKI	RLRPGGKKQY	RLKHLVWASR	ELERFALNPS
362	A_SE_SE853	...RASVLSG	.GRLDWEKI	RLRPGGKKKY	RMKHLVWASR	ELDRFALNPS
363	A_SE_SE889	...RASKLSG	.EKKDAWEKM	RLRPGGKKKY	KLKHMVWARR	ELEKSALNPS
364	A_SE_UGSE8	MGARASVLSG	.GKLDWEKI	RLRPGGNKKY	RLKHLVWASR	ELEKFALNPG
365	A_UG_92UG0	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
366	A_UG_U455_	MGARASVLSG	.KKLDSWEKI	RLRPGGNKKY	RLKHLVWASR	ELEKFTLNPG
367	AC_IN_2130	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MIKHLVWASR	ELERFALNPG
368	AC_RW_92RW	MGARASILRG	.GKLDWEKI	KLKPGGKKTY	MMKHLVWASR	ELERFALNPD
369	AC_SE_SE94	...RASVLSG	.GKLDWEKI	RLRPGGKKKY	RMKHLVWASR	ELDRFALNPS
370	ACD_SE_SE8	MGARASILSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELDRFALNPS

371	ACG_BE_VI1	MGARASVLTG	.GKLDTWERI	RLRPAGKKKY	RMKLLVWASR	ELERFAINPG
372	AD_SE_SE69	MGARASVLSG	.ERLDEWEKI	QLRPGGKKRY	RLKHIVWASR	ELERFALNPG
373	AD_SE_SE71	...RASVLSG	.GKLDaweKI	RLRPGGRKKY	KLKHIVWASR	ELERFALNPS
374	ADHK_NO_97	MGARASILSG	.GKLDKWEKI	RLRPGGKKQY	RLKHLVWASR	ELDRFALNPS
375	ADK_CD_MAL	MGARASVLSG	.GKLDaweKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
376	AG_BE_VI11	MGARASVLSG	.GKLDaweKI	RLRPGGKKKY	RMKHLVWASR	ELERFAINPG
377	AG_NG_92NG	MGARASVLSG	.GKLDaweKI	RLRPGGKKKY	RMKHLVWASR	ELERFALNPD
378	AGHU_GA_VI	MGARASILSG	.GKLDaweKI	RLRPGGKKKY	QIKHIVWASR	ELERFALNPG
379	AGU_CD_Z32	MGARASVLSG	.GKLDKWEKI	RLRPGGKKQY	KLKHIVWASR	ELERFALNPG
380	AJ_BW_BW21	MGARASVLSG	.GKLDaweKI	RLRPGGKKQY	RMKHLVWASR	ELERFALNPG
381	B_AU_VH_AF	MGARASVLSG	.GELDRWEKI	RLRPGGKKTY	KLKHIVWASR	ELERFAVNPG
382	B_CN_RL42	MGARASVLSG	.GQLDRWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFAVNPG
383	B_DE_D31_U	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	RLKHIVWASR	ELERFAVNPG
384	B_DE_HAN_U	MGARASVLSG	.GELDKWEKI	RLRPGGKKKY	QLKHIVWASR	ELERFAVNPG
385	B_FR_HXB2	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPG
386	B_GA_OYI	MGARASVLSG	.GELDKWEKI	RLRPGGKKKY	QLKHIVWASR	ELERFAINPG
387	B_GB_CAM1	MGARASVLSG	.GELDKWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPG
388	B_GB_GB8_A	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	RLKHVVWASR	ELERFAVNPG
389	B_GB_MANC	MGARASVLSG	.GKLDREWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFTVNLG
390	B_KR_WK_AF	MGARASILSG	.GELDQWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFAVNPG
391	B_NL_3202A	MGARASVLSG	.GELDKWEKI	RLRPGGKKRY	KLKHIVWASR	ELERFAVNPG
392	B_TW_TWCYS	MGARASILSA	.GELDKWERY	RLRPGGKKKY	RLKHLVWASR	ELERFAVNPG
393	B_US_BC_L0	MGARASVLSG	.GKLDKWEKI	RLRPGGKKKY	KLKHLVWASR	ELERFAVNPG
394	B_US_DH123	MGARASVLSG	.GKLDSWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPG
395	B_US_JRCFS	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	RLKHIVWASR	ELERFAVNPG
396	B_US_MNCG	MGARASVLSG	.GELDRWENI	RLRPGGKKKY	KLKHVVWASR	ELERFAVNPG
397	B_US_P896	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPS
398	B_US_RF_M1	MGARASVLSG	.GKLDKWEKI	RLRPRGKKRY	KLKHIVWASR	ELERFAVNPS
399	B_US_SF2_K	MGARASVLSG	.GELDKWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPG
400	B_US_WEAU1	MGARASVLSG	.GELDRWEKI	RLRPGGNKKY	KLKHIVWASR	ELERFAVNPG
401	B_US_WR27	MGARASMLSG	.GELDKWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFAVNPG
402	B_US_YU2_M	MGARASVLSA	.GELDKWEKI	RLRPGGKKQY	RLKHIVWASR	ELERFAVDPG
403	BF1_BR_93B	MGARASVISG	.GELDKWEKI	RLRPGGHKKY	RLKHIVWASR	ELERFAVNPG
404	C_BR_92BR0	MGARASILRG	.GKLDawERI	KLKPGGKKHY	MMKHLVWASR	ELERFALDPG
405	C_BW_96BW0	MGARASILRG	.GKLDaweKI	RLRPGGKKQY	RIKHLVWASR	ELERFALNPG
406	C_BW_96BW1	MGARASILRG	.GKLDTWeki	RLRPGGKKRY	MIKHLVWASR	ELERFALNPG
407	C_BW_96BW1	MGARASILRG	.EKLDTWeki	RLRPGGKKRY	MMKHLVWASR	ELENFALNPA
408	C_BW_96BW1	MGARASISRG	.EKLDTWeki	RSRPGGKKCY	MLKHIVWASR	ELERFALNPG
409	C_ET_ETH22	MGARASILRG	.EKLDaweKI	KLKPGGKKHY	MLKHLVWANR	ELEKFALNPD
410	C_IN_93IN1	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
411	C_IN_93IN9	MGARASILRG	.EKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELDRFALNPG
412	C_IN_93IN9	MGARASILRG	.EKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELDRFALNPG
413	C_IN_94IN1	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELEKFALNPG
414	C_IN_95IN2	MGARASILRG	.GKLDKWEKI	RLRPGGKKRY	MLKHLVWASR	ELDRFAVNPG
415	CRF01_AE_C	MGARASVLSG	.GKLDaweKI	RLRPGGKKKY	RMKHLVWASR	ELERFALNPG
416	CRF01_AE_C	MGARASILSG	.GKLDaweKI	RLRPGGKKQY	RMKHLVWASR	ELERFALNPG
417	CRF01_AE_C	MGARASVLSG	.GKLDaweKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
418	CRF01_AE_T	MSARASVLSG	.EKLNAWEKI	RLRPGGRKKY	KLKHLVWASR	ELEKFALNPG
419	CRF01_AE_T	MGARASVLSG	.KLDaleKI	RLRPGGKKKY	KMKHLVWASR	ELERFALNPG
420	CRF01_AE_T	MGARASVLSG	.GKLDaweKI	RLRPGGKKKY	KMKHLVWASR	ELERFALNPG
421	CRF01_AE_T	MGAKASVLSG	.GKLDaweKI	RLRPGGRKKY	HLKHIVWASR	ELERFALNPG
422	CRF01_AE_T	MGARASVLSG	.GKLDaweKI	RLRPGGRKKY	RLKHLVWASR	ELERFALNPS
423	CRF01_AE_T	MGARASILSG	.GKLDaweKI	RLRPGGRKKY	RMKHLVWASR	ELERFALNPG
424	CRF02_AG_F	MGARASVLSG	.GKLDSWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
425	CRF02_AG_F	MGARASVLSG	.GKLDSWEKI	RLRPAGKKKY	RLKHLVWASR	ELERFALNPG
426	CRF02_AG_G	MGARVSVLRG	.GQLDTWEKI	RLRPGGKKKY	KMKLLVWASR	ELERFAVNPG
427	CRF02_AG_N	MGARASVLSG	.GKLDaweKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
428	CRF02_AG_S	MGARASVLSG	.GKLDaweKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
429	CRF02_AG_S	.GARASVLSG	.GKLDawERI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
430	CRF03_AB_R	MGARASVLSG	.GKLDaweKI	RLRPGGKEY	RIKHLVWASR	ELERFALNPS
431	CRF03_AB_R	MGARASVLSG	.GKLDaweKI	RLRPGGKKKY	RIKHLVWASR	ELERFAINPS

432	CRF04_cpx_	MGARASVLSG	.GKLDAWERI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
433	CRF04_cpx_	MGARASVLSG	.GKLDAWERI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
434	CRF04_cpx_	MGARASVLSG	.GRLDAWEKI	RLRPGGKKRY	RIKHLIWASR	ELERFALNPG
435	CRF05_DF_B	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
436	CRF05_DF_B	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RLKHIVWASR	ELERFALNPG
437	CRF06_cpx_	MGARASVLSG	.GKLDEWEKI	RLRPGGKKKY	KMKHLVWASR	ELERFALNPG
438	CRF06_cpx_	MGARASVLSG	.GKLDEWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
439	CRF06_cpx_	MGARASVLSG	.GKLDEWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFALNPG
440	CRF06_cpx_	MGARASVLSG	.GKLDEWEKI	RLRPGGKKKY	RLKHLVWASR	ELDRFALNPG
441	CRF11_cpx_	MGARASVLSG	.GKLDSWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
442	CRF11_cpx_	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
443	D_CD_84ZR0	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFALNPG
444	D_CD_ELI_K	MGARASVLSG	.GKLDKWEKI	RLRPGGKKKY	RLKHIVWASR	ELERYALNPG
445	D_CD_NDK_M	MGARASVLSG	.GKLDTWERI	RLRPGGKKKY	ALKHLIWASR	ELERFTLNPG
446	D_UG_94UG1	MGARASVLSG	.GKLDEWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
447	F1_BE_VI85	MGARASILSG	.GKLDEWEKI	QLRPGGKKRY	KMKHLIWASR	ELERFALDPG
448	F1_BR_93BR	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALDPG
449	F1_FI_FIN9	MGARASVLSG	.GKLDAWEKI	RLRPGGKKQY	RIKHLVWASR	ELERFAIDPG
450	F1_FR_MP41	MGARASVLSG	.GKLDAWERI	RLRPGGKKKY	RMKHLVWASR	ELERFAVDPG
451	F2_CM_MP25	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RLKHIVWASR	ELKRFALNPG
452	F2KU_BE_VI	MGARASVLSG	.GKLDSWEKI	RLRPGGRKKY	RLKHLVWASR	ELERFALNPG
453	G_BE_DRCBL	MGARASVLSG	.GKLDAWEKI	RLRPGGKKRY	RMKHLVWASR	ELDRFALNPG
454	G_NG_92NG0	VGARASVLSG	.GKLDSWEKI	RLRPGGRKKY	KLKHIVWASR	ELGRFALNRD
455	G_SE_SE616	MGARASVLTG	.GKLDAWEKI	RLRPGGRKSY	KIKHLVWASR	ELERFALNPD
456	H_BE_VI991	MGARASVLSG	.GKLDAWEKI	RLRPGGRKKY	RLKHLVWASR	ELERFALNPD
457	H_BE_VI997	MGARASVLSG	.GRLDTLEKI	RLRPGGKKKY	RLKHIVWASR	ELERFALNPG
458	H_CF_90CF0	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
459	J_SE_SE702	MGARASILSG	.GKLDDWEKI	RLRPGGKKQY	RIKHLVWASR	ELDRFALNPG
460	J_SE_SE788	MGARASILSG	.GKLDDWEKI	RLRPGGKKKY	RIKHLVWASR	ELDRFALNPG
461	K_CD_EQTB1	MGARASVLSG	.GKLDKWEKI	QLRPGGKKKY	RLKHLVWASR	ELERFALNPN
462	K_CM_MP535	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	KLKHLVWASR	ELERFALNPG
463	N_CM_YBF30	MGARASVLTG	.GKLDQWESI	YLRPGGKKKY	RMKHLVWASR	ELERFACNPG
464	O_CM_ANT70	MGASASVLTG	.SKLDAWEKI	RLKPGSKKKY	RLKHLVWASR	ELERFACNPE
465	O_CM_MVP51	MGARASVLTG	.SKLDAWEKI	RLRPGSKKKY	RLKHLVWASR	ELERYACNPG
466	O_SN_99SE_	MGARASVLTG	.SKLDAWEKI	RLKPGCKKKY	RLKHLVWASR	ELDRSACNPE
467	O_SN_99SE_	MGARASVLSG	.SKLDTWEKI	RLKPGCKKKY	RLKHLVWASR	ELERFACNPE
468	U_CD___83C	MGARASVLSG	.GKLDAWEKI	RLRPGGRKKY	RLKHLVWASR	ELEKFAINPG

51

100

00BW0762_1	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLY	NTVATLYCVH	KKIDVRDTKE
00BW0768_2	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATPYCVH	EKIEVRDTKE
00BW0874_2	LLETAEGCRQ	IIKQLHPALQ	TGTEELRSLY	NTVATLYCVH	RGIEVRDTKE
00BW1471_2	LLETADGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATLYCVH	KGIQVQDTKE
00BW1616_2	LLETSDGCKQ	IMKQLQPALQ	TGTEELKSLF	NTVATLYCVH	ANIDVRDTKE
00BW1686_8	LLETSDGCKQ	IIQQLQPALK	TGTEELRSLF	NTVATLYCAH	KGISIQDTKE
00BW1759_3	LLETAEGCKR	IIKQLQPALQ	TGTEELKSLH	NTVATLYCVH	KEIDVRDTKE
00BW1773_2	LLETAEGCKQ	IIKQLQPALQ	TGTEELKSLY	NTVATLYCVH	AGIEVRDTKE
00BW1783_5	LLETSEGCKQ	IIQQLQPALK	TGTEELRSLY	NTVATLYCVH	AKIEVRDTKE
00BW1795_6	LLETSEGCKQ	IMKQLQPAIQ	TGTEELRSLF	NTVATLYCVH	EGIDVQDTKE
00BW1811_3	LLETAAGCKQ	IIROLHPALQ	TGTEELRSLY	NTVATLYCVH	AEIEVRDTKE
00BW1859_5	LLETSEGCRQ	IMRQLQPALQ	TGTEELRSLF	NTVATLYCVH	EKIPVRDTKE
00BW1880_2	LLETAEGCKQ	IIROLHPALQ	TGTQELRSLY	NTVATLYCVH	KDIEVRDTKE
00BW1921_1	LLETSEGCKQ	IIQQLQPALQ	TGTEELRSLY	NTVATLYCVH	KGIEVQDTKE
00BW2036_1	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	KKIQVQDTKE
00BW2063_6	LLETADGCKQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	EGIDVRDTKE
00BW2087_2	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATLYCVH	KGIEVRDTKE
00BW2127_2	LLETSEGCRQ	IIKQLQPALQ	TGTEELRSLY	NTIATLYCAH	QRIQVQDTKE
00BW2128_3	LLETSEGCKQ	IIKQLHPALQ	TGTEELKSLY	NTVATLYCVH	AGIAVRDTKE
00BW2276_7	LLETSEGCKQ	IMQQLQPALK	TGTEELISLY	NTVATLYCVH	EKIQVQDTKE
00BW3819_3	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLY	NTVATLYCVH	QKIEIRDTEKE
00BW3842_8	LMETSEGCKQ	IIQQLQPALQ	TGTEELRSLF	NTIATLYCVH	KGIQVQDTKE

00BW3871_3	LLETSDGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATLYCVH	KGIKVQDTKE
00BW3876_9	LLETSEGCEQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	ARIEVKDTKE
00BW3886_8	LLETAEGCTQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	AGIDVQDTKE
00BW3891_6	LLETSDGCKQ	IIQQLQPALK	TGTEELRSLY	NTVATLYCVH	NNIEIRDTE
00BW3970_2	LLETSEGCKQ	IIKQLQPALQ	TGTEELKSLF	NTVATLYCVH	EKIEIRDTE
00BW5031_1	LLETADGCKQ	IIKQLQPALK	TGTEELRSLY	NTVATLYCVH	RNIEVQDTKE
96BW01B21	LLETSEGCKQ	IMEQLQPALQ	TGTEELKSLY	NTVATLYCVH	ENIEVRDTKE
96BW0407	LLETSEGCKQ	IIRQLHPALQ	TGSEELKSLF	NTVATLYCVH	EKIEVRDTKE
96BW0502	LLETAEGCKQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	AGIEVRDTKE
96BW06_J4	LLETSEGCKQ	IMQQLQPALQ	TGTEELRSLF	NTVATLYCVH	KGIKVQDTKE
96BW11_06	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	EGIEVQDTKE
96BW1210	LLETAEGCKQ	IMKQLQPALK	TGTEELKSLY	NTVATLYCVH	EKIEVRDTKE
96BW15B03	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	EKIKVQDTKE
96BW16_26	LLETSEGCRQ	IMIQLQPALK	TGTEELKSLY	NTVAVLFCVH	AGIEVQDTKE
96BW17A09	LLETAEGCKQ	IIKQLQPALQ	TGTEELKSLY	NTVATLYCVH	QGIEVRDTKE
96BWM01_5	LLETSEGCKQ	IIKQLQPTIQ	TGTEELKSLY	NTVATLYCVH	KGIDVRDTKE
96BWM03_2	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLY	NTVATLYCVH	EKIEVRDTKE
98BWMC12_2	LLETAEGCTQ	IMRQLQPALQ	TGTEELRSLY	NTVATLYCVL	KGIKVRDTKE
98BWMC13_4	LLETSEGCKQ	IMRQLQPAIQ	TGTEELRSLF	NTVATLYCVH	EGIDVKDTKE
98BWMC14_a	LLETSEGCCQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	MGIEVRDTKE
98BWM014_1	LLETAEGCKQ	IIQQLQPALK	TGTEELRSLF	NTVATLYWVH	KNVEVRDTKE
98BWM018_d	LLETSEGCRK	IMKQLQPSIQ	TGTEELRSLY	NTIATLYCVH	EKIEVRDTKE
98BWM036_a	LLETAEGCKQ	ILQQLQPALK	TGTEELKSLY	NTVATLYCVH	QGIEVRDTKE
98BWM037_d	LENSEGCKQ	IMKQLQPALQ	TGTEELKSLF	NTVATLYCVH	EKIEVRDTKE
99BW3932_1	LLETADGCKQ	IIKQLQPAFQ	TGTEELRSLY	NSIAVLYCVH	RRLTIQDTKE
99BW4642_4	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	ERIQVRDTKE
99BW4745_8	LLETTEGCRQ	IIRQLQPALQ	TGTEELKSLY	NTVATLYCVH	NNIEIRDTE
99BW4754_7	LLETAEGCKQ	IIKQLHPALQ	TGTEELRSLY	NTVATLYCVH	NKIEVQDTKE
99BWMC16_8	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLY	NTIATLYCVH	ESIEVRDTKE
A2_CD_97CD	LLETETGCRR	IFGQLQPALE	TGTEELRSLY	NTIAVLYFVH	QKIEVKDTKE
A2_CY_94CY	LLETPEGCRQ	IIRQLQPALQ	TGTEELKSLY	NTVVVLYWVH	QRVDVKDTKE
A2D_97KR	LLETSEGCKQ	IIGQLEPSIK	TGSEELKSLF	NAVVTLYCVH	QRIEVRDTKE
A2G_CD_97C	LLETAAGCRQ	ILGQLQPALQ	TGTEELRSLY	NTVAVLYCVH	QKIEVKDTKE
A_BY_97BL0	LLETSEGCCQ	ILEQLQPTLK	TGSEELKSLY	NTVATLYCVH	QRIEIKDTKE
A_KE_Q23_A	LLETADGCQQ	IMEKLQPALK	TGTEELKSLF	NTVATLYCVH	QRIDVKDTKE
A_SE_SE659	LLETTEGCQQ	IIEQQLPALN	TGTEELKSLF	NTVATLYCVH	QRIDVKDTKE
A_SE_SE725	LLETTEGCQQ	IMEQLQSALK	TGTEELRSLF	NTVAVLYCVH	QRIEIKDTKE
A_SE_SE753	LLETAEGCQQ	IMKQLQPALK	TGTEELRSLY	NTVATLYCVH	QRINVTDTKE
A_SE_SE853	LLETTEGCQQ	IIGQLQPAFK	TGTEELKSLY	NTVATLWCVH	QRIDVKDTKE
A_SE_SE889	LLETTEGCQQ	IMDKLQPALR	TGTEELRSLY	NTVATLYCVH	QKIAVKDTKE
A_SE_UGSE8	LLETAEGCQQ	IIEQQLSAPK	TGTEELRSLY	NTVATLYCVH	QRIDVKDTKE
A_UG_92UG0	LLETTEGCQQ	IMEQLQSALR	TGTEELRSLY	NTVATLYCVH	QRIEVRDTKE
A_UG_U455_	LLETAEGCQQ	ILGQLQPALQ	TGTEELRSLY	NTVAVLYCVH	QRIDVKDTKE
AC_IN_2130	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLH	NTVATLYCVH	AGIEIRDTE
AC_RW_92RW	LLETPEGCKQ	IMRQLQPALQ	TGTEELRSLY	NTVATLYCVH	QKIDVKDTKE
AC_SE_SE94	LLETSEGCCQ	ILEQLQPALK	TGTEELKSLF	NTVATLYCVH	QRIEVRDTKE
ACD_SE_SE8	LLETTEGCQQ	IMDQLQPALK	TGTEELRSLY	NTVATLWCVH	KRIDVKDTKE
ACG_BE_VI1	LLETAEGCQQ	IIEQQLSTLK	TGSEELKSLF	NTVATLWCVH	LRIEIKDTKE
AD_SE_SE69	LLETPEGCKQ	IMGQLQPAIQ	TGSEELKSLF	NTVATLYCVH	AKIKVTDTE
AD_SE_SE71	LLETTKGCQQ	IMEQLQPAFK	TGTEELKSLY	NTVATLYCVH	QQIEVKDTKE
ADHK_NO_97	LLETSEGCCQ	VMEQLQPALK	TGSEELKSLF	NLVAVLWCVH	QRIDVKDTKE
ADK_CD_MAL	LLETTEGCQQ	IMEQLQSTLK	TGSEELKSLY	NTVATLYCVH	QRIDVKDTKE
AG_BE_VI11	LLETAEGCQQ	IIEQQLSTLR	TGSEELKSLY	NTLATLWCVH	KKIEVRDTKE
AG_NG_92NG	LLETTEGCQQ	IMRQLQPSLQ	TGTEELKSLF	NTVATLYCVH	QRIEVRDTKE
AGHU_GA_VI	LLETAEGCQQ	IMEQLQSALK	TGSEELKSLF	NTVATLYCVH	QKIDVKDTKE
AGU_CD_Z32	LLETTEGCQQ	ILSQFQPALK	TGTEELRSLY	NTVATLYCVH	QNIEVKDTKE
AJ_BW_BW21	LLETAEGCQQ	IMEQLQSALK	TGSEELRSLY	NTVATLYCVH	QRIEVRDTKE
B_AU_VH_AF	LLETSEGCRQ	ILVQLQPSLP	TGSEELKSLF	NTVATLYCVH	QKIEIRDTE
B_CN_RL42_	LLETSEGCRQ	ILEQLQPALQ	TGSEELRSLF	NTVATLYCVH	LRIEIKDTKE
B_DE_D31_U	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLF	NTVATLYCVH	QRIEVRDTKE
B_DE_HAN_U	LLETSEGCRQ	IMGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QKIEVKDTKE

B_FR_HXB2_	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QRIEIKDTKE
B_GA_OYI_	LLETSEGCRQ	ILGQLQPSLK	TGSEEBIRSLY	NTVATLYCVH	QKIEVKDTKE
B_GB_CAM1_	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QKIDVKDTKE
B_GB_GB8_A	LLETSEGCRQ	ILEQLQPSLQ	TGSEERRSLF	NTVATLYCVH	QRIDVKDTKE
B_GB_MANC_	LLETSEGCRQ	ILVQLQPSLQ	TGSEELKSLY	NTVAVLYCVH	QGIEVKDTKE
B_KR_WK_AF	LLETSEGCRQ	ILGQLQPSLQ	TGSEELKSLF	NAVAVLYCVH	QRIEIKDTKE
B_NL_3202A	LLETAEGCRQ	ILGQLQPALQ	TGSEELRSLF	NTVAVLYCVH	QRIEIKDTKE
B_TW_TWCYS	LLETSEGCRQ	ILGQLQSSLQ	TGSEELRSLY	NTVATLYCIH	QKIEIKDTKD
B_US_BC_L0	LLETAEGCRQ	ILGQLQPSLQ	TGSEELKSLY	NTIAVLYCVH	QMIDVKDTKE
B_US_DH123	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	ERIEVKDTKE
B_US_JRCSF	LLESSEGCRQ	ILGQLQPSLK	TGSEELTSLY	NTVATLYCVH	QRIEIKDTKE
B_US_MNCG_	LLETSEGCRQ	ILGQLQPSLQ	TGSEELKSLY	NTVATLYCVH	QKIEIKDTKE
B_US_P896_	LLETSEGCRQ	ILGQLQSSLQ	TGSEELKSLY	NTVATLYCVH	QRIEIKDTKE
B_US_RF_M1	LLETAEGCRQ	ILGQLQPALQ	TGSEELKSLY	NAVATLYCVH	QNIEVRDTKE
B_US_SF2_K	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QRIDVKDTKE
B_US_WEAU1	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVAVLYCVH	QKIEVKDTKE
B_US_WR27_	LLETAEGCRQ	ILRQLQPSLQ	TGSEELRSLF	NTVATLYCVH	QRIGVKDTKE
B_US_YU2_M	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QKIEVKDTKE
BF1_BR_93B	LLETSEGCRQ	ILEQLQPALK	TGSEELRSLY	NTVATLYCVH	QKIDVKDTKE
C_BR_92BR0	LLETSEGCKQ	IMKQLQPALQ	TGTELISLH	NTVATLYCVH	EKIDVRDTKE
C_BW_96BW0	LLETSEGCKQ	IIQQLQPALQ	TGTEELRSLF	NTVATLYCVH	KKIEVRDTKE
C_BW_96BW1	LLGTSEGCKQ	IMKQLQPALQ	TGTEEBIRSLY	NTVATLYCVH	EGIEVQDTKE
C_BW_96BW1	LLETAEGCKQ	IMKQLQPALK	TGTEELKSLY	NTVATLYCVH	EKIEVRDTKE
C_BW_96BW1	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	EKIKVKDTKE
C_ET_ETH22	LLDTSAGCKQ	IIKQLQPALQ	TGTEELKSLF	NTVATLYCVH	QKIEIKDTKE
C_IN_93IN1	LLETAEGCKQ	IIKQLQPALQ	TGTEELKSLH	NTVATLYCVH	AGIEVRDTKE
C_IN_93IN9	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLH	NTVVTLYCVH	AGIEVRDTKE
C_IN_93IN9	LLEAAEGCKQ	IIKQLQPALQ	TGTEELRSLH	NTVATLYCVH	EGIEVRDTKE
C_IN_94IN1	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	AEIEVRDTKE
C_IN_95IN2	LLETAEGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATLYCVH	AGIEVRDTKE
CRF01_AE_C	LLETAEGCQQ	LIEQLQSNLK	TGSEEIKSLF	NTIATLWCVH	QRIDVKDTKE
CRF01_AE_C	LLETAEGCQQ	LIEQLQSTIK	TGSEELKSLF	NTIATLWCVH	QRIDVKDTKE
CRF01_AE_C	LLETAEGCQQ	LLEQLQSTLK	TGSEELKSLF	NTIATLWCVH	QRINVTDTKE
CRF01_AE_T	LLETAEGCQQ	LIEQLQSTLK	TGSEELKSLF	NTIATLWCVH	QKIEVKDTKK
CRF01_AE_T	LLETAEGCQQ	IIIEQLQSALK	TGSEELKSLY	NTVVTLWCVH	QRIDVKDTKE
CRF01_AE_T	LLETAEGCQQ	LIEQLQSTLK	TGSEELKSLY	NTIATLWCVH	QRIEIKDTKE
CRF01_AE_T	LLETAEGCQQ	LIEQLQSTLK	TGSEELRSLF	NTIVTLWCVH	QRIEIKDTKE
CRF01_AE_T	FLETAEGCQQ	IIIEQLQSTLK	TGLEELKSLF	NTVATLWCVH	QRIEIKDTKE
CRF01_AE_T	LLETAEGCQQ	LIGQLQSNLK	TGSEELRSLF	NTVATLWCVH	QRIEIKDTKE
CRF02_AG_F	LLETAEGCQQ	LIEQLQALG	TGSEELKSLY	NTIATLWCVH	KRIDIKDTKE
CRF02_AG_F	LLETAEGCQQ	LMKQLQSALG	TGSEELKSLY	NTIATLWCVH	QRIDIKDTKE
CRF02_AG_G	LLETTEGCQQ	ILEQLQPALG	AGSEELKSLY	NTVATLYCVH	QKIDVRDTKE
CRF02_AG_N	LLETAEGCQQ	LMEQLQSALR	TGSEELKSLF	NTIATLWCVH	QRIDIKDTKE
CRF02_AG_S	LLETAEGCQQ	LMEQLQSTLR	TGSEELKSLF	NTIATLWCVH	QRIDIKDTKE
CRF02_AG_S	LLETAEGCQQ	IIIEQLQSTLK	TGSEELKSLF	NTVATLYCVH	QRIEIKDTKE
CRF03_AB_R	LLETSEGCCQ	ILEQLQPTLK	TGSEELKSLY	NTVATLYCVH	QRIEIKDTKE
CRF03_AB_R	LLETSEGCCQ	ILEQLQPTLK	TGSEELKSLY	NTVATLYCVH	RRIEIKDTKE
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CRF04_cpx_	LLETAEGCQQ	LMEQLQPTLR	TGSEEVKSLF	NTLATLWCVH	QRIDVKDTKE
CRF04_cpx_	LLETAEGCQQ	LMEQLQSTLK	TGSEELKSLF	NLIATLWCVH	QRIEIKDTKE
CRF05_DF_B	LLETSEGCKQ	IIISQLQPAIQ	TGTEELKSLY	NTVATLYCVH	ERIEVKDTKE
CRF05_DF_B	LLETSEGCKQ	IIAQQLQPAIQ	TGSEELRSLY	NTVATLYCVH	EKIEVKDTKE
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CRF06_cpx_	LLETPEGCQQ	IMEQLQSTLR	TGSEELKSLY	NTVATLYCVH	QRIKVTDTKE
CRF06_cpx_	LLETAEGCQQ	IIIEQLQSALK	TGSEELRSLF	NTVATLYCVH	QRIKVTDTKE
CRF11_cpx_	LLETGEGCQQ	LMGQLQPALG	TGTEELRSLY	NTLATLYCVH	HRIEIKDTKE
CRF11_cpx_	LLETGEGCKQ	IMGQLQPALG	TGTEELRSLY	NTVAALYCVH	LRIEVKDTKE
D_CD_84ZR0	LLETSEGCKQ	IMEQLQPALK	TGSEELRSLY	NTVATLYCVH	KRIEIKDTKE
D_CD_ELI_K	LLETSEGCKQ	IIIGQLQPAIQ	TGTEELRSLY	NTVATLYCVH	KGIDVKDTKE
D_CD_NDK_M	LLETSEGCKQ	IIIGQLQPSIQ	TGSEEBIRSLY	NTVATLYCVH	ERIEVKDTKE

D_UG_94UG1	LLETSEGCRCQ	IIRQLQPSIQ	TGSEEIKSLY	NTVVTLYCVH	ERIKVASTKE
F1_BE_VI85	LLETSEGCQK	IIRQLQPSLQ	TGSEELKSLF	NTVAVLYYVH	QRAGVTDTK
F1_BR_93BR	LLETSEGCRK	IIGQLQPSLQ	TGSEELKSLY	NTIAVLYYVH	QKVEVKDTKE
F1_FI_FIN9	LLETSEGCQK	IIAQIQPSIQ	TGSEELRSLY	NTIAVLYFVH	QKIEVKDTKE
F1_FR_MP41	LLETPEGCKQ	IIRQLQPSLQ	TGSEELRSLF	NTVAVLYCVH	QKIEIKDTKE
F2_CM_MP25	LLETTEGCKK	IIGQLQPSLQ	TGSEELKSLF	NTIVVLYYVH	QKIEVRDTKE
F2KU_BE_VI	LLESANGCRQ	IIEQIQPALQ	TGSEELRSLF	NTVVTLYWVH	QRIEVKDTKE
G_BE_DRCBL	LLETAEGCQK	IMAQLQPALQ	TGTEEIKSLF	NTVATLYCVH	QKIEVRDTKE
G_NG_92NG0	LLETAEGCVQ	IMKQLQP.AL	TGTEELRSLF	NTVATLYCVH	QKIEVKDTKE
G_SE_SE616	LLETAEGCQQ	IMRQLQPSLQ	TGTEEIKSLY	NAVATLYCVH	QRIEVKDTKE
H_BE_VI991	LLETADGCQQ	ILGQLQPALQ	TGTEDLQSLY	NTIAVLYCVH	QRIDVKDTKE
H_BE_VI997	LLESAEGCLQ	IIEQLRPSIK	TGTEELXSLF	NTVATLYCVL	QRIEVKDTKE
H_CF_90CF0	LLETPEGCLQ	IIEQIQPAIK	TGTEELKSLF	NLVAVLYCVH	RKIDVKDTKE
J_SE_SE702	LLESAKGCQQ	ILVQLQPALQ	TGTEEIKSLY	NTVATLYCVH	QRIEIKDTKE
J_SE_SE788	LLESAKGCQQ	ILVQLQPALQ	TGTQEIKSLY	NTVATLYCVH	QRIEIKDTME
K_CD_EQTB1	LLETVEGCRQ	IIRQLQPSLQ	TGSEELRSLF	NTVATLYWVH	QSIQVRDTKE
K_CM_MP535	LLETTEGCRQ	IITQIQPSIQ	TGSEEIKSLY	NTIAVLYFVH	QKIEVKDTKE
N_CM_YBF30	LMDTADGCAK	LLNQLEPALK	TGSEELRSLY	NALAVLYCVH	SRIQIHNTQE
O_CM_ANT70	LLETAEGNEK	LLQQLEPALK	TGSDSLQSLW	NAIVVLWCVH	NRYKIGDTQQ
O_CM_MVP51	LLETAEGTEQ	LLQQLEPALK	TGSEDLKSLW	NAIAVLWCVH	NRFDIRDRTQQ
O_SN_99SE_	LLETAEGNEK	LLQQLEPALK	TGSESLQSLW	NTIAVLWCVH	NRIKVEDTQQ
O_SN_99SE_	LLETAEGNEE	LLQQLEPALK	TGSESLQSLW	NTIAVLWCVH	KRFKVEDTQQ
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	101			150
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00BW0874_2	ALDKIEKEQNESQQ	KTQQAKAADG	K..... VSQNYPIVQN
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00BW1783_5	ALDKIEEEQN	KCQQK.....	.TQQAECTQQ	AGAA...GGK VSQNYPIVQN
00BW1795_6	ALDKVEEEQN	KSQQ.....	KMQQAEEADK	KVS..... ..QNYPIVQN
00BW1811_3	ALDKIEEEQN	KSQQK.....	.TQQAQEATA	TG.....K VSQNYPIVQN
00BW1859_5	ALDKIEEEQN	KCQQ.....	KTQQTEAAAG	K..... VSQNYPIVQN
00BW1880_2	ALDKIEEEQN	KSQQK.....	.AQQAEEADK	Q..... VSQNYPIVQN
00BW1921_1	ALDKIEEEQN	KSQQ.....	KTQQAEEAAAG	K..... VSQNYPIVQN
00BW2036_1	ALDKIEEEQN	TCQQ.....	KTQQAEEAAAG	K..... ISQNYPIVQN
00BW2063_6	ALDKIEEEQK	KSQQ.....	KTQQAEEADK	KVS..... ..QNYPIVQN
00BW2087_2	ALDKIEEEQN	KCQQK.....	.TQQAKAADK	G.....E VSQNYPIVQN
00BW2127_2	ALDEIEEEQN	KCQQK.....	.AQQEKATDGK VSQNYPIVQN
00BW2128_3	ALDKIEEEQN	KIQQK.....	.TQQAKEADKK VSQNYPIVQN
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00BW3871_3	ALDKIEEEQN	KSQQ.....	KTQQAEEAAE	K..... VSQNYPIVRN
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00BW3886_8	ALDKIEEEQN	KSQQK.....	.TQQAQAADKK VSQNYPIVQN
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00BW3970_2	ALDKIEEEQK	KSQQK.....	.TQQAKAADG	KI.....S ..QNYPIVQN
00BW5031_1	ALDKVEEEQN	NCQQK.....	.TQQAEEAAGGK ISQNYPIVQN
96BW01B21	ALDKIEEEQN	KSQQK.....	.TQQAKTDD.	.G.....K ISPNYPIVQN
96BW0407	ALDKIEEEQN	KCQQK.....	.IQQAEEADK	G.....K VSQNYPIVQN
96BW0502	ALDKIEEEQN	KSQQK.....	.TQQAKEADG	K..... VSQNYPIVQN
96BW06_J4	ALDKIEEEQN	KSQQ.....	KTQQAEEAAAG	K..... VSQNYPIVQN
96BW11_06	AVDKIEEEQN	KSQQ.....	KTQQAEEADK	KVS..... ..QNYPIVQN
96BW1210	ALDKIEEEQN	KCQQK.....	.EQQAEEAAK	G.....K VSQNYPIVQN
96BW15B03	ALDKIEEEQN	KSQE.....	KTQQAEEAAAG	K..... ISQNYPIVQN
96BW16_26	ALDKIEEEQN	KSQQK.....	.TQQAKEATG	K..... VSQNYPIVQN

96BW17A09	ALDKIEEEQN	K.....	FQQQAKAADG	K.....	VSQNYPIVQN
96BWM01_5	ALDKIEEEQN	KIQQ.....	KMQQAEAADK	KISQ...DKK	ISQNYPIVQN
96BWM03_2	ALDRIEEEQN	KCQQK.....	AQQQEEA.AA	K.....	VSQNYPIVQN
98BWMC12_2	ALDKIEEEQNKSKQ	KTQQAKAADE	K.....	VSQNYPIVQN
98BWMC13_4	ALDKVEEEQN	KIQQ.....	KMQQAESADK	KVS.....	..QNYPIVQN
98BWMC14_a	ALDKIEEEQN	KVQQ.....	KTQQAEAAAAG	K.....	VSQNYPIVQN
98BWM014_1	ALDKIEEEQN	KSQQK.....	TQQAEAADKG	K.....	VSQNYPIVQN
98BWM018_d	ALDKVEEEQN	QCQQR.....	.TQQAEAADK	G.....K	VSQNYPIVQN
98BWM036_a	ALDKIEEEQN	KIQQQ.....	.TQKATAADK	G.....K	VSQNYPIVQN
98BWM037_d	ALDKIEEEQN	KSQK.....	..K.TQQADG	KV.....S	..QNYPIVQN
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99BW4642_4	ALDKIEEEQN	KCQS.....	KTQQAEAAAAG	K.....	VSQNYPIVQN
99BW4745_8	ALDRIEEEQNKSQK	KAQQAKAAEG	K.....	VSQNYPIVQN
99BW4754_7	ALDKIEEEQN	KSQQK.....	.TTQAEAADK	K.....	VSQNYPIVQN
99BWMC16_8	ALDKIEEEQN	KCQQK.....	.TQQAEAADK	.G.....K	VSQNYPIVQN
A2_CD_97CD	ALDKIEEEQN	KCKQK.....	.TQQAADTG	SSSSQNYRGS	SSQNYPIVQN
A2_CY_94CY	ALDKIEEEQN	..KQK.....	.TQHAAADTG	NS.....S	S.QNYPIVQN
A2D_97KR	ALDKLEEEQN	KHKQK.....	.TQPAAADTG	SS.....	GSQNYPIVQN
A2G_CD_97C	ALDKIEEEQN	TCKQR.....	.TQHAAADTG	SSRSQDYRGS	SSQNYPIVQN
A_BY_97BL0	ALDKIEEIQN	XSKQ.....	KTQQAATGTG	S.....SS.K	VSQNYPIVQN
A_KE_Q23_A	ALDKIEEIKN	KSKQ.....	KTQQAADTG	N.....SS.N	VSQNYPIVQN
A_SE_SE659	ALDKIEEMQK	KSKQ.....	KTSQATADTG	S.....SS.K	VSQNYPIVQN
A_SE_SE725	ALDKIEEIQK	KSKQ.....	KAQQAADTG	N.....SS.K	VSQNYPIVQN
A_SE_SE753	ALDKIEEIQN	KSEQ.....	KTQQAADTG	N.....S..K	VSQNYPIVQN
A_SE_SE853	ALDKLEEIQK	KSKQ.....	KTQQAVADTG	S.....SS.K	VSHNYPVVQN
A_SE_SE889	ALDKIEEIQN	KNKQ.....	KTQQAADTG	N.....SS.N	VSRNYPVVQN
A_SE_UGSE8	ALDKIEEIQN	KSKQ.....	KKEQAAADTG	N.....SS.K	VSQNYPIVQN
A_UG_92UG0	ALDKIEEIQK	KSKQ.....	KTQQAADTG	S.....SS.K	VSQNYPIVQN
A_UG_U455_	ALNKIEEMQN	KNKQR.....	.TQQAANTG	SS.....	..QNYPIVQN
AC_IN_2130	ALDKIEEEQN	KSQQK.....	.TQQAADTG	K.....	VSQNYPIVQN
AC_RW_92RW	ALDKIEEEQN	KSQQK.....	.TQQAADTG	G.....K	VSQNYPIVQN
AC_SE_SE94	ALDKIEEIKN	KSKQ.....	KAQQAADTG	N.....SG.K	VSQNYPIVQN
ACD_SE_SE8	ALDKIEEIQK	KSKQ.....	KAQQAADTG	N.....SS.N	VSQNYPIVQN
ACG_BE_VI1	ALDKLEEVQN	KSKQR.....	.TQQAANTGS	GSQNFPIVQN
AD_SE_SE69	ALDKIEEEQN	KSK.....K	KAQQATADTK	N.....SS.Q	VSQNYPIVQN
AD_SE_SE71	ALDKIEEMQN	RSKQ.....	KTQQAADTG	N.....NS.K	VSQNYPIVQN
ADHK_NO_97	ALDKIEEIQN	KSKQ.....	KTQQAANTG	N.....GS.N	ISQNYPIVQN
ADK_CD_MAL	ALDKIEEIQN	KSRQKTQQA	AAQQAANTG	N.....SS.S	VSQNYPIVQN
AG_BE_VI11	AVDKIEEMQN	KSKQ.....	KTQQAANTG	G.....S	SSQNYPIVQN
AG_NG_92NG	ALEEVEKIQK	NSQEQ.....	.TQKAAMGKG	N.....SS.Q	VSQNYPIVQN
AGHU_GA_VI	ALDKIEEIQN	KSKQ.....	KTQQAANTG	N.....SS.K	VSQNYPIVQN
AGU_CD_Z32	ALDEVEKAQK	SSQQK.....	.TQKATMAEE	N.....SSNQ	VSKNFPPIVQN
AJ_BW_BW21	ALDKIEEIQN	KSKQ.....	KAQQAANTG	N.....SS.S	VSQNYPIVQN
B_AU_VH_AF	ALEKIEEEQN	KSKKKAQQ.A	AADAAAADAG	N.....SS.K	VSQNYPIVQN
B_CN_RL42_	ALEKIEEEQN	KSKK.....	KAQQTAAAGTG	NNS.....Q	ASQNYPIVQN
B_DE_D31_U	ALDKIEEEQN	KSKK.....	KAQPAARDAG	N.....NS.Q	VSQNYPIVQN
B_DE_HAN_U	ALDKVEEEQN	NSKK.....	KAQQAADAG	N.....RN.Q	VSQNYPIVQN
B_FR_HXB2_	ALDKIEEEQN	KSKK.....	KAQQAADTG	H.....SN.Q	VSQNYPIVQN
B_GA_OYI_	ALDKIEEEQN	KSKK.....	KAQQTAAADTG	NSS.....Q	VSQNYPIVQN
B_GB_CAM1_	ALEKIEEEQN	KSKK.....	KAQQAAGTG	N.....SS.Q	VSQNYPIVQN
B_GB_GB8_A	ALDKIEEEQN	KSKK.....	KAQQAADKG	NSNS...N.Q	VSQNYPIVQN
B_GB_MANC_	ALDKIEEEQN	KSKK.....	KAQPAADTG	N.....SS.Q	VSHNYPVVQN
B_KR_WK_AF	ALEKIEEEQN	KSKK.....	KAQQTADTG	S.....SS.Q	VSQNYPIVQN
B_NL_3202A	ALDKIEEEQN	KSKK.....	KAQQAADTG	N.....SS.Q	VSQNYPIVQN
B_TW_TWCYS	ALEKIEEEQN	KSKK.....	KAQQAATGTG	NNS.....P	VSQNYPIVQN
B_US_BC_L0	ALEKIEEEQN	NSKK.....	KAQQAADTG	N.....SS.Q	VSRNYPVVQN
B_US_DH123	ALDKVEEEQN	KSKK.....	KAQQAADTG	N.....SS.Q	VSQNYPIVQN
B_US_JRCSF	ALEKIEEEQN	KSMK.....	KAQQAADTG	N.....SS.Q	VSQNYPIVQN
B_US_MNCG_	ALEKIEEEQN	KSKK.....	KAQQAADTG	NRG.N.SS.Q	VSQNYPIVQN
B_US_P896_	ALDKIEEEQN	KSKK.....	KAQQAADTG	N.....SS.Q	VSQNYPIVQN
B_US_RF_M1	ALDKIEEEQN	KSKK.....	KAQQAADTG	N.....GS.Q	VSQNYPIVQN

B_US_SF2_K	ALEKIEEEQN	KSKK.....	KAQQAAAAAG	TG..N.SS.Q	VSQNYPIVQN
B_US_WEAU1	ALDKIEEEQN	KSKK.....	KAQQAADTE	N....RN.Q	VSQNYPIVQN
B_US_WR27	ALEKIEEEQN	KSKK.....	KAQQAADTG	N....NS.K	VSQNYPIVQN
B_US_YU2_M	ALEKIEEEQN	KSKK.....	KAQQAADTG	N....SS.Q	VSQNYPIVQN
BF1_BR_93B	ALEKIEEEQN	.SKK.....	KAQQAANTG	NNS.....Q	VSQNYPIVQN
C_BR_92BR0	ALDKIEEEQN	KSQK.....	.TQQAADK	G.....K	VSQNYPIVQN
C_BW_96BW0	ALDKIEEEQN	KCQK.....	.IQQAADK	G.....K	VSQNYPIVQN
C_BW_96BW1	AVDKIEEEQN	KSQK.....	KTQQAADK	RVS.....	..QNYPIVQN
C_BW_96BW1	ALDKIEEEQN	KCQK.....	.EQQAADK	G.....K	VSQNYPIVQN
C_BW_96BW1	ALDKIEEEQN	KSQE.....	KTQQAADK	K.....	ISQNYPIVQN
C_ET_ETH22	ALDKIEEEQN	ESQK.....	.TQQAADR	G.....K	DSQNYPIVQN
C_IN_93IN1	ALDKIEEEQN	KIQK.....	.TQQAADG	K.....	VSQNYPIVQN
C_IN_93IN9	ALDKIEEEQN	KNQK.....	.TQQAADG	K.....	VSQNYPIVQN
C_IN_93IN9	ALDKIEEEQN	KSQK.....	.TQQAADG	K.....	VSQNYPIVQN
C_IN_94IN1	ALDKIEEEQN	KSQK.....	.TQQAADSQNYPIVQN
C_IN_95IN2	ALDKIEEEQN	KIKK.....	.TQQAEDD	K.....	VSQNYPIVQN
CRF01_AE_C	ALDKIEEVQN	KNKQ.....	KTQQAAGTG	S....NS.K	VSQNYPIVQN
CRF01_AE_C	ALDKIEEVQN	KSKQ.....	KAQQAAGTG	S....SS.K	VSQNYPIVQN
CRF01_AE_C	ALDKIEEIQN	KNKQ.....	KTQQAADTG	S....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEVQK	KSQK.....	KTQQAAGTG	S....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEVQN	KSQK.....	KTQQAAGTG	S....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEVQK	KSQK.....	KTQQAADTG	S....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEVQN	KSQK.....	KTQQAAGTG	S....SS.T	VSHNYPIVQN
CRF01_AE_T	ALDKIEEVQN	KSQR.....	KTQQAAGTG	S....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEAQK	KSQK.....	KTQQAAGTG	S....SS.K	VSQNYPIVQN
CRF02_AG_F	ALEKIEEVQN	KSKQ.....	KTQQAAGTGS	SSQNYPIVQN
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CRF02_AG_N	ALDKMEEIQN	KSKQ.....	KVQQTAAATGS	SSQNYPIVQN
CRF02_AG_S	ALDKVEEVQK	KSKQ.....	KTQQAAGTGS	SSQNYPIVQN
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CRF03_AB_R	ALDKIEEIQN	KSKQ.....	KTQQAATGTG	S....SS.K	VSQNYPIVQN
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CRF04_cpx_	ALDKIEEIQS	KSKQ.....	KTQQAAGTG	G....SS.N	VSQNYPIVQN
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CRF05_DF_B	ALEKIEEEQN	KSKR.....K	KAQQAAGTG	N....SS.Q	ASQNYPIVQN
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CRF06_cpx_	AVDKVEEIQN	KSKQK.....	.TQTTAATG	N....SS.N	LSQNYPIVQN
CRF11_cpx_	ALDKIEEIQN	KSKQ.....	KTQQAADTG	N....SS.N	VSQNYPIVQN
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D_CD_NDK_M	AVEKMEEEQN	KSK.....K	KTQQAADSS.Q	VSQNYPIVQN
D_UG_94UG1	ALDKIEEEQA	KSK.....K	KAQQAADTR	N....SS.Q	VSQNYPIVQN
F1_BE_VI85	ALDKLEEEQN	KSQK.....	.KTQQAADKG	VSQNYPIVQN
F1_BR_93BR	ALEKLEEEQN	KGRQ.....	.KTQQAADKG	VSQNYPIVQN
F1_FI_FIN9	ALDKLEEEQN	KSQK.....	.QQAADKG	VSQNYPIVQN
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F2_CM_MP25	ALDKLQEEQD	KHQQ.....	.KTQQAADK	GVSK....G	VSQNYPIVQN
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G_BE_DRCBL	ALEEVEKIQK	KSQK.....KEN	S....SS.Q	VSQNYPIVQN
G_NG_92NG0	ALEEVEKIQK	NSQE.....	.IQQAADK	N....SN.P	VSQNYPIVQN
G_SE_SE616	ALEEVEKIQK	KSQE.....	.IQQAADK	N....SN.Q	VSQNYPIVQN
H_BE_VI991	ALGKIEEIQN	KNKQR.....	.TQQAADK	K.EK...DSK	ISQNYPIVQN
H_BE_VI997	ALGKIEEIQN	KRQK.....	.TQQAADK	..ER...DNK	VSQNYPIVQN
H_CF_90CF0	ALDKIEEIQN	KSQK.....	.TQQAADK	..EK...DNK	VSQNYPIVQN
J_SE_SE702	ALDKIEEIQN	KNKQK.....	.TQQAADK	DNS.....Q	VSQNYPIVQN

J_SE_SE788	ALEKIEEIQN	KNKQQ.....	.AQKAETDKK	DNS.....Q	VSQNYPIVQN
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N_CM_YBF30	ALDKIKEKQE	QHKPE....P	KNPEAGAAAA	TDS.....N	ISRNPLVQT
O_CM_ANT70	AIQKLKEVMG	SRKS.....	.ADAAKEDTS	A.....R..Q	AGQNYPIVSN
O_CM_MVP51	AIQKLKEVMA	SRKS.....	.AEAAKEETS	P.....R..Q	TSQNYPIVTN
O_SN_99SE_	AIQKLKEVMG	SRKS.....	.AGTAKEDTS	A.....R..Q	TGQNYPIVTN
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A2D___97KR	AQGQMTYQNL	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
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A_BY_97BL0	AQGQMTHQSM	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
A_KE_Q23_A	AQGQMIHQSL	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
A_SE_SE659	AQGQMIHQSL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNTM
A_SE_SE725	AQGQMVHQSL	SPRTLNAWVK	VVEEKAFSPE	VIPVFSALSE	GATPQDLNTM
A_SE_SE753	AQGQMVHQSL	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
A_SE_SE853	AQGQMIHQNL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNTM
A_SE_SE889	AQGQMVHQSL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNTM
A_SE_UGSE8	AQGQMVHQVM	SPRTLNAWVK	VVEERAFSPE	VIPMFSALSE	GATPHDLNMM
A_UG_92UG0	AQGQMIHQSL	SPRTLNAWVK	VVEEKALSPE	VIPMFSALSE	GATPQDLNTM
A_UG_U455_	AQGQPVHQAL	SPRTLNAWVK	VVEDKAFSPE	VIPMFSALSE	GATPQDLNTM
AC_IN_2130	LQGQMVHQAL	SPRTLNAWVK	VVEEKAFSPE	IIPMFTALSE	GATPQDLNTM
AC_RW_92RW	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
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ACD_SE_SE8	AQGQMVHQSL	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
ACG_BE_VI1	AQEQMVHQSM	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
AD_SE_SE69	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GAAPQDLNTM
AD_SE_SE71	AQGQMIHQAL	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
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ADK_CD_MAL	AQGQMIHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
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B_US_BC_L0	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_DH123	LQGQMVHQAL	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_JRCSF	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_MNCG_	IEGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_P896_	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_RF_M1	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_SF2_K	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_WEAU1	LQGQMVHQAL	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_WR27_	LQGQMVHQAL	SPRTLFAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_YU2_M	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
BF1_BR_93B	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
C_BR_92BR0	LQGQMVHQPI	SARTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_BW_96BW0	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_BW_96BW1	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_BW_96BW1	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	IIPMFTALSE	GATPQDLNTM
C_BW_96BW1	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_ET_ETH22	MQGQMVHQPI	SARTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_93IN1	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_93IN9	LQGQMVHQAL	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_93IN9	LQGQMVHQPI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM

C_IN_94IN1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_95IN2	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
CRF01_AE_C	AQGQMVHQPL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_C	AQGQMVHQAL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_C	AQGQMIHQAL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMVHQPV	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMVHQPL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMVHQPL	SPRTLNAWVK	VIEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMVHQPI	SPRTLNAWVK	VIEEKGFSPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMAHQPL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMVHQPV	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF02_AG_F	AQGQMT HQPM	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNMM
CRF02_AG_F	AQGQMT HQPM	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNMM
CRF02_AG_G	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNMM
CRF02_AG_N	AKGQMT HQSM	SPRTLNAWVK	VIEEKGFSPE	VIPMFSALSE	GATPQDLNMM
CRF02_AG_S	AQGQMT HQSI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF02_AG_S	AQGQMVHQSI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF03_AB_R	AQGQMT HQSM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF03_AB_R	AQGQMT HQSM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF04_cpx_	AQGQMVHQSI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF04_cpx_	AQGQMVHQAM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF04_cpx_	AQGQMVHQSI	SPRTLNAWVK	VVEEKGFSPE	VIPMFSALSE	GATPQDLNMM
CRF05_DF_B	IQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNNTM
CRF05_DF_B	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNNTM
CRF06_cpx_	AQGQMVHQAM	SPRTLNAWVK	VIEDKAFSPE	VIPMFTALSE	GATPQDLNMM
CRF06_cpx_	AQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF06_cpx_	AQGQMIHQAI	SPRTLNAWVK	AIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF06_cpx_	AQGQMVHQAI	SPRTLNAWVK	AIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF11_cpx_	AQGQMVHQPV	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF11_cpx_	AQGQMVHQAM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
D_CD_84ZR0	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFNPE	VIPMFSALSE	GATPQDLNNTM
D_CD_ELI_K	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNNTM
D_CD_NDK_M	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNNTM
D_UG_94UG1	LQGQMVHHPL	SPRTLNAWVK	VIEEKAFNPE	VIPMFSALSE	GATPQDLNNTM
F1_BE_VI85	LQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPTDLNNTM
F1_BR_93BR	LQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNNTM
F1_FI_FIN9	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNNTM
F1_FR_MP41	LQGQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNNTM
F2_CM_MP25	LQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNNTM
F2KU_BE_VI	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNNTM
G_BE_DRCBL	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNNTM
G_NG_92NG0	AQGQMIHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNNTM
G_SE_SE616	AQGQMVHQAI	TPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNLM
H_BE_VI991	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNAM
H_BE_VI997	AQGQMVHQPI	SXRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNAM
H_CF_90CF0	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNAM
J_SE_SE702	LQGQPVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNNTM
J_SE_SE788	LQGQPVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNNTM
K_CD_EQTB1	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNNTM
K_CM_MP535	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNNTM
N_CM_YBF30	AQGQMVHQPL	TPRTLNAWVK	VIEEKAFSPE	VIPMFMALSE	GATPSDLNNTM
O_CM_ANT70	AQGQMVHQAI	SPRTLNAWVK	AVEEKAFNPE	IIPMFMALSE	GAISYDINTM
O_CM_MVP51	AQGQMVHQAI	SPRTLNAWVK	AVEEKAFNPE	IIPMFMALSE	GAVPYDINTM
O_SN_99SE_	AQGQMVHQSL	SPRTLNAWVK	AVEEKAFNPE	IIPMFMALSE	GAIPYDTNNTM
O_SN_99SE_	AQGQMVHQSL	SPRTLNAWVK	AVEEKAFNPE	IIPMFMALSE	GAIPYDTNNTM
U_CD___83C	MQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNNTM

201

00BW0762_1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
00BW0768_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PAHAGPVAPG	QMREPRGSDI
00BW0874_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPVAPG	QMREPRGSDI

250

00BW1471_2	LNTVGGHQ.A	AMQMLKDTIN	EEVAEWDR LH	PVQAGPIAPG	QMRDPRGSDI
00BW1616_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR MH	PVQAGPVAPG	QMRDPRGSDI
00BW1686_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
00BW1759_3	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
00BW1773_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
00BW1783_5	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVQAGPVAPG	QIREPRGSDI
00BW1795_6	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
00BW1811_3	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
00BW1859_5	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIAPG	QMREPRGSDI
00BW1880_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMRDPRGSDI
00BW1921_1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QLREPRGSDI
00BW2036_1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPNPAG	QMREPRGSDI
00BW2063_6	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPAAPG	QMREPRGSDI
00BW2087_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
00BW2127_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
00BW2128_3	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIAPG	QMREPRGSDI
00BW2276_7	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
00BW3819_3	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
00BW3842_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVQAGPVAPG	QIREPRGSDI
00BW3871_3	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
00BW3876_9	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR IH	PVHAGPVAPG	QMRDPRGSDI
00BW3886_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
00BW3891_6	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
00BW3970_2	LNAVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QLREPRGSDI
00BW5031_1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
96BW01B21	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR TH	PVHAGPVAPG	QLREPRGSDI
96BW0407	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIAPG	QMREPRGSDI
96BW0502	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVQAGPVAPG	QMRDPRGSDI
96BW06_J4	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVQAGPVAPG	QMRDPRGSDI
96BW11_06	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
96BW1210	LNTVGGHQ.A	AMQMLKDTIN	EEAAGWDR LH	PVHAGPVAPG	QMREPRGSDI
96BW15B03	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
96BW16_26	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIAPG	QMREPRGSDI
96BW17A09	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
96BWM01_5	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
96BWM03_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR MH	PVHAGPVAPG	QMREPRGSDI
98BWMC12_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
98BWMC13_4	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVQAGPVAPG	QIREPRGSDI
98BWMC14_a	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMRDPRGSDI
98BWM014_1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR TH	PVHAGPVAPG	QMREPRGSDI
98BWM018_d	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
98BWM036_a	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
98BWM037_d	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVQAGPIAPG	QIREPRGSDI
99BW3932_1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR TH	PVHAGPVAPG	QMREPRGSDI
99BW4642_4	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
99BW4745_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR IH	PVHAGPVAPG	QMREPRGSDI
99BW4754_7	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIAPG	QIREPRGSDI
99BWMC16_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR TH	PVHAGPIAPG	QMREPRGSDI
A2_CD_97CD	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVQAGPIPPG	QMREPRGSDI
A2_CY_94CY	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
A2D_97KR	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
A2G_CD_97C	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGS..
A_BY_97BL0	LNIVGGHQ.A	AMQMLKDTIN	EEAAXXDR LH	PAQAGPFP PG	QMREPRGSDI
A_KE_Q23_A	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
A_SE_SE659	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGS..
A_SE_SE725	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PAHAGPVAPG	QMREPRGS..
A_SE_SE753	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
A_SE_SE853	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGS..
A_SE_SE889	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGS..
A_SE_UGSE8	LNIVGGHQ.A	AMEMLKDTIN	EEAAEWDR TH	PIHAGPVAPG	QMREPRGSDI
A_UG_92UG0	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI

A_UG_U455_	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
AC_IN_2130_	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PAQAGPIAPG	QMREPRGSDI
AC_RW_92RW	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVQAGPVAPG	QIREPRGSDI
AC_SE_SE94	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PAQAGPVAPG	QMREPRGS..
ACD_SE_SE8	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR IH	PVHAGLIAPG	QMREPRGSDI
ACG_BE_VI1	LNIVGGHQ.A	AMQMLKDTIN	EEAADWDR TH	PVHAGPNPPG	QMREPRGSDI
AD_SE_SE69	LSTVGGHQ.A	AMQILKETIN	EEAADWDR LH	PVHAGPNAPG	QMREPRGSDI
AD_SE_SE71	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGS..
ADHK_NO_97	LNIVGGHQ.A	AMQMLKDTIN	EEAADWDR LH	PVHAGPIPPG	QMREPRGSDI
ADK_CD_MAL	LNIVGGHQ.A	AMQMLKDTIN	EEAADWDR VH	PVHAGPIPPG	QMREPRGSDI
AG_BE_VI11	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
AG_NG_92NG	LNTVGGHQ.A	AMQMLKDSIN	EEAAEWDR LH	PQQAGPIPPG	QIREPRGSDI
AGHU_GA_VI	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR IH	PVQAGPIPPG	QIREPRGSDI
AGU_CD_Z32	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PPQAGPIPPG	QIREPRGSDI
AJ_BW_BW21	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
B_AU_VH_AF	LNTVGGHQAA	AMQMLKETIN	EEAADWDR LH	PVHAGPIAPG	QMREPRGSDI
B_CN_RL42_	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
B_DE_D31_U	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
B_DE_HAN_U	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
B_FR_HXB2_	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR VH	PVHAGPIAPG	QMREPRGSDI
B_GA_OYI_	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
B_GB_CAM1_	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
B_GB_GB8_A	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR VH	PVHAGPVAPG	QMREPRGSDI
B_GB_MANC_	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
B_KR_WK_AF	LNTVGGHQ.A	AMQMLKETIN	EEAADWDR LH	PVHAGPIAPG	QMREPRGSDI
B_NL_3202A	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
B_TW_TWCYS	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
B_US_BC_L0	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVQAGPVAPG	QMREPRGSDI
B_US_DH123	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
B_US_JRCSF	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
B_US_MNCG_	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPITPG	QMREPRGSDI
B_US_P896_	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVQAGPVAPG	QMREPRGSDI
B_US_RF_M1	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
B_US_SF2_K	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR VH	PVHAGPIAPG	QMREPRGSDI
B_US_WEAU1	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
B_US_WR27_	LNTVGGHQ.A	AMQMLKETIN	DEAAEWDR LH	PVQAGPVAPG	QMREPRGSDI
B_US_YU2_M	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
BF1_BR_93B	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
C_BR_92BR0	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
C_BW_96BW0	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
C_BW_96BW1	LTTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
C_BW_96BW1	LNTVGGHQ.A	AMQMLKDTIN	EEAAGWDR LH	PVHAGPVAPG	QMREPRGSDI
C_BW_96BW1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
C_ET_ETH22	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMRDPRGSDI
C_IN_93IN1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PIHAGPIAPG	QMREPRGSDI
C_IN_93IN9	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PIHAGPIAPG	QMREPRGSDI
C_IN_93IN9	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QIREPRGSDI
C_IN_94IN1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR IH	PVHAGPIAPG	QMREPRGSDI
C_IN_95IN2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVPAGPIAPG	QLREPRGSDI
CRF01_AE_C	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_C	LNIVGGHQ.A	AMQILKDTIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGADI
CRF01_AE_C	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGEHQ.A	AMQMLKETIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGGHQ.A	AMQMLKETIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGGHQ.A	AMQMLKETIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGGHQ.A	AMQMLKETIN	EEPAEWDR VH	PVHAGPIPPG	QIREPRGSDI
CRF01_AE_T	LNIVGGHQ.A	AMQMLKETIN	EEPAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGGHQ.A	AMQMLKETIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF02_AG_F	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF02_AG_F	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF02_AG_G	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR TH	PIHAGPNPPG	QMREPRGSDI

CRF02_AG_N	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
CRF02_AG_S	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
CRF02_AG_S	LNIVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
CRF03_AB_R	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PAQAGPFPPG	QMREPRGSDI
CRF03_AB_R	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PAQAGPFPPG	QMREPRGSDI
CRF04_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
CRF04_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEASEWDRAH	PVHAGPIPPG	QMREPRGSDI
CRF04_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PAHAGPNPAG	QMREPRGSDI
CRF05_DF_B	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVQAGPVAPG	QMRDPRGSDI
CRF05_DF_B	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDRVH	PAQAGPIAPG	QIREPRGSDI
CRF06_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QIREPRGSDI
CRF06_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
CRF06_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRMH	PVQAGPMPPG	QMREPRGSDI
CRF06_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PAQAGPIPPG	QIRDPRGSDI
CRF11_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVQAGPIAPG	QMRDPRGSDI
CRF11_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPAPPG	QMREPRGSDI
D_CD_84ZR0	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVQAGPVAPG	QMREPRGSDI
D_CD_ELI_K	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
D_CD_NDK_M	LNTVGGHQ.A	AMQMLKETIN	DEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
D_UG_94UG1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QLREPRGSDI
F1_BE_VI85	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPAPPG	QMREPRGSDI
F1_BR_93BR	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PTQAGPIPPG	QIREPRGSDI
F1_FI_FIN9	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
F1_FR_MP41	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PAHAGPILPG	QMREPRGSDI
F2_CM_MP25	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
F2KU_BE_VI	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
G_BE_DRCBL	LNTVGGHQ.A	AMQMLKETIN	DEAAEWDR LH	PQQAGPIAPG	QIRDPTGSDI
G_NG_92NG0	LNTVGGHQ.A	AMQMLKDTIN	DEAAEWDR LH	PQQAGPIPPG	QIREPSGSDI
G_SE_SE616	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR MH	PQQAGPFPPG	QIREPRGSDI
H_BE_VI991	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
H_BE_VI997	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
H_CF_90CF0	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
J_SE_SE702	LNTIGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPVAPG	QVREPRGSDI
J_SE_SE788	LNTIGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIAPG	QVREPRGSDI
K_CD_EQTB1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR MH	PVQAGPIPPG	QIREPRGSDI
K_CM_MP535	LNTVGGHQ.A	AMQMLKDTIN	DEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
N_CM_YBF30	LNTVGGHQ.A	AMQMLKEVIN	EEAADWDRTH	PVPVGPLPPG	QLRDPRGSDI
O_CM_ANT70	LNAIGGHQ.G	ALQVLKEVIN	EEAVEWDRTH	PPPVGPLPPG	QIREPTGSDI
O_CM_MVP51	LNAIGGHQ.G	ALQVLKEVIN	EEAAEWDRTH	PPAMGPLPPG	QIREPTGSDI
O_SN_99SE_	LNAIGGHQ.G	ALQVLKEVIN	EEAAEWDRTH	PPAAGPLPVG	QIREPTGSDI
O_SN_99SE_	LNAIGGHQ.G	ALQVLKEVIN	EEAAEWDRTH	PQAAGPLPPG	QIREPTGSDI
U_CD___83C	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDR LH	PVHAGPIPPG	QMREPRGSDI

00BW0762_1	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW0768_2	AGTTSNLQEQ	IAWMTA.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW0874_2	AGTTSTLQEQ	IAWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1471_2	AGTTSTLQEQ	VAWMTS.NPP	VPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1616_2	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1686_8	AGTTSNLQEQ	VAWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1759_3	AGTTSTLQEQ	IAWMTS.NPP	VPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1773_2	AGTTSTLQEQ	ITWMTS.NPP	VPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1783_5	AGTTSTLQEQ	ITWMTS.NPP	IPVGGDIYKRW	IVLGLNKIVR	MYSPPVSILDI
00BW1795_6	AGTTSTLQEQ	IAWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1811_3	AGTTSTLQEQ	IAWMTN.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1859_5	AGTTSTLQEQ	IAWMTG.NPP	VPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1880_2	AGTTSTLQEQ	ITWMTS.NPP	IPVGGDIYKRW	IVLGLNKIVR	MYSPPVSILDI
00BW1921_1	AGTTSTLQEQ	IAWMTN.NPP	VPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW2036_1	AGTTSTLQEQ	IAWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW2063_6	AGTTSTLAEQ	IAWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW2087_2	AGTTSTLQEQ	IAWMTN.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW2127_2	AGTTTTLQEQ	INWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW2128_3	AGTTSTLQEQ	IAWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW2276_7	AGTTSTLQEQ	IAWMTS.NPA	IPVGGDIYKRW	IILGLDKIVR	MYSPPVSILDI
00BW3819_3	AGTTSTLQEQ	VAWMTS.NPP	VPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW3842_8	AGTTSNLQEQ	ITWMTS.NPP	IPVGEIYKRW	IVLGLNKIVR	MYSPPVSILDI
00BW3871_3	AGTTSTLQEQ	IDWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW3876_9	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW3886_8	AGTTSTLQEQ	IAWMTN.NPP	VPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW3891_6	AGTTSNLQEQ	INWMTA.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW3970_2	AGTTSTLQEQ	IAWMTN.NPP	VPVGGDIYKRW	IVLGLNKIVR	MYSPPVSILDI
00BW5031_1	AGTTSTLQEQ	IAWMTS.NPP	VPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
96BW01B21	AGTTSNLQEQ	IAWMTA.NPP	VPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
96BW0407	AGTTSTLQEQ	IAWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
96BW0502	AGATSTLQEQ	IAWMTS.NPP	VPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
96BW06_J4	AGTTSTLQEQ	IGWMTN.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
96BW11_06	AGTTSTLQEQ	IAWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
96BW1210	AGTTSNLQEQ	INWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
96BW15B03	AGTTSTLQEQ	IAWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
96BW16_26	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
96BW17A09	AGTTSTLQEQ	IAWMTN.NPP	IPVGGDIYKRW	ITMGLNKIVR	MYSPPVSILDI
96BWM01_5	AGTTSTLQEQ	IAWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
96BWM03_2	AGSTSTLQEQ	IAWMTS.NPP	VPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
98BWMC12_2	AGSTSNLQEQ	IAWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
98BWMC13_4	AGTTSTLQEQ	IAWMTN.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
98BWMC14_a	AGTTSTLQEQ	VGWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
98BWM014_1	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
98BWM018_d	AGTTSTLQEQ	IAWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
98BWM036_a	AGTTSTLQEQ	IAWMTS.NPP	IPVGGDIYKRW	IIMGLNKIVR	MYSPPVSILDI
98BWM037_d	AGTNSTLQEQ	IAWMTN.NPP	VPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
99BW3932_1	AGTTSTLQEQ	IQWMTS.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
99BW4642_4	AGTTSTLQEQ	VTWMTS.NPP	VPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
99BW4745_8	AGTTSTLQEQ	INWMTG.NPP	IPVGGDIYKRW	IIMGLNKIVR	MYSPPVSILDI
99BW4754_7	AGTTSTLQEQ	ITWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
99BWMC16_8	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
A2_CD_97CD	AGATSNLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
A2_CY_94CY	AGTTSTLQEQ	IGWMTS.DPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
A2D_97KR	AGTTSTLQEQ	IGWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
A2G_CD_97C
A_BY_97BL0	AGTTSTLQEQ	IGXMTS.NPP	IPXGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
A_KE_Q23_A	AGTTSTPQEQ	IGWMTG.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI
A_SE_SE659
A_SE_SE725
A_SE_SE753	AGTTSTPQEQ	IGWMTG.NPP	IPVGGDIYKRW	IILGLNKIVR	MYSPPVSILDI

A_SE_SE853
A_SE_SE889
A_SE_UGSE8	AGTTSTLQEQ	IAWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
A_UG_92UG0	AGTTSTPQEQ	IAWMTG.NPP	IPVGDIYKRW	MILGLNKIVR	MYSPPVSILDI
A_UG_U455_	AGTTSTVQEQ	IGWMTG.NPP	IPVGDIYRRW	IILGLNKIVR	MYSPPVSILDI
AC_IN_2130	AGTTSTLQEQ	IAWMTG.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AC_RW_92RW	AGTTSTLQEQ	IAWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AC_SE_SE94
ACD_SE_SE8	AGTTSTLQEQ	IAWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
ACG_BE_VI1	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AD_SE_SE69	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AD_SE_SE71
ADHK_NO_97	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
ADK_CD_MAL	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
AG_BE_VI11	AGSTSTLQEQ	VGWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
AG_NG_92NG	AGTTSTLQEQ	ITWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AGHU_GA_VI	AGTTSTTQEQ	IGWMTG.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AGU_CD_Z32	AGTTSTLQEQ	IRWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AJ_BW_BW21	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_AU_VH_AF	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_CN_RL42_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTCILDI
B_DE_D31_U	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_DE_HAN_U	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_FR_HXB2_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_GA_OYI_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_GB_CAM1_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_GB_GB8_A	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
B_GB_MANC_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_KR_WK_AF	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPASILDI
B_NL_3202A	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_TW_TWCYS	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_US_BC_L0	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPSSILDI
B_US_DH123	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IIMGLNKIVR	MYSPTSILDI
B_US_JRCSE	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_MNCG_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPSSILDI
B_US_P896_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPSSILDI
B_US_RF_M1	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPISILDI
B_US_SF2_K	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_US_WEAU1	AGTTSTLQEQ	IAWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_WR27_	AGXTSTLXXX	IGWMTN.XPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_US_YU2_M	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
BF1_BR_93B	AGTTSTLQEQ	IQWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPTSILGI
C_BR_92BR0	AGTTSTLQEQ	ITWMTN.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_BW_96BW0	AGTTSTLQEQ	IAWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_BW_96BW1	AGTTSTLQEQ	IAWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_BW_96BW1	AGTTSTLQEQ	INWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_BW_96BW1	AGTTSTLQEQ	IAWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_ET_ETH22	AGTTSTLQEQ	IAWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_IN_93IN1	AGTTSSLQEQ	IAWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_IN_93IN9	AGTTSSLQEQ	IAWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_IN_93IN9	AGTTSTLQEQ	IAWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_IN_94IN1	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDT
C_IN_95IN2	AGTTSTLQEQ	IAWMTN.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_C	XGTTSTNLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_C	AGTTSTLHEQ	IGWMTS.NPP	IPVGEIYKKW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_C	AGTTSTLQEQ	IGWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_T	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYRPPVSILDI
CRF01_AE_T	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_T	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYQPPVSILDI
CRF01_AE_T	AGTTTTLQEQ	IGWMTN.NPP	IPVGSIIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_T	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI

CRF01_AE_T	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF02_AG_F	AGTTSTPQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF02_AG_F	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF02_AG_G	AGTTSTNLQEQ	IAWMTG.NPP	IPVGEIYKRW	IVLGLNKIVR	MYSPPVGILDI
CRF02_AG_N	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IVLGLNKIVR	MYSPPVSILDI
CRF02_AG_S	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IVLGLNKIVR	MYSPPVSILDI
CRF02_AG_S	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF03_AB_R	AGSSSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF03_AB_R	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF04_cpx_	AGTTSTLQEQ	IGWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	TYSPISILDI
CRF04_cpx_	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF04_cpx_	AGTTSTLQEQ	VGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF05_DF_B	AGTTSTLQEQ	IAWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF05_DF_B	AGTTSTLQEQ	ITWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF06_cpx_	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVGILDI
CRF06_cpx_	AGTTSTLQEQ	IGWMTG.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF06_cpx_	AGTTSTLLEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF06_cpx_	AGTTSTLQEQ	IRWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF11_cpx_	AGTTSTLQEQ	IGWMTG.NPP	IPVGDIYRRW	IILGLNKIVR	MYSPPVSILDI
CRF11_cpx_	AGTTGNLQEQ	IGWMTG.NPP	IPVGEIYRRW	IILGLNKIVR	MYSPPVSILDI
D_CD_84ZR0	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
D_CD_ELI_K	AGTTSTLQEQ	IAWMTS.NPP	IPVGEIYKRW	IIVGLNKIVR	MYSPPVSILDI
D_CD_NDK_M	AGTTSTLQEQ	IAWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
D_UG_94UG1	AGTTSTNLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
F1_BE_VI85	AGTTSTLQEQ	IQWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
F1_BR_93BR	AGTTSTLQEQ	IQWMTG.NPP	VPVGEMYKRW	IILGLNKIVR	MYSPPVGILDI
F1_FI_FIN9	AGTTSTLQEQ	IQWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
F1_FR_MP41	AGTTSTLQEQ	IQWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
F2_CM_MP25	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
F2KU_BE_VI	AGATSNLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
G_BE_DRCBL	AGATSTLQEQ	IRWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
G_NG_92NG0	AGTTSTLQEQ	IRWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
G_SE_SE616	AGTTSSLQEQ	ITWMTG.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
H_BE_VI991	AGTTSTLQEQ	VAWMTG.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
H_BE_VI997	AGTTSTLQEQ	IAWMTG.NPS	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
H_CF_90CF0	AGTTSTLQEQ	IAWMTG.NPA	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
J_SE_SE702	AGTTSTNLQEQ	IGWMTG.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
J_SE_SE788	AGTTSTLQEQ	IGWMTG.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
K_CD_EQTB1	AGTTSTLQEQ	ITWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
K_CM_MP535	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
N_CM_YBF30	AGTTSTLAEQ	VAWMTA.NPP	VPVGDIYRRW	IVLGLNRIVR	MYSPPVSILEI
O_CM_ANT70	AGTTSTQQEQ	IHWTTTRPNQP	IPVGDIYRKW	IVLGLNKMVK	MYSPPVSILDI
O_CM_MVP51	AGTTSTQQEQ	IIWTTTRGANS	IPVGDIYRKW	IVLGLNKMVK	MYSPPVSILDI
O_SN_99SE_	AGTTSTQQEQ	VHWITRPNQP	IPVGDIYRKW	IVLGLNKVVK	MYSPPVSILDI
O_SN_99SE_	AGTTSTQQEQ	VHWITRPNQP	IPVGDIYRKW	IVLGLNKVVK	MYSPPVSILDI
U_CD___83C	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI

301

350

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ACD_SE_SE8	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKTILK
ACG_BE_VI1	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
AD_SE_SE69	RQGPKEPFRD	YVDRFFKTLR	AEQASQDVKN	WMTETLLVQN	ANPDCKTILK
AD_SE_SE71
ADHK_NO_97	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILK
ADK_CD_MAL	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKTILK

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A2_CY_94CY	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSHVQSTN.	..T.NIMMQR
A2D_97KR	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQVQNTN.	..SNIMMMQK
A2G_CD_97C
A_BY_97BL0	ALGSEATLEE	MMTACQGVGG	PGHKAXVXAE	AMSQVQN...	...ANIMMQK
A_KE_Q23_A	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQH...	...TNIMMQR
A_SE_SE659
A_SE_SE725
A_SE_SE753	ALGAGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQH...	...PNIMMQR
A_SE_SE853
A_SE_SE889
A_SE_UGSE8	GLGAGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAQQ...	...TNIMMQR
A_UG_92UG0	ALGAGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQH...	...TNIMMQR
A_UG_U455_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQQT...	...SIMMQR
AC_IN_2130	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN...	...NSILMQR
AC_RW_92RW	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQQ...	...PNIMMQR
AC_SE_SE94
ACD_SE_SE8	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN...	..ANTAIMMQR
ACG_BE_VI1	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...TVMMQR
AD_SE_SE69	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQATNN..	..INAAIMMQR
AD_SE_SE71
ADHK_NO_97	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQN...	...VSVMQR
ADK_CD_MAL	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	..STAAIMMQR
AG_BE_VI11	ALGTGATLEE	MVTACQGVGG	PGHKARVLAE	AMSQVH...	..QTNIMMQR
AG_NG_92NG	ALGAGATLEE	MLTACQGVGG	PSHKARVLAE	AMSRAT.G..	..TSAAIMMQK
AGHU_GA_VI	GLGAGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVHN...	...TSIMMQR
AGU_CD_Z32	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAS.S..	..TAAAIMMQK
AJ_BW_BW21	ALGAGATLEE	MMTACQGVG.	PGHKAKILAE	AMSQVQN...	...TNIMMQR
B_AU_VH_AF	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT...	..NSATIMMQR
B_CN_RL42_	ALGPAATLEE	MMTACQGVGG	PSHKARILAE	AMSQVTNSAI	TNSATIMMQR
B_DE_D31_U	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT...	..NSATVMMQR
B_DE_HAN_U	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT...	..GSAAIMMQR
B_FR_HXB2_	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT...	..NSATIMMQR
B_GA_OYI_	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVN...	..SVTVMMQK
B_GB_CAM1_	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT...	..NSATIMMQR
B_GB_GB8_A	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVN...	..SATIMMQK
B_GB_MANC_	ALGPAATLEE	MMTACQGVGG	PSHKARILAE	AMSQVT...	..NSATIMMQR

B_KR_WK_AF	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAT....	.NSATIMMQR
B_NL_3202A	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_TW_TWCYS	ALGPAATLEE	MMTACQGVGG	PSHKARVLAE	AMSRVP....	.NSTNIMMQR
B_US_BC_L0	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_US_DH123	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQITN...	.TSATIMMQG
B_US_JRCSF	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NPATIMMQR
B_US_MNCG_	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_US_P896_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_US_RF_M1	ALGPAATLEE	MMTACQGVGG	PSHKARILAE	AMSQVT....	.NSATIMLQK
B_US_SF2_K	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NPANIMMQR
B_US_WEAU1	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NTATMMMQR
B_US_WR27_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.GSNAIMMQK
B_US_YU2_M	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
BF1_BR_93B	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSGTIMMQR
C_BR_92BR0	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSKVNN...	...TNIMMQR
C_BW_96BW0	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQT.N...	...TNVMMQR
C_BW_96BW1	ALGPGASLEE	MMTACQGVGG	PSHKARILAE	AMSQANN...	...SNIMMQK
C_BW_96BW1	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSHAGN...	...AGIMMQR
C_BW_96BW1	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQATS...	...ANILMQR
C_ET_ETH22	ALGPGASLEE	MMTACQGVGG	PAHKARVLAE	AMSQVNN...	...TTIMMQK
C_IN_93IN1	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN....	...STILMQR
C_IN_93IN9	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	...SAILMQK
C_IN_93IN9	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN....	...SNILMQR
C_IN_94IN1	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	...SAILMQR
C_IN_95IN2	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	...SAILMQR
CRF01_AE_C	ALGTGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	...HANIMMQR
CRF01_AE_C	ALGTGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVH....	...HTNIMMQK
CRF01_AE_C	ALGTGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	...HANIMMQR
CRF01_AE_T	SLGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHAQ....	...HANIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAQ....	...HANIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAQ....	...HANIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHAQ....	...QANIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHAQ....	...HATIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHVQ....	...QANIMMQR
CRF02_AG_F	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	...QSNIMMQR
CRF02_AG_F	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	...QSNIMMQR
CRF02_AG_G	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQSP...	...NILMQR
CRF02_AG_N	ALGTGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	...QANVMMQR
CRF02_AG_S	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQVQ....	...QPNIMMQR
CRF02_AG_S	ALGPGATLEE	MMSACQGVGG	PGHKARVLAE	AMSQAQ....	...QSNIMMQR
CRF03_AB_R	ALGSGATLEE	MMTVCQGVGG	PGHKARVLAE	AMSQVQN...	...ANIMMQK
CRF03_AB_R	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQN...	...ANIMMQK
CRF04_cpx_	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQASN...	...AAAAIMMQK
CRF04_cpx_	ALGTGATLEE	MMTACQGVGG	PAHKARVLAE	AMSQASN...	...AAAAIMMQK
CRF04_cpx_	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQASS...	...AAAAIMMQK
CRF05_DF_B	ALGQQATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	...SAATAMMQR
CRF05_DF_B	ALGPQATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATG...	...SPAVMMQ.R
CRF06_cpx_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQAS...	...VGAIMMQ.K
CRF06_cpx_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQASGT..	...LTAIMMQ.K
CRF06_cpx_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQASGT..	...VAAAIMMQK
CRF06_cpx_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVSGA...	...TAAIMMQ.K
CRF11_cpx_	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQVQQ...	...TNVMMQR
CRF11_cpx_	ALGVGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAQH...	...TNIMMQR
D_CD_84ZR0	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATS...	...ASAAIMMQK
D_CD_ELI_K	ALGPQATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	...SVTTAMMQR
D_CD_NDK_M	ALGPQATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVTG...	...SATAVMMQR
D_UG_94UG1	ALGPAATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	...ANTAIMMQR
F1_BE_VI85	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAN....	...SAIMMQK
F1_BR_93BR	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	...TAIMMQK
F1_FI_FIN9	GLGIGATLEE	MMTACQGVGG	PGHKARILAE	AMSQAN....	...TTIMMQK
F1_FR_MP41	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQATN...	...AAIMMQK

F2_CM_MP25	ALGPGATLEE	MMTACQGVGG	PSHKARILAE	AMSKATG...	...AAIMMQK
F2KU_BE_VI	ALGPGASLEE	MMTACQGVGG	PAHKARVLAE	AMSQATN...	...TAIMMQK
G_BE_DRCBL	GLGQGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAS.G...	...AAAAIMMQK
G_NG_92NG0	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQASGA...	...AAAAIMMQK
G_SE_SE616	ALGQGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQAS.G...	...AAAAIMMQK
H_BE_VI991	ALGRGASIEE	MMTACQGVGG	PSHKARVLAE	AMSQVTNAS...	...AAIMMQK
H_BE_VI997	ALGQGASIEE	MMTACQGVGG	PSHKARVLAE	AMSQVTNAN...	...AAIMMQK
H_CF_90CF0	ALGQGASIEE	MMTACQGVGG	PSHKARVLAE	AMSQVTNTN...	...TAIMMQK
J_SE_SE702	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVTN...	...TNIMMQK
J_SE_SE788	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVTN...	...TNIMMQK
K_CD_EQTB1	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVTN...	...SAVMMQK
K_CM_MP535	ALGPGASLEE	MMTACQGVGG	PSHKARILAE	AMSQVTN...	...PVVMMQK
N_CM_YBF30	ALGPGATLEE	MMTACQGVGG	PAHKARVLAE	AMSQVQQP...	...TTSVFAQR
O_CM_ANT70	SLGPGATLEE	MMVACQGVGG	PTHKARVLAE	AMATAQQDLK	GGYTAVFMQR
O_CM_MVP51	ALGPEATLEE	MMVACQGVGG	PTHKAKILAE	AMASAQQDLK	GGYTAVFMQR
O_SN_99SE	SLGPGATLEE	MMIACQGVGG	PTHKARVLAE	AMA.AAQDLK	GGYTAVFMQR
O_SN_99SE	SLGPGATLEE	MMIACQGVGG	PTHKARVLAE	AMS.AAQDLK	GGYSAVFMQR
U_CD___83C	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	...TAIMMQK

401

450

00BW0762_1	NNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW0768_2	SNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW0874_2	SNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1471_2	GNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1616_2	SNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1686_8	SNFKGSK.RV	KCFNCGKEGH	IARNCRAPRK	RGCWKCCKEG	HQMKDCT..E
00BW1759_3	SNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1773_2	SNFKGPRRTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1783_5	NNLKGTTRTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1795_6	NNFKGPRRII	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1811_3	SNFKGSKRSV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1859_5	SNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1880_2	SNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1921_1	SNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW2036_1	GNFKGPKRII	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW2063_6	NNFKGPRRLV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW2087_2	SNFKGSKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW2127_2	GNFKGAKRSV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW2128_3	SNFKGSKRSV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW2276_7	SNFKGPRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW3819_3	SNFKGSKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW3842_8	SNFKGPKRTI	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW3871_3	SNFKGPRRII	KCFNCGKEGH	IARNCRAPRK	RGCWKCCKEG	HQMKDCT..E
00BW3876_9	GNFKGSKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW3886_8	GNFKGAKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW3891_6	SNFKGSRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW3970_2	SNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW5031_1	NNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW01B21	SNFKNPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW0407	SNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW0502	SNFKGPRRNV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW06_J4	GNFKGPKRII	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW11_06	NNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW1210	GNFKGPRKIP	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW15B03	SNFKGPKRII	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW16_26	SNFKGPRRSV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW17A09	GNFKGPRRTI	KCFNCGKEGH	IARNCRAPRK	XGCWKCCKEG	HQMKDCT..E
96BWM01_5	NNFKGPRRTI	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BWM03_2	GNFKGPKRII	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWMC12_2	SNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWMC13_4	SNFKGPKRII	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E

98BWM014_a	GNFKGPRRII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWM014_1	SHFKGSKRTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWM018_d	GNFKGPRRII	KCSNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWM036_a	SNFKGPKRTV	KCFNCGKEGH	VARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWM037_d	GNFKGSKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BW3932_1	SNFKGPKRII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BW4642_4	SNFKGPKRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BW4745_8	SNFKGPRRTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BW4754_7	XNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BWM016_8	SNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A2_CD_97CD	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A2_CY_94CY	GNFRGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A2D_97KR	GNFRGQK..I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A2G_CD_97C
A_BY_97BL0	SNFRGPKR.I	KCXNCGKEGH	LARNCRAPRK	XGCWKCCKEG	HQMKDCT..E
A_KE_Q23_A	GNFKGQKR.I	KCFNCGKEGH	LARNCRALRK	KGCWKCCKEG	HQMKDCT..E
A_SE_SE659
A_SE_SE725
A_SE_SE753	GNFRGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A_SE_SE853
A_SE_SE889
A_SE_UGSE8	GNFRGQKK.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A_UG_92UG0	GNFKGQKR.I	KCFNCGKEGH	LAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A_UG_U455	GNFRGPRR.I	KCFNCGKEGH	LAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AC_IN_2130	SNFKGFKRTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AC_RW_92RW	GNFKGQRRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AC_SE_SE94
ACD_SE_SE8	GNFKGPKKII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
ACG_BE_VI1	GNFKGPKRII	KCFNCGKEGH	VARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AD_SE_SE69	GNFKGQRKII	KCFNCGKLGH	IARNCKAPRK	KGCWKCCKEG	HQMKDCT..E
AD_SE_SE71
ADHK_NO_97	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
ADK_CD_MAL	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AG_BE_VI11	GNFRGQKT.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AG_NG_92NG	NNFKGPRRGI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AGHU_GA_VI	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AGU_CD_Z32	SNFKGPRKTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AJ_BW_BW21	SNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_AU_VH_AF	GNFRNQRKTV	KCFNCGKEGH	IARNCRAPRK	RGCWKCCKEG	HQMKDCT..E
B_CN_RL42	GNFRNQRKIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_DE_D31_U	GNFRNQRKTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_DE_HAN_U	GNFRNQRKTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_FR_HXB2	GNFRNQRKIV	KCFNCGKEGH	TARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_GA_OYI	GNFKNQRKTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_GB_CAM1	GNFRNQRKTV	KCFNCGKVGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_GB_GB8_A	GNFRSQRKTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_GB_MANC	GNFRNQRKTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_KR_WK_AF	GNFRNQRRTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_NL_3202A	GNFRNQRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_TW_TWCYS	GNFRNQRKTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_US_BC_L0	GNFRNQRKTV	KCFNCGKEGH	IARNCKAPRK	RGCWKCCKEG	HQMKDCT..E
B_US_DH123	GNFRNQRK.I	KCFNCGKEGH	ISKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_US_JRCSF	GNFRNQRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_US_MNCG	GNFRNQRKII	KCFNCGKEGH	IAKNCRAPRK	RGCWKCCKEG	HQMKDCT..E
B_US_P896	GNFRNQRKTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_US_RF_M1	GNFRDQRKIV	KCFNCGKVGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_US_SF2_K	GNFRNQRKTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_US_WEAU1	GNFRSPRKTI	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
B_US_WR27	GNFRNQRKTV	KCXNCGKEGH	XARXCKAPRK	RGCWKCCKEG	HQMKDCT..E
B_US_YU2_M	GNFRNQRKTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
BF1_BR_93B	GNFRNQRKTI	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E

C_BR_92BR0	SNCKGPKRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQVKDCT..E
C_BW_96BW0	SNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_BW_96BW1	NNFKGPRTRIV	KCFNCGKEGH	IARNCKAPRK	KGCWKCCKEG	HQMKDCT..E
C_BW_96BW1	GNFKGPRKIP	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCS..E
C_BW_96BW1	SNFKGPKRII	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_ET_ETH22	SNFKGPKRAI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_IN_93IN1	SNFKGSKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_IN_93IN9	SNFKGSKRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_IN_93IN9	SNFKGSKRTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_IN_94IN1	SNFKGSKRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_IN_95IN2	SNFKGSKRIV	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
CRF01_AE_C	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	RGCWKCCKEG	HQMKDCTE..
CRF01_AE_C	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF01_AE_C	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF01_AE_T	GNFKGPRR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQTR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQKR.I	KCFNCGKEGH	LARNCRALRK	KGCWKCCKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQKR.I	KCFNCGREGH	LARNCRAPRK	QGCWKCCKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF02_AG_F	GNFRGQRT.I	KCFNCGKEGH	LARNCKAPRK	KGCWKCCKEG	HQMKDCTE..
CRF02_AG_F	GNFRGQRT.I	KCFNCGKEGH	LARNCKAPRK	KGCWKCCKEG	HQMKDCTE..
CRF02_AG_G	GNFKGQK.RI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
CRF02_AG_N	GNFRGQRT.I	KCFNCGKEGH	LARNCKAPRK	RGCWKCCKEG	HQMKDCTE..
CRF02_AG_S	GNFRGQRP.I	KCFNCGKEGH	LARNCKAPRK	KGCWKCCKEG	HQMKDCTE..
CRF02_AG_S	GNFRGQRT.I	KCFNCGKEGH	LARNCKAPRK	RGCWKCCKEG	HQMKDCTE..
CRF03_AB_R	SNFRGPKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF03_AB_R	SNFRGPKR.I	KCFNCGKDGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCNE..
CRF04_cpx_	SKFKGQRRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF04_cpx_	SNFRGQKR.II	KCFNCGKEGH	LARNCRAPRK	RGRWKCCKEG	HQMKDCTE..
CRF04_cpx_	SNFKGPRRSI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCPE..
CRF05_DF_B	GNFKGPRKII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF05_DF_B	GNFKGPRKSI	KCFNCGKEGH	TAKNCRAPRK	RGCWKCCKEG	HQMKDCIE..
CRF06_cpx_	SNFKGPKRSI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF06_cpx_	SNYKGPKRSI	KCFNCGREGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF06_cpx_	SNFKGP.RKI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF06_cpx_	SNFKGQRKNI	KCFNCGKEGH	TARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF11_cpx_	SNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF11_cpx_	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	K.GCKCKEG	HQMKDCTE..
D_CD_84ZR0	SNFKGTRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
D_CD_ELI_K	GNFKGPRKII	KCFNCGKEGH	IAKNCRAPRK	KGCWRCCKEG	HQLKDCTE..
D_CD_NDK_M	GNFKGPRKSI	KCFNCGKEGH	TAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
D_UG_94UG1	GNFKGPKKII	KCFNCGKEGH	TAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
F1_BE_VI85	SNFKGQRRVV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
F1_BR_93BR	SNFKGQRRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
F1_FI_FIN9	SNFRGQRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
F1_FR_MP41	SNYKGPRRFI	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
F2_CM_MP25	SNFKGQRRIV	KCFNCGKEGH	IARNCRAPRK	RGCWKCCKEG	HQMKDCT..E
F2KU_BE_VI	GNFKGPRRDV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
G_BE_DRCBL	SNFKGPRRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKECTE..
G_NG_92NG0	SNFKGPRRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKECTE..
G_SE_SE616	SNFKGPRRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
H_BE_VI991	GNFKGPRRTV	KCSNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..G
H_BE_VI997	SNFKGPRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
H_CF_90CF0	GNFKGQRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
J_SE_SE702	GNFRDHKRIV	KCFNCGKQGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
J_SE_SE788	GNFRDHKRIV	KCFNCGKQGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
K_CD_EQTB1	GNFKGQRRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCS..E
K_CM_MP535	GNFKGHRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
N_CM_YBF30	GNFKGIRKPI	KCFNCGKEGH	LARNCKAPRR	GGCWKCCKEG	HQMKDCKNEG
O_CM_ANT70	GQNPIRKGTI	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCRN.G

O_CM_MVP51	GQNPNRKGPI	KCFNCGKEGH	IAKNCRAPRK	RGCWKCGQEG	HQMKDCKN.G
O_SN_99SE_	GQNPSRKGP	KCFNCGKEGH	LARNCRAPRK	KGCWKCGQEG	HQMKDCKN.G
O_SN_99SE_	GQNPGRKGPI	KCFNCGKEGH	LARNCRAPRK	KGCWKCGQEG	HQMKDCRN.G
U_CD___83C	GNFKGPRRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGREG	HQMKDCT..E

	451				500
00BW0762_1	RQANFLGKIW	PSHKG.RPGN	FLQSR.....PEP	TAPPAESFK.
00BW0768_2	RQANFLGKIW	PSHKG.RPGN	FLQNRPEP..	TAPPAESFK.
00BW0874_2	RQANFLGKIW	PSHKG.RPGN	FLQNRPEPSA	PPAESLRPEP	SAPPAESLR.
00BW1471_2	RQANFLGKIW	PSQKG.RPGN	FLQNRPEP..	SAPPAESFR.
00BW1616_2	RQANFLGKIW	PSHKG.RPGN	FLQSRPEPTA	PP....APVP	TAPPAESFR.
00BW1686_8	RQANFLGKIW	PSHKG.RPGN	FLQNRPEP..	SAPPAESFK.
00BW1759_3	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPAESFR.
00BW1773_2	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESFR.
00BW1783_5	RQANFLGKIW	PSQKGGRPGN	FLQNRPA...ESRLEP	TAPPAESFR.
00BW1795_6	RQANFLGKIW	PSHKG.RPGN	FLQNRPE...P	TAPPAESFR.
00BW1811_3	RQANFLGRIW	PSHKG.RPGN	FLQNRPEPTA	P.....LEP	TAPPAESFR.
00BW1859_5	RQANFLGKIW	PSHKG.RPGN	FLQNRPEP..	TAPPAESFR.
00BW1880_2	RQANFLGKIW	PSHKG.RPGN	FLQSR.....PEP	TAPPAESFK.
00BW1921_1	RQANFLGKIW	PSHKG.RPGN	FLQSRPEP..	TAPPAESFR.
00BW2036_1	RQANFLGKIW	PSNKG.RPGN	FLQNRTPAPPVEP	TAPPAESFR.
00BW2063_6	RQANFLGKIW	PSHKG.RPGN	FLQSRLE...P	TAPPAESF..
00BW2087_2	RQANFLGKIW	PSHKGGRPGN	FLQSRPEPTA	P.....PAEP	TAPPAESFR.
00BW2127_2	RQANFLGKIW	PSHKG.RPGN	FLQNRPEPTA	P.....RPEP	SAPPAESFR.
00BW2128_3	RQANFLGRIW	PSNKG.RPGN	FLQNRPEPTA	PPAE.NRPEP	TAPPAESFR.
00BW2276_7	RQANFLGKLW	PSNKG.RPGN	FLQNRTEPTA	P.....LEP	TAPPADSFK.
00BW3819_3	RQANFLGKIW	PSHKG.RPGN	FLQNRPE...	P.....TAP	TAPPAESFR.
00BW3842_8	RQANFLGKIW	PSRGG.RPGN	FLQNRTEPTA	P.....PEP	TAPPAESFR.
00BW3871_3	RQANFLGKIW	PSHKG.RPGN	FLQNRPEP..	TAPPAESFR.
00BW3876_9	RQANFLGKIW	PSHKG.RPGN	FLQNRPE...P	TAPPAESFR.
00BW3886_8	RQANFLGKIW	PSHKG.RPGN	FLQNRPEPTA	P.....PAEP	TAPPAESFR.
00BW3891_6	RQANFLGRIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESFR.
00BW3970_2	RQANFLGRFW	PSQKG.RPGN	FLQ.....SRSEP	TAPPAESFR.
00BW5031_1	RQANFLGKIW	PSNKG.RPGN	FLQSRPEPTA	P.....PMP	TAPPAESFR.
96BW01B21	RQANFLGKIW	PSHKG.RPGN	FLQNR.....LEP	SAPPAESFR.
96BW0407	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPAESFR.
96BW0502	RQANFLGKIW	PSHKG.RPGN	FLQNRSEPA.APTVP	TAPPAESFR.
96BW06_J4	RQANFLGKIW	PSHKGGRPGN	FLQSRPEP..	TAPPAESFR.
96BW11_06	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESL..
96BW1210	RQANFLGKIW	PSHKG.RPGN	FLQSR.....PEP	SAPPAESFR.
96BW15B03	RQANFLGKIW	PSHKG.RPGN	FLQNRTEP..	TAPPAESFK.
96BW16_26	RQADFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESFR.
96BW17A09	RQANFLGKIW	PSHKGGRPGN	FLQNRPEP..	TAPPAESFR.
96BWM01_5	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAEIL..
96BWM03_2	RQANFLGKIW	PSHKG.RPGN	FLQSRPEP..	TAPPAERFR.
98BWMC12_2	RQANFLGRLW	PSHKG.RPGN	FPQNR.....VEP	TAPPAESLR.
98BWMC13_4	KQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESL..
98BWMC14_a	RQANFLGKIW	PSHKG.RPGN	FLQSRPEP..	SAPPAESFR.
98BWM014_1	RQANFLGKIW	PSHKGGRPGN	FLQRRPEP..	TAPPAESFR.
98BWM018_d	RQANFLGKIW	PSHKG.RPGN	FIQNRPAPT.APPVEP	TAPPAESFR.
98BWM036_a	RQANFLGRIW	PSHKG.RPGN	FLQSRPEPTA	P.....PAEP	TAPPAESFR.
98BWM037_d	RQANFLGKIW	PSHKG.RPGN	FLQ.....KRPEP	TAPPAESFR.
99BW3932_1	RQVNFLGKIW	PSNKG.RPGN	FLQNRTPVPTA	PPAESFRIEP	TAPPAESFR.
99BW4642_4	RQANFLGKIW	PSHKG.RPGN	FFQNRTEP..	TAPPAESFR.
99BW4745_8	RQANFLGKIW	PSNKG.RPGN	FLQNRPEPTA	P.....LEP	TAPPAESFR.
99BW4754_7	RQANFLGKIW	PSNKG.RPGN	FLQSR.....PEP	TAPPAESFK.
99BWMC16_8	RQANFLGKIW	PSNKG.RPGN	FLQNRPEPT.APLEP	TAPPAESFR.
A2_CD_97CD	RQANFLGKIW	PSNKG.RPGN	FPQSRTE...P	TAPPME....
A2_CY_94CY	RQANFLGKIW	PSNKG.RPGN	FPQSRTE...P	TAPPAENLR.
A2D___97KR	RQANFLGKIW	PSHSG.RPGN	FPQSRTE...P	TAPPAEDFG.
A2G_CD_97C

A_BY_97BL0	RQANFLGRIW	PSSKG.RPGN	FPQSRPE...PS	APP.AENFR.
A_KE_Q23_A	RQANFLGKIW	PSRKG.RPGN	FPQNRLE...PT	APP.AETCG.
A_SE_SE659
A_SE_SE725
A_SE_SE753	RQANFLGRIW	PSSKG.RPGN	FPQSRLE...PT	APP.AEIFG.
A_SE_SE853
A_SE_SE889
A_SE_UGSE8	RQANFLGKIW	PSHKG.RPGN	FPQSRPE...PS	APP...AEM.
A_UG_92UG0	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PT	APPAAEIFG.
A_UG_U455_	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...P	TAPPAEIFG.
AC_IN_2130	RQANFLGKIW	PSHKG.RPGN	FLQ.....NRPEP	TAPPAESFR.
AC_RW_92RW	RQANFLGKIW	PSNKG.RPGN	FPQSRL....EP	TAPPA.....
AC_SE_SE94
ACD_SE_SE8	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...PT	APPA.ESFG.
ACG_BE_VI1	RQANFLGKIW	PSNKG.RPGN	FPQSRPEPTA	PP.....AEP	TAPPAESFG.
AD_SE_SE69	RQANFLGKIW	PSSKG.RPGN	FLQSRP....EP	TAPPAESFG.
AD_SE_SE71
ADHK_NO_97	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PS	APPA.ESFG.
ADK_CD_MAL	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...PT	APPA.ESFG.
AG_BE_VI11	RQANFLGKIW	PSSKG.RPGN	FPQSRLE...PT	APPA.ESLG.
AG_NG_92NG	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPAESFG.
AGHU_GA_VI	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...PT	APPA.ESFG.
AGU_CD_Z32	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPAESFE.
AJ_BW_BW21	RQANFLGKIW	PSNKG.RPGN	FLQSRPE...PT	APPA.ESFG.
B_AU_VH_AF	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_CN_RL42_	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_DE_D31_U	RQANFLGKIW	PSYKG.RPGN	FLQRRPE...P	TAPPEESFR.
B_DE_HAN_U	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_FR_HXB2_	RQANFLGKIW	PSYKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_GA_OYI__	RQANFLGKIW	PSHKG.RPGN	FLQNRPE...P	TAPPAESFG.
B_GB_CAM1_	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_GB_GB8_A	RQANFLGKIW	PSHKG.RPGN	FLQSRPEPIA	PP.....EP	TAPPEESFR.
B_GB_MANC_	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_KR_WK_AF	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	SAPPEESFR.
B_NL_3202A	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_TW_TWCYS	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_US_BC_L0	RQANFLGKIW	PSHKG.RPGN	FPQSRLE...P	TAPPEESFR.
B_US_DH123	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	SAPPEESFR.
B_US_JRCSF	RQANFLGKIW	PSYKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_US_MNCG_	RQANFLGKIW	PSCKG.R.RN	FPQSRTE...P	TAPPEESFR.
B_US_P896_	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_US_RF_M1	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_US_SF2_K	RQANFLGKIW	PSYKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_US_WEAU1	RQANFLGKIW	SSQKG.RPGN	FPQSRLE...P	TAPPEESFR.
B_US_WR27_	RQAXFLGXIR	PSHXG.RPGX	FLQNRPE...P	SAPPAESFR.
B_US_YU2_M	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPSEESVR.
BF1_BR_93B	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESFR.
C_BR_92BR0	RQANFLGKIW	PSHRG.RPGN	LLQNRTE...EP	TAPPE.....
C_BW_96BW0	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPAESFR.
C_BW_96BW1	RRANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESF..
C_BW_96BW1	GQANFLGKIW	PSHKG.RPGN	FLQSR.....PEP	SAPPAESFR.
C_BW_96BW1	RQANFLGKIW	PSHKG.RPGN	FLQNRTEP..	TAPPAESFK.
C_ET_ETH22	RQANFLGRLW	PSNKG.RPGN	FLQSRP....EP	TAPPESLRPE
C_IN_93IN1	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPAESFR.
C_IN_93IN9	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPAESFR.
C_IN_93IN9	RQANFLGKIW	PSHKG.RPGN	FLQNRPEPTA	PP...ARPEP	TAPPAESFR.
C_IN_94IN1	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPAESFR.
C_IN_95IN2	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPAESFR.
CRF01_AE_C	RQANFLGKIW	PLNKG.RPGN	FPQSRLE...PT	APPA.ESLG.
CRF01_AE_C	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PT	APPM.ESLG.
CRF01_AE_C	RQANFLGRIW	PSSKG.RPGN	FPQSRPE...PT	APPA.ESLG.

CRF01_AE_T	RQANFLGKFW	PSNKG.RPGN	FPQSRPE...PT	APPA.ENWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...PT	APP..AEWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSKPE...PT	APPA.ENWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...PT	APPA.ENWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...PT	APPA.ENWG.
CRF02_AG_F	GQANFLGKIW	PSSKG.RPGN	FPQSRPE...PT	APPA.ESLG.
CRF02_AG_F	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PT	APPA.ESFG.
CRF02_AG_G	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...	P.....	SAPPAESFG.
CRF02_AG_N	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PT	APPA.ESFG.
CRF02_AG_S	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PT	APPA.ESLG.
CRF02_AG_S	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PT	APPA.ESFG.
CRF03_AB_R	RQANFLGRIW	PSSKG.RPGN	FPQSRPE...PS	APP.AENFG.
CRF03_AB_R	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PS	APP.AENFG.
CRF04_cpx_	RQANFLGRMW	PSSKG.RPGN	FLQNRPE...PT	APPA.ECLE.
CRF04_cpx_	RQANFLGRMW	PSSKG.RPGN	FLQSRPE...PT	APPA.ESLE.
CRF04_cpx_	RQANSLGRMW	PSSKG.RPGN	FLQSRTE...PT	APPA.ESFE.
CRF05_DF_B	RQANFLGKVW	PSHKG.RPGN	FLQSRP....EP	SAPPAESFR.
CRF05_DF_B	GQANFLGRVW	LSHKG.RPGN	FLQSRP....EP	SAPPAESFG.
CRF06_cpx_	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPIESFG.
CRF06_cpx_	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPAESFG.
CRF06_cpx_	RQANFLGRIW	PSSKG.RPGN	FLQNRPE...P	TAPPAESFG.
CRF06_cpx_	RQANFLGKIW	PSHKG.RPGN	FLQNRPEQNR	P.....EP	SAPPAESFG.
CRF11_cpx_	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...PT	APPA.ESFG.
CRF11_cpx_	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...PT	APPA.ESFG.
D_CD_84ZR0	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAE.FG.
D_CD_ELI_K	RQANFLGRIW	PSHKG.RPGN	FLQSRP....EP	TAPPAESFG.
D_CD_NDK_M	RQANFLGKIW	PSHKG.RPGN	FLQSRP....EP	TAPPAESFG.
D_UG_94UG1	RQANFLGKIW	PSHNG.RPGN	FLQSRPPA..EP	TAPPAEIFG.
F1_BE_VI85	RQANFLGKIW	PSNKG.RPGN	FLQSRPE...P	TAPPAESFG.
F1_BR_93BR	RQANFLGKIW	PSNKG.RPGN	FIQNRPE...P	SAPPAESFR.
F1_FI_FIN9	RQANFLGKIW	PSNKG.RPGN	FLQSRPE...P	TAPPAESLG.
F1_FR_MP41	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPAESFG.
F2_CM_MP25	RQANFLGKMW	PSNKG.RPGN	FLQNRPE...P	TAPPAESFG.
F2KU_BE_VI	RQANFLGKIW	PSNKG.RPGN	FLQSRPE...P	TAPPAESFG.
G_BE_DRCBL	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPAENFG.
G_NG_92NG0	RQANFLGKIW	PSNKG.RPGN	FLQNRTE...P	TAPPAESFG.
G_SE_SE616	RQANFLGKIW	PSNKG.RPGN	FLQNRTE...P	TAPPAESLG.
H_BE_VI991	RQANFLGKIW	PSSKG.RPGN	FPQKRLE...P	TAPPAESFG.
H_BE_VI997	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...P	TAPPAESFG.
H_CF_90CF0	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...P	TAPPAESFG.
J_SE_SE702	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...P	TAPPAESLG.
J_SE_SE788	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...P	TAPPAESLG.
K_CD_EQTB1	RQANFLGKFW	PLNKE.RPGN	FLQNRPE...P	TAPPAESFG.
K_CM_MP535	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESFG.
N_CM_YBF30	RQANFLGKSW	SPFKG.RPGN	FPQTTTRK..EP	TAPPLESYG.
O_CM_ANT70	KQANFLGKYW	PP.GGTRPGN	YVQRPAAH...P	SAPPMEEVK
O_CM_MVP51	RQANFLGKYW	PP.GGTRPGN	YVQKQVS...P	SAPPMEEAVK
O_SN_99SE_	RQANFLGKYW	PP.GGTRPGN	YAQRQVS...P	SAPPMTEEMK
O_SN_99SE_	KQANFLGKYW	PP.GGTRPGN	YAQRQVS...P	SAPPMTEEMK
U_CD___83C	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPAESFG.

501

00BW0762_1FE...	..ETNPTP..	...KQE....	PKDRE.....	PLTSLKSLFG
00BW0768_2FE...	..ETTPAP..	...KQE....	LKDR.....E	PLTALKSLFG
00BW0874_2FE...	..ETTPAL..	...KRE....	LKER.....E	PLISLKSLFG
00BW1471_2FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSLKSLFG
00BW1616_2F....	..GETTPSP..	...RQE....	AKDRE.....	PLISLKSLFG
00BW1686_8FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSLKSLFG
00BW1759_3FE...	..ETTPAP..	...KQE....	PKDRE.....	TLTSLRSLFG
00BW1773_2FE...	..ETTPAP..	...KQE....	PKDRE.....	PLTSLKSLFG

550

00BW1783_5FE...	..ETTPVQ..	...KQE....	TKDRE.....	PLTSLKSLFG
00BW1795_6F....	.EETTPSP..	...KQE....	LKDKE.....	PLTSLKSLFG
00BW1811_3FE...	..ETTPAS..	...KQE....	KKDRE.....	TLTSLKSLFG
00BW1859_5FE...	..ETTPAP..	...KQE....	QKDR.....E	PLTSLKSLFG
00BW1880_2FE...	..ETTPAP..	...KQE....	PKDRE.....	PLTSLKSLFG
00BW1921_1FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSLKSLFG
00BW2036_1FE...	..ETTPAP..	...KQE....	LKDR.....E	PLISLKSLFG
00BW2063_6EETTPAP..	...KQE....	MKDKE.....	PLISLKSLFG
00BW2087_2FE...	..ETTPAS..	...KQD....	LKDRE.....	PLTSLKSLFG
00BW2127_2FE...	..ETTHAP..	...KQE....	LKDRE.....	ALTSLKSLFG
00BW2128_3FE...	..ETTPAP..	...KQE....	PKNRE.....	PLTSLKSLFG
00BW2276_7FE...	..ETTPEL..	...KQG....	PKDR.....E	PLTSLKSLFG
00BW3819_3FE...	..EITPAP..	...KQE....	TKDRE.....	PLTSLKSLFG
00BW3842_8FE...	..ETTPAP..	...KQE....	PKDRGPY.RE	PLISLKSLFG
00BW3871_3FE...	..ETTPVP..	...KQE....	PTDR.....E	PLTSLKSLFG
00BW3876_9FE...	..ETTPTL..	...KQE....	LKDRE.....	PLTSLKSLFG
00BW3886_8FE...	..ETTPVP..	...KQE....	QKDRE.....	ALTSLKSLFG
00BW3891_6FE...	..EITPVP..	...KQE....	PKDR.....E	PLTSLKSLFG
00BW3970_2FE...	..ETTPAP..	...KQE....	PKDRE.....	PLISLKSLFG
00BW5031_1FG...	..ETTPAP..	...KQE....	MKERE.....	PLISLKSLFG
96BW01B21FE...	..ETTPAP..	...KQE....	PKDRE.....	PLTSLKSLFG
96BW0407FE...	..ETTPGQ..	...KQE....	SKDRE.....	TLTSLKSLFG
96BW0502FE...	..ETTPAP..	...KQE....	PKDREPY.RE	PLTSLKSLFG
96BW06_J4FE...	..ETTPAL..	...KQE....	PKDK.....E	PLTSLKSLFG
96BW11_06EETTPAP..	...KQE....	TKDRE.....	PLISLKSLFG
96BW1210FE...	..ETTPAQ..	...KQE....	PKDREP....	PLASLKSLFG
96BW15B03FE...	..ETTPAP..	...KQE....	PKDR.....E	PLISLKSLFG
96BW16_26FG...	..ETTPAP..	...KQE....	PKDRE.....	PLTSLKSLFG
96BW17A09FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSLKSLFG
96BWM01_5EETTPAP..	...KQE....	MKDKEPY.KE	PLISLKSLFG
96BWM03_2PE...	..PTAPPAE..	...RQE....	SKDR.....E	PLISLKSLFG
98BWMC12_2LE...	..ETTPAS..	...KQE....	MKDR.....E	PLISLKSLFG
98BWMC13_4EETTPAP..	...KQE....	PKDKE.....	PLISLKSLFG
98BWMC14_aFE...	..ETTPAP..	...KQE....	QKDR.....E	PLTSLKSLFG
98BWM014_1FESRP	EPTAPPAES.	..FRQE....	PKDR.....E	PLTSLKSLFG
98BWM018_dFE...	..ETTPAL..	...KQE....	PKDREA....	PLTSLKSLFG
98BWM036_aFE...	..ETNLAP..	...KQE....	PKDRE.....	PLTSLKSLFG
98BWM037_dFE...	..ETTPAP..	...RQE....	AKDKE.....	PLNSLKSLFG
99BW3932_1FE...	..ETTPAP..	...KQE....	LKDRE.....	ALTSLKSLFG
99BW4642_4FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSLKSLFG
99BW4745_8FE...	..GATPTP..	...KQE....	PRDR.....E	PLTSLKSLFG
99BW4754_7FE...	..ETTPAQ..	...KQE....	SKDRE.....	PLTSLKSLFG
99BWMC16_8FE...	..ETNPAP..	...KQE....	LKNRE.....	TLTSLKSLFG
A2_CD_97CDEEITSSL..	...KQE....	NREPS....T	PAISLKSLFG
A2_CY_94CYMGEEITSSL..	..KQEL...E	TREPY....N	PAISLKSLFG
A2D_97KRMGEETPLQ..	..KQEL...K	NREQH....T	PAISLKSLFG
A2G_CD_97C
A_BY_97BL0	MGEEIT....	PSLK.Q...E	QKDRE..QYP	PSISLKSLFG
A_KE_Q23_A	MGEETV....	SPLK.Q...E	QKDRE..QAQ	PLVSLKSLFG
A_SE_SE659
A_SE_SE725
A_SE_SE753	MREEIA....	SPPK.Q...E	Q...KG..QDP	PLVSLKSLFG
A_SE_SE853
A_SE_SE889
A_SE_UGSE8	MGEEIA....	SPPK.Q...E	Q.....NNP	PSVSLKSLFG
A_UG_92UG0	MREEIV....	SPPK.Q...E	QNDRE..QNP	PSVSLKSLFG
A_UG_U455_MGEKMTSPA..	..KQEL...K	DREQ....T	PLVSLKSLFG
AC_IN_2130FE...	..ETTPAL..	...KQE....	QKDRE.....	PLTSLKSLFG
AC_RW_92RWENFG	MGEEIASPL..	..K.QE....	QKDRE.....	PLISLKSLFG
AC_SE_SE94
ACD_SE_SE8	FGEEITP....	S.QK.Q...E	QKDKE...LY	PLASLKSLFG

ACG_BE_VI1	KEDAIDSS..	..PKQE....	PRDKG..LYP	PLTSLKSLFG
AD_SE_SE69	FGEEIAP...	.SQKQE...Q	KDK....ELY	PLASLKSLFG
AD_SE_SE71
ADHK_NO_97	IGEEIT....	SYQK.Q...E	QKDRE..PPP	PLVSLKSLFG
ADK_CD_MAL	FGEEIK....	PSQK.Q...E	QKDKE..L.Y	PLASLKSLFG
AG_BE_VI11	MEEEIT....	PSQK.Q...E	PRDTG..LYP	PLTSLKSLFG
AG_NG_92NG	FGEEIAP...	S.LK.Q...E	PREKE..SPP	L.TSLKSLFG
AGHU_GA_VI	FGEEIA....	PSPR.P...E	PREKE..R.Y	PLTSLKSLFG
AGU_CD_Z32	TKEEITS...	S.PK.Q...E	PRDKE..LYP	PLASLKSLFG
AJ_BW_BW21	FGEETA....	PSPK.Q...E	GKDKE..L.Y	PLTSLKSLFG
B_AU_VH_AF	FGEETTPP..	.SQKQE....	PIDK...ELY	PLASLRSLFG
B_CN_RL42_	FGEETTPP..	.SQKQE....	PIDK...ELY	PLASLRSLFG
B_DE_D31_U	FGEETATP..	.FQKQE....	PIDK...ELY	PLASLRSLFG
B_DE_HAN_U	FGEATAP...	.SQKQE....	PIDK...ELY	PLASLKSLFG
B_FR_HXB2_	SGVETTPP..	.PQKQE....	PIDK...ELY	PLTSLRSLFG
B_GA_OYI_	FGEETTPP..	.PQKQE....	PIDK...GLY	PLTSLRSLFG
B_GB_CAM1_	FGEEKTPP..	.SQKQE....	PIDK...ELY	PLASLRSLFG
B_GB_GB8_A	FGGETTPP..	.SQKQE....	PINK...EPY	PLASLRSLFG
B_GB_MANC_	FGEETTPP..	.AQKQE....	PIDK...ELY	PLASLRPLFG
B_KR_WK_AF	FGEETTPP..	.SQKQE....	PIDK...ELY	PLASLRSLFG
B_NL_3202A	FGEETTPP..	.SQKQE....	PRDK...ELY	PLASLRSLFG
B_TW_TWCYS	FGEQTPP..	.SQKQE....	PIDK...DLY	PLASLESFLG
B_US_BC_L0	FGEETTPP..	.PQKQERE..	..DK...EMY	PLASLRSLFG
B_US_DH123	FGEETATP..	.SQKQE....	..PK...ELY	PLASLKSLFG
B_US_JRCSF	FGEETATP..	.SQKQEQKQE	PIDK...ELY	PLTSLRSLFG
B_US_MNCG_	FGEETTPP..	.YQKQEKQKE	TIDK...DLY	PLASLKSLFG
B_US_P896_	FGEETTPP..	.SQKQE....	PIDK...ELY	PLASLRSLFG
B_US_RF_M1	FGEETTPP..	.SQKQE....	KIDK...ELY	PLASLKSLFG
B_US_SF2_K	FGEEKTPP..	.SQKQE....	PIDK...ELY	PLTSLRSLFG
B_US_WEAU1	FREETTPP..	.SQKQE....	PIDK...ELY	PLTSLKSLFG
B_US_WR27_	FGXETTPP..	.SQKQE....	PIDK...ELY	PLASLRSLFV
B_US_YU2_M	FGEETTPP..	.SQKQE....	PIDK...ELY	PLASLRSLFG
BF1_BR_93B	FGEEVTPP..	.SQKQE....	PIDK...EMY	PLASLRSLFG
C_BR_92BR0	ESFR FGEETTPPS.	..RKQE....	TIDKEL....	PLTSLKSLFG
C_BW_96BW0	FE... ..ETTPVP..	...KQE....	PKDRE....	PLTSLKSLFG
C_BW_96BW1ETTPAP..	...KQE....	TKDRE....	PLISLKSLFG
C_BW_96BW1	FE... ..ETTPAQ..	...KQE....	PKDREP....	PLASLKSLFG
C_BW_96BW1	FE... ..ETTPAP..	...KQE....	PKDR....E	PLISLKSLFG
C_ET_ETH22	PTAPPPESFR	FEEATPSPK.	..Q..E....	LKDRE....	ALTSLKSLFG
C_IN_93IN1	FE... ..ETTPAP..	...KQE....	PKDRE....	PLTSLKSLFG
C_IN_93IN9	FE... ..ETPPAP..	...KQE....	PKDRE....	PLTSLRSLFG
C_IN_93IN9	FE... ..ETTPAL..	...KQE....	PKDRE....	PLTSLKSLFG
C_IN_94IN1	FE... ..ETPPAP..	...KQE....	PKERE....	PLTSLRSLFG
C_IN_95IN2	FE... ..ETTPAP..	...KQE....	PKDRE....	PLTSLRSLFG
CRF01_AE_C	MGEEIT....	SFPK.Q...E	QKDKE..HPS	PLVSLKSLFG
CRF01_AE_C	MGEEIT....	SFPK.Q...E	QKDKK..QPP	PLVSLKSLFG
CRF01_AE_C	MGEEIT....	SFSR.Q...E	QKDRE..HPP	PLVSLKSLFG
CRF01_AE_T	MGEETT....	.SLLKQ...E	QKDKE..HHP	PLVSLKSLFG
CRF01_AE_T	MGEEIT....	SLPK.Q...E	QKDKD..PPP	.LVSLKSLFG
CRF01_AE_T	MGEE.....	QKDKE..HPP	PSVSLKSLFG
CRF01_AE_T	MGEETT....	SSLK.Q...E	QKDKE..PPP	PLISLKSLFG
CRF01_AE_T	MGEEITGEEI	TSLPKQ...E	QKDKE..HPP	PLVSLKSLFG
CRF01_AE_T	MGEEIT....	SFLK.Q...E	QKDKE..HPP	PSVSLKSLFG
CRF02_AG_F	MGEEIT....	SPPK.Q...E	ARDQG..LYP	PLASLKSLFG
CRF02_AG_F	MGEEIT....	SPPK.Q...E	PRDQG..LYP	PLASLKSLFG
CRF02_AG_G	TREEITSS..	..PQQE....	PRDKG..LYP	PLTSLKSLFG
CRF02_AG_N	MGEEIP....	PSPQ.Q...E	PRDKG..LYP	PLTSLKSLFG
CRF02_AG_S	IGEEIT....	SSQK.Q...E	PGDKG..LYP	PLASLKSLFG
CRF02_AG_S	MGEEIT....	SSPK.Q...E	PGDKG..LYP	PLTSLKSLFG
CRF03_AB_R	MGEEIT....	PSLK.Q...E	QKDRE..QHP	PSISLKSLFG
CRF03_AB_R	MGEEIT....	PSLK.Q...E	QKDRG..QHP	PSISLKSLFG

CRF04_cpx_	RKEETTS...	S.LK.Q...E	PRDKE..LYP	.LTSLKSLFG
CRF04_cpx_	MKEETTS...	S.PK.Q...E	PRDKE..LYP	.LTSLKSLFG
CRF04_cpx_	MKEETTS...	S.PK.Q...E	QRDKE..LYP	.ITSLKSLFG
CRF05_DF_B	FGEEIAS...	.SPKQE...Q	KDEG...LYP	PLASLKSLFG
CRF05_DF_B	FGEEITP...	.SPKQE...Q	KDEG...LYP	PLASLKSLFG
CRF06_cpx_	FGEEIAP...	S.PK.Q...E	SKEKEEKGLY	PLASLKSLFG
CRF06_cpx_	FGEEITP...	S.PE.Q...K	PKEKE...LY	PLTSLRSLFG
CRF06_cpx_	FGEEITP...	S.LK.Q...E	PKEKEKE.LY	PLASLKSLFG
CRF06_cpx_	FGEEIAP...	S.PK.Q...E	PKEKE...LY	PLASLKSLFG
CRF11_cpx_	FGEEIAP...	.SPK.Q...E	PKEKEK.ELY	PLTSLKSLFG
CRF11_cpx_	FGEEITP...	.SPK.Q...E	PKEK...ELY	PITSLKSLFG
D_CD_84ZR0	FGEEITP...	.SQKQEQK..	DKDK...ELY	PLASLKSLFG
D_CD_ELI_K	FGEEITP...	.SQKQE...Q	KDK...ELY	PLTSLKSLFG
D_CD_NDK_M	FGEEITP...	.SQKQE...Q	KDK...ELY	PLASLKSLFG
D_UG_94UG1	LGEEITP...	.PQKQE...Q	KDK...ELY	PLTSLKSLFG
F1_BE_VI85FR...	.EEITPSP..	...KQE....	QKDGL..YP	PLASLKSLFG
F1_BR_93BRFG...	.EETTPSP..	...KQE....	QKDEGL..YP	PLASLKSLFG
F1_FI_FIN9IR...	.EEVTPSP..	...RQE....	QKEEGQ..YP	PLASLKSLFG
F1_FR_MP41FK...	.EEITPSP..	...KQE....	QKDEGQGLYP	PLASLKSLFG
F2_CM_MP25FG...	.EEIAPSP..	...KQE....	QKDKEQ..VP	PLISLKSLFG
F2KU_BE_VIFG...	.EEINPSP..	...RQE....	TKDKGQ..EP	PLTSLKSLFG
G_BE_DRCBL	FGEEIAP...	S.PK.Q...E	QKEKE..LYP	L.SSLKSLFG
G_NG_92NG0	FGEEIAP...	S.PK.Q...E	PKEKE..LYP	L.TSLKSLFG
G_SE_SE616	FGEEIAP...	S.PK.Q...E	MKEKE..LYP	...SLKSLFG
H_BE_VI991FG...	.EEITPSP..	...RQE....	LKEQE....P	PLTSLRSLFG
H_BE_VI997FG...	.EEMTSSP..	...KQE....	LKDKE....P	PFASLKSLFG
H_CF_90CF0FG...	.EEMTPSP..	...KQE....	LKDKE....P	PLASLRSLFG
J_SE_SE702FG...	.EEIPSP..	...KQE....	PKDKE...LY	PLTSLRSLFG
J_SE_SE788LG...	.EEIPSP..	...KQE....	PKDKE...LY	PLTSLKSLFG
K_CD_EQTB1FG...	.EKITPSL..	...RQE....	MKDQEQ..GP	PLTSLKSLFG
K_CM_MP535FG...	.EEITPSP..	...RQE....	TKDKEQ..SP	PLTSLKSLFG
N_CM_YBF30FQ...	.EEKSTQ..	GKEMQE...N	QERTENSLYP	PLTSLRSLFG
O_CM_ANT70GQENQEQ..	...KGG....	PNE.....LY	PFASLKSLFG
O_CM_MVP51EQENQSQ..	...KGD....	QEE.....LY	PFASLKSLFG
O_SN_99SE_GQENQEQ..	...KED....	QNE.....LY	PFASLRSLFG
O_SN_99SE_GQENQEQ..	...KGD....	QNE.....LY	PFASLKSLFG
U_CD___83CFG...	.EETTPSP..	...KQE....	PRDKESL.YP	PLTSLKSLFG

551

00BW0762_1	SDPLSQ
00BW0768_2	SDPLSQ
00BW0874_2	NDPLSQ
00BW1471_2	SDPLSQ
00BW1616_2	SDPLSQ
00BW1686_8	SDPLSQ
00BW1759_3	SDPLSQ
00BW1773_2	SDPLSQ
00BW1783_5	SDPLSQ
00BW1795_6	SDPLSQ
00BW1811_3	SDPLSQ
00BW1859_5	SDPLSQ
00BW1880_2	NDPLSQ
00BW1921_1	SDPLSQ
00BW2036_1	SDPLSQ
00BW2063_6	NDPLSQ
00BW2087_2	SDPLSQ
00BW2127_2	SDPLSQ
00BW2128_3	SDPWSQ
00BW2276_7	SDPLSQ
00BW3819_3	SDPLSQ
00BW3842_8	SDPLSQ

00BW3871_3	SDPLSQ
00BW3876_9	SDPLSQ
00BW3886_8	SDPLSQ
00BW3891_6	SDPLSQ
00BW3970_2	SDPLSQ
00BW5031_1	SDPLSQ
96BW01B21	SDPLSQ
96BW0407	NDPLSQ
96BW0502	SGPLSQ
96BW06_J4	SDPLSQ
96BW11_06	SDPLSQ
96BW1210	NDPLSQ
96BW15B03	SDPLSQ
96BW16_26	NDPLSQ
96BW17A09	SDPLSQ
96BWMO1_5	SDPLSQ
96BWMO3_2	SDPLSQ
98BWMC12_2	NDPLSQ
98BWMC13_4	SDPLSQ
98BWMC14_a	NDPLSQ
98BWMO14_1	SDPLSQ
98BWMO18_d	SDPLSQ
98BWMO36_a	SDPLSQ
98BWMO37_d	SDPLSQ
99BW3932_1	SDPLSQ
99BW4642_4	SDPLSQ
99BW4745_8	SDPLSQ
99BW4754_7	NDPLSQ
99BWMC16_8	GDPLSQ
A2_CD_97CD	NDLLSQ
A2_CY_94CY	NDPLLQ
A2D___97KR	NDPLLQ
A2G_CD_97C
A_BY_97BL0	NDPLSQ
A_KE_Q23_A	NDLLSQ
A_SE_SE659
A_SE_SE725
A_SE_SE753	NDLLSQ
A_SE_SE853
A_SE_SE889
A_SE_UGSE8	NDLLSQ
A_UG_92UG0	NDLLSQ
A_UG_U455_	NDPLSQ
AC_IN_2130	SDPLSQ
AC_RW_92RW	NDPLSQ
AC_SE_SE94
ACD_SE_SE8	NDP...
ACG_BE_VI1	NDP...
AD_SE_SE69	NDP...
AD_SE_SE71
ADHK_NO_97	NDPLSQ
ADK_CD_MAL	NDQLSQ
AG_BE_VI11	NDP...
AG_NG_92NG	NDP...
AGHU_GA_VI	SDP...
AGU_CD_Z32	SDP...
AJ_BW_BW21	SDP...
B_AU_VH_AF	NDPSSQ
B_CN_RL42_	NDPSSQ
B_DE_D31_U	NDPSSQ
B_DE_HAN_U	SDPSSQ

B_FR_HXB2_	NDPSSQ
B_GA_OYI_	NDPSSQ
B_GB_CAM1_	NDPSSQ
B_GB_GB8_A	NDPSSQ
B_GB_MANC_	NDPSSQ
B_KR_WK_AF	NDPSSQ
B_NL_3202A	NDPSSQ
B_TW_TWCYS	NDPSSQ
B_US_BC_L0	NDPSSQ
B_US_DH123	NDP...
B_US_JRCSF	NDPSSQ
B_US_MNCG_	NDPLSQ
B_US_P896_	NDPSSQ
B_US_RF_M1	NDPSSQ
B_US_SF2_K	NDPSSQ
B_US_WEAU1	NDPSSQ
B_US_WR27_	NDPSSQ
B_US_YU2_M	SDPSSQ
BF1_BR_93B	NDPSSQ
C_BR_92BR0	SDPLST
C_BW_96BW0	SDPLSQ
C_BW_96BW1	SDPLSQ
C_BW_96BW1	NDPLSQ
C_BW_96BW1	SDPLSQ
C_ET_ETH22	NDHLLQ
C_IN_93IN1	SDLLSQ
C_IN_93IN9	SDPLSQ
C_IN_93IN9	SDPLSQ
C_IN_94IN1	SDPLSQ
C_IN_95IN2	SDPLSQ
CRF01_AE_C	NDPLSQ
CRF01_AE_C	NDPLSQ
CRF01_AE_C	NDPLSQ
CRF01_AE_T	NDPSSQ
CRF01_AE_T	NDPLSQ
CRF01_AE_T	NDPLSQ
CRF01_AE_T	NDPLSQ
CRF01_AE_T	NDPLSQ
CRF01_AE_T	NDPLSQ
CRF02_AG_F	NDP...
CRF02_AG_F	NDP...
CRF02_AG_G	NDP...
CRF02_AG_N	NDP...
CRF02_AG_S	NDP...
CRF02_AG_S	NDPYSQ
CRF03_AB_R	DDPLSQ
CRF03_AB_R	NDPLSQ
CRF04_cpx_	SDPLSQ
CRF04_cpx_	NHPLSQ
CRF04_cpx_	SDPLSR
CRF05_DF_B	NDPLSQ
CRF05_DF_B	NDPLSQ
CRF06_cpx_	SDP...
CRF06_cpx_	NDP...
CRF06_cpx_	NDP...
CRF06_cpx_	SDP...
CRF11_cpx_	SDP...
CRF11_cpx_	SDPLSQ
D_CD_84ZR0	NDPLSQ
D_CD_ELI_K	NDPLSQ
D_CD_NDK_M	NDPSSQ

D_UG_94UG1	NDPLSQ
F1_BE_VI85	NDP...
F1_BR_93BR	NDP...
F1_FI_FIN9	NDP...
F1_FR_MP41	SDP...
F2_CM_MP25	SDQ...
F2KU_BE_VI	SDPLLQ
G_BE_DRCBL	NDQ...
G_NG_92NG0	SDP...
G_SE_SE616	SDP...
H_BE_VI991	NDQ...
H_BE_VI997	NDPLSQ
H_CF_90CF0	SDPLLQ
J_SE_SE702	SDPLSQ
J_SE_SE788	SDPLSQ
K_CD_EQTB1	SDPLSQ
K_CM_MP535	NDPLSQ
N_CM_YBF30	NDPSSQ
O_CM_ANT70	TDQ...
O_CM_MVP51	TDQ...
O_SN_99SE_	TDQ...
O_SN_99SE_	TDQ...
U_CD___83C	SDPSLQ

Table 12. HIV Env Sequence Alignment
GCG Multiple Sequence File.
Written by Omega 1.1

Name: 00BW0762_1	SEQ	ID NO: 469	Len: 962	Check: 4645	Weight: 1.00
Name: 00BW0768_2	SEQ	ID NO: 470	Len: 962	Check: 9565	Weight: 1.00
Name: 00BW0874_2	SEQ	ID NO: 471	Len: 962	Check: 7745	Weight: 1.00
Name: 00BW1471_2	SEQ	ID NO: 472	Len: 962	Check: 9593	Weight: 1.00
Name: 00BW1616_2	SEQ	ID NO: 473	Len: 962	Check: 792	Weight: 1.00
Name: 00BW1686_8	SEQ	ID NO: 474	Len: 962	Check: 3744	Weight: 1.00
Name: 00BW1759_3	SEQ	ID NO: 475	Len: 962	Check: 9808	Weight: 1.00
Name: 00BW1773_2	SEQ	ID NO: 476	Len: 962	Check: 3500	Weight: 1.00
Name: 00BW1783_5	SEQ	ID NO: 477	Len: 962	Check: 9684	Weight: 1.00
Name: 00BW1795_6	SEQ	ID NO: 478	Len: 962	Check: 8410	Weight: 1.00
Name: 00BW1811_3	SEQ	ID NO: 479	Len: 962	Check: 2068	Weight: 1.00
Name: 00BW1859_5	SEQ	ID NO: 480	Len: 962	Check: 5692	Weight: 1.00
Name: 00BW1880_2	SEQ	ID NO: 481	Len: 962	Check: 1901	Weight: 1.00
Name: 00BW1921_1	SEQ	ID NO: 482	Len: 962	Check: 5923	Weight: 1.00
Name: 00BW2036_1	SEQ	ID NO: 483	Len: 962	Check: 7035	Weight: 1.00
Name: 00BW2063_6	SEQ	ID NO: 484	Len: 962	Check: 4853	Weight: 1.00
Name: 00BW2087_2	SEQ	ID NO: 485	Len: 962	Check: 2085	Weight: 1.00
Name: 00BW2127_2	SEQ	ID NO: 486	Len: 962	Check: 4015	Weight: 1.00
Name: 00BW2128_3	SEQ	ID NO: 487	Len: 962	Check: 5884	Weight: 1.00
Name: 00BW2276_7	SEQ	ID NO: 488	Len: 962	Check: 8913	Weight: 1.00
Name: 00BW3819_3	SEQ	ID NO: 489	Len: 962	Check: 9390	Weight: 1.00
Name: 00BW3842_8	SEQ	ID NO: 490	Len: 962	Check: 8867	Weight: 1.00
Name: 00BW3871_3	SEQ	ID NO: 491	Len: 962	Check: 7069	Weight: 1.00
Name: 00BW3876_9	SEQ	ID NO: 492	Len: 962	Check: 4761	Weight: 1.00
Name: 00BW3886_8	SEQ	ID NO: 493	Len: 962	Check: 7681	Weight: 1.00
Name: 00BW3891_6	SEQ	ID NO: 494	Len: 962	Check: 379	Weight: 1.00
Name: 00BW3970_2	SEQ	ID NO: 495	Len: 962	Check: 8001	Weight: 1.00
Name: 00BW5031_1	SEQ	ID NO: 496	Len: 962	Check: 4902	Weight: 1.00
Name: 96BW01B21	SEQ	ID NO: 497	Len: 962	Check: 5774	Weight: 1.00
Name: 96BW0407	SEQ	ID NO: 498	Len: 962	Check: 4260	Weight: 1.00
Name: 96BW0502	SEQ	ID NO: 499	Len: 962	Check: 4658	Weight: 1.00
Name: 96BW06_J4	SEQ	ID NO: 500	Len: 962	Check: 9749	Weight: 1.00
Name: 96BW11_06	SEQ	ID NO: 501	Len: 962	Check: 4328	Weight: 1.00
Name: 96BW1210	SEQ	ID NO: 502	Len: 962	Check: 3855	Weight: 1.00
Name: 96BW15B03	SEQ	ID NO: 503	Len: 962	Check: 9133	Weight: 1.00
Name: 96BW16_26	SEQ	ID NO: 504	Len: 962	Check: 5	Weight: 1.00
Name: 96BW17A09	SEQ	ID NO: 505	Len: 962	Check: 6458	Weight: 1.00
Name: 96BWM01_5	SEQ	ID NO: 506	Len: 962	Check: 9487	Weight: 1.00
Name: 96BWM03_2	SEQ	ID NO: 507	Len: 962	Check: 8766	Weight: 1.00
Name: 98BWMC12_2	SEQ	ID NO: 508	Len: 962	Check: 2722	Weight: 1.00
Name: 98BWMC13_4	SEQ	ID NO: 509	Len: 962	Check: 2526	Weight: 1.00
Name: 98BWMC14_a	SEQ	ID NO: 510	Len: 962	Check: 7761	Weight: 1.00
Name: 98BWM014_1	SEQ	ID NO: 511	Len: 962	Check: 93	Weight: 1.00
Name: 98BWM018_d	SEQ	ID NO: 512	Len: 962	Check: 279	Weight: 1.00
Name: 98BWM036_a	SEQ	ID NO: 513	Len: 962	Check: 134	Weight: 1.00
Name: 98BWM037_d	SEQ	ID NO: 514	Len: 962	Check: 9669	Weight: 1.00
Name: 99BW3932_1	SEQ	ID NO: 515	Len: 962	Check: 3527	Weight: 1.00
Name: 99BW4642_4	SEQ	ID NO: 516	Len: 962	Check: 1175	Weight: 1.00
Name: 99BW4745_8	SEQ	ID NO: 517	Len: 962	Check: 8117	Weight: 1.00
Name: 99BW4754_7	SEQ	ID NO: 518	Len: 962	Check: 5709	Weight: 1.00
Name: 99BWMC16_8	SEQ	ID NO: 519	Len: 962	Check: 285	Weight: 1.00
Name: A2_CD_97CD	SEQ	ID NO: 520	Len: 962	Check: 2892	Weight: 1.00
Name: A2_CY_94CY	SEQ	ID NO: 521	Len: 962	Check: 8628	Weight: 1.00
Name: A2D_97KR	SEQ	ID NO: 522	Len: 962	Check: 471	Weight: 1.00
Name: A2G_CD_97C	SEQ	ID NO: 523	Len: 962	Check: 939	Weight: 1.00
Name: A_BY_97BL0	SEQ	ID NO: 524	Len: 962	Check: 4291	Weight: 1.00
Name: A_KE_Q23_A	SEQ	ID NO: 525	Len: 962	Check: 1190	Weight: 1.00

Name: A_SE_SE659	SEQ	ID NO: 526	Len: 962	Check: 6674	Weight: 1.00
Name: A_SE_SE725	SEQ	ID NO: 527	Len: 962	Check: 4925	Weight: 1.00
Name: A_SE_SE753	SEQ	ID NO: 528	Len: 962	Check: 2482	Weight: 1.00
Name: A_SE_SE853	SEQ	ID NO: 529	Len: 962	Check: 1860	Weight: 1.00
Name: A_SE_SE889	SEQ	ID NO: 530	Len: 962	Check: 2102	Weight: 1.00
Name: A_SE_UGSE8	SEQ	ID NO: 531	Len: 962	Check: 5063	Weight: 1.00
Name: A_UG_92UG0	SEQ	ID NO: 532	Len: 962	Check: 6685	Weight: 1.00
Name: A_UG_U455_	SEQ	ID NO: 533	Len: 962	Check: 8657	Weight: 1.00
Name: AC_IN_2130	SEQ	ID NO: 534	Len: 962	Check: 7784	Weight: 1.00
Name: AC_RW_92RW	SEQ	ID NO: 535	Len: 962	Check: 4676	Weight: 1.00
Name: AC_SE_SE94	SEQ	ID NO: 536	Len: 962	Check: 2949	Weight: 1.00
Name: ACD_SE_SE8	SEQ	ID NO: 537	Len: 962	Check: 1464	Weight: 1.00
Name: ACG_BE_VI1	SEQ	ID NO: 538	Len: 962	Check: 2980	Weight: 1.00
Name: AD_SE_SE69	SEQ	ID NO: 539	Len: 962	Check: 8959	Weight: 1.00
Name: AD_SE_SE71	SEQ	ID NO: 540	Len: 962	Check: 7056	Weight: 1.00
Name: ADHK_NO_97	SEQ	ID NO: 541	Len: 962	Check: 487	Weight: 1.00
Name: ADK_CD_MAL	SEQ	ID NO: 542	Len: 962	Check: 2555	Weight: 1.00
Name: AG_BE_VI11	SEQ	ID NO: 543	Len: 962	Check: 6342	Weight: 1.00
Name: AG_NG_92NG	SEQ	ID NO: 544	Len: 962	Check: 1272	Weight: 1.00
Name: AGHU_GA_VI	SEQ	ID NO: 545	Len: 962	Check: 1974	Weight: 1.00
Name: AGU_CD_Z32	SEQ	ID NO: 546	Len: 962	Check: 4356	Weight: 1.00
Name: AJ_BW_BW21	SEQ	ID NO: 547	Len: 962	Check: 9995	Weight: 1.00
Name: B_AU_VH_AF	SEQ	ID NO: 548	Len: 962	Check: 5833	Weight: 1.00
Name: B_CN_RL42_	SEQ	ID NO: 549	Len: 962	Check: 4092	Weight: 1.00
Name: B_DE_D31_U	SEQ	ID NO: 550	Len: 962	Check: 5486	Weight: 1.00
Name: B_DE_HAN_U	SEQ	ID NO: 551	Len: 962	Check: 3480	Weight: 1.00
Name: B_FR_HXB2_	SEQ	ID NO: 552	Len: 962	Check: 6939	Weight: 1.00
Name: B_GA_OYI_	SEQ	ID NO: 553	Len: 962	Check: 9780	Weight: 1.00
Name: B_GB_CAM1_	SEQ	ID NO: 554	Len: 962	Check: 9716	Weight: 1.00
Name: B_GB_GB8_C	SEQ	ID NO: 555	Len: 962	Check: 4180	Weight: 1.00
Name: B_GB_MANC_	SEQ	ID NO: 556	Len: 962	Check: 9762	Weight: 1.00
Name: B_KR_WK_AF	SEQ	ID NO: 557	Len: 962	Check: 6641	Weight: 1.00
Name: B_NL_3202A	SEQ	ID NO: 558	Len: 962	Check: 7168	Weight: 1.00
Name: B_TW_TWCYS	SEQ	ID NO: 559	Len: 962	Check: 3591	Weight: 1.00
Name: B_US_BC_L0	SEQ	ID NO: 560	Len: 962	Check: 7266	Weight: 1.00
Name: B_US_DH123	SEQ	ID NO: 561	Len: 962	Check: 6905	Weight: 1.00
Name: B_US_JRCSF	SEQ	ID NO: 562	Len: 962	Check: 9381	Weight: 1.00
Name: B_US_MNCG_	SEQ	ID NO: 563	Len: 962	Check: 9951	Weight: 1.00
Name: B_US_P896_	SEQ	ID NO: 564	Len: 962	Check: 5855	Weight: 1.00
Name: B_US_RF_M1	SEQ	ID NO: 565	Len: 962	Check: 6075	Weight: 1.00
Name: B_US_SF2_K	SEQ	ID NO: 566	Len: 962	Check: 1434	Weight: 1.00
Name: B_US_WEAU1	SEQ	ID NO: 567	Len: 962	Check: 5451	Weight: 1.00
Name: B_US_WR27_	SEQ	ID NO: 568	Len: 962	Check: 4262	Weight: 1.00
Name: B_US_YU2_M	SEQ	ID NO: 569	Len: 962	Check: 5841	Weight: 1.00
Name: BF1_BR_93B	SEQ	ID NO: 570	Len: 962	Check: 5506	Weight: 1.00
Name: C_BR_92BR0	SEQ	ID NO: 571	Len: 962	Check: 8769	Weight: 1.00
Name: C_BW_96BW0	SEQ	ID NO: 572	Len: 962	Check: 6197	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 573	Len: 962	Check: 8144	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 574	Len: 962	Check: 1160	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 575	Len: 962	Check: 2736	Weight: 1.00
Name: C_ET_ETH22	SEQ	ID NO: 576	Len: 962	Check: 8219	Weight: 1.00
Name: C_IN_93IN1	SEQ	ID NO: 577	Len: 962	Check: 4068	Weight: 1.00
Name: C_IN_93IN9	SEQ	ID NO: 578	Len: 962	Check: 3674	Weight: 1.00
Name: C_IN_93IN9	SEQ	ID NO: 579	Len: 962	Check: 1581	Weight: 1.00
Name: C_IN_94IN1	SEQ	ID NO: 580	Len: 962	Check: 9352	Weight: 1.00
Name: C_IN_95IN2	SEQ	ID NO: 581	Len: 962	Check: 6988	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 582	Len: 962	Check: 8684	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 583	Len: 962	Check: 3342	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 584	Len: 962	Check: 5017	Weight: 1.00
Name: CRF01_AE_T	SEQ	ID NO: 585	Len: 962	Check: 9124	Weight: 1.00
Name: CRF01_AE_T	SEQ	ID NO: 586	Len: 962	Check: 2718	Weight: 1.00

Name:	CRF01_AE_T	SEQ	ID NO:	587	Len:	962	Check:	2104	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	588	Len:	962	Check:	8495	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	589	Len:	962	Check:	4076	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	590	Len:	962	Check:	948	Weight:	1.00
Name:	CRF02_AG_F	SEQ	ID NO:	591	Len:	962	Check:	9298	Weight:	1.00
Name:	CRF02_AG_F	SEQ	ID NO:	592	Len:	962	Check:	9278	Weight:	1.00
Name:	CRF02_AG_G	SEQ	ID NO:	593	Len:	962	Check:	4373	Weight:	1.00
Name:	CRF02_AG_N	SEQ	ID NO:	594	Len:	962	Check:	8955	Weight:	1.00
Name:	CRF02_AG_S	SEQ	ID NO:	595	Len:	962	Check:	252	Weight:	1.00
Name:	CRF02_AG_S	SEQ	ID NO:	596	Len:	962	Check:	5147	Weight:	1.00
Name:	CRF03_AB_R	SEQ	ID NO:	597	Len:	962	Check:	2239	Weight:	1.00
Name:	CRF03_AB_R	SEQ	ID NO:	598	Len:	962	Check:	2671	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	599	Len:	962	Check:	4892	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	600	Len:	962	Check:	8070	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	601	Len:	962	Check:	5453	Weight:	1.00
Name:	CRF05_DF_B	SEQ	ID NO:	602	Len:	962	Check:	174	Weight:	1.00
Name:	CRF05_DF_B	SEQ	ID NO:	603	Len:	962	Check:	2694	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	604	Len:	962	Check:	7351	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	605	Len:	962	Check:	5073	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	606	Len:	962	Check:	661	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	607	Len:	962	Check:	8440	Weight:	1.00
Name:	CRF11_cpx	SEQ	ID NO:	608	Len:	962	Check:	2217	Weight:	1.00
Name:	CRF11_cpx	SEQ	ID NO:	609	Len:	962	Check:	8216	Weight:	1.00
Name:	D_CD_84ZR0	SEQ	ID NO:	610	Len:	962	Check:	4843	Weight:	1.00
Name:	D_CD_ELI_K	SEQ	ID NO:	611	Len:	962	Check:	8403	Weight:	1.00
Name:	D_CD_NDK_M	SEQ	ID NO:	612	Len:	962	Check:	5813	Weight:	1.00
Name:	D_UG_94UG1	SEQ	ID NO:	613	Len:	962	Check:	9407	Weight:	1.00
Name:	F1_BE_VI85	SEQ	ID NO:	614	Len:	962	Check:	2982	Weight:	1.00
Name:	F1_BR_93BR	SEQ	ID NO:	615	Len:	962	Check:	8919	Weight:	1.00
Name:	F1_FI_FIN9	SEQ	ID NO:	616	Len:	962	Check:	6761	Weight:	1.00
Name:	F1_FR_MP41	SEQ	ID NO:	617	Len:	962	Check:	478	Weight:	1.00
Name:	F2_CM_MP25	SEQ	ID NO:	618	Len:	962	Check:	9292	Weight:	1.00
Name:	F2KU_BE_VI	SEQ	ID NO:	619	Len:	962	Check:	567	Weight:	1.00
Name:	G_BE_DRCBL	SEQ	ID NO:	620	Len:	962	Check:	6261	Weight:	1.00
Name:	G_NG_92NG0	SEQ	ID NO:	621	Len:	962	Check:	4508	Weight:	1.00
Name:	G_SE_SE616	SEQ	ID NO:	622	Len:	962	Check:	6733	Weight:	1.00
Name:	H_BE_VI991	SEQ	ID NO:	623	Len:	962	Check:	7498	Weight:	1.00
Name:	H_BE_VI997	SEQ	ID NO:	624	Len:	962	Check:	8345	Weight:	1.00
Name:	H_CF_90CF0	SEQ	ID NO:	625	Len:	962	Check:	2490	Weight:	1.00
Name:	J_SE_SE702	SEQ	ID NO:	626	Len:	962	Check:	4446	Weight:	1.00
Name:	J_SE_SE788	SEQ	ID NO:	627	Len:	962	Check:	1662	Weight:	1.00
Name:	K_CD_EQTB1	SEQ	ID NO:	628	Len:	962	Check:	7406	Weight:	1.00
Name:	K_CM_MP535	SEQ	ID NO:	629	Len:	962	Check:	512	Weight:	1.00
Name:	N_CM_YBF30	SEQ	ID NO:	630	Len:	962	Check:	1733	Weight:	1.00
Name:	O_CM_ANT70	SEQ	ID NO:	631	Len:	962	Check:	75	Weight:	1.00
Name:	O_CM_MVP51	SEQ	ID NO:	632	Len:	962	Check:	3290	Weight:	1.00
Name:	O_SN_99SE	SEQ	ID NO:	633	Len:	962	Check:	6963	Weight:	1.00
Name:	O_SN_99SE	SEQ	ID NO:	634	Len:	962	Check:	6278	Weight:	1.00
Name:	U_CD_83C	SEQ	ID NO:	635	Len:	962	Check:	9044	Weight:	1.00

SEQ	ID	NO	1	
469	00BW0762_1	...	MRVMGI	MRNC.QQWWI WV.ILGFWML MVCN.VIGNL WVTVYYGVPV
470	00BW0768_2	...	MRVREI	LRNC.QQWWT WG.SLGFWMV MIYS.VVGEL WVTVYYGVPV
471	00BW0874_2	...	MRAMGT	QRNC.RQWWI WG.ILGFWML MTCS.GVG.E MVTVYYGVPV
472	00BW1471_2	...	MRVMGI	LRSC.QQWWI WG.ILGFWML MICS.VLGNL WVTVYYGVPV
473	00BW1616_2	...	MRVMGI	QRNC.QRWWI WG.ILGFWMI Y.N.VVGNL WVTVYYGVPV
474	00BW1686_8	...	MRVKG	QRNW.PQWWI WG.SLGFWML MFYS.VMGNL WVTVYYGVPV
475	00BW1759_3	...	MRVRGI	PRNW.QQWWI WG.ILGFCMI ITCK.VVGNL WVTVYYGVPV
476	00BW1773_2	...	MRVREI	LRSY.QHWWM WS.ILGLWIL IISN.VVGNL WVTVYYGVPV
477	00BW1783_5	...	MRVMGI	KRNC.PPWWI WG.ILGFWML MICN.VMGNL WVTVYYGVPV
478	00BW1795_6	...	TRVMGI	RRNW.QQWWI WG.ILGFWML IICN.VMGNM WVTVYYGVPV

479	00BW1811_3MRVRGT	LKNY.QRWWI	WG.ILGLWIL	LINI.VVGNL	WVTVYYGVPV
480	00BW1859_5MRVRGI	PRNW.QQWWI	WG.ILGFWIL	MICN.VVGNL	WVTVYYGVPV
481	00BW1880_2MRVTGI	MRNC.QQWWI	WV.ILGFWML	MICN.VIGNL	WVTVYYGVPV
482	00BW1921_1MRVRGI	QRNW.QQWWI	WG.SLGFWVM	A.CS.VVGNL	WVTVYYGVPV
483	00BW2036_1MRVRGI	SRNW.QQWWI	WG.ILGFWMF	MICS.VLGNL	WVTVYYGVPV
484	00BW2063_6MRVMGI	MRNW.PPWWI	WG.ILGFWML	MICN.VMGNL	WVTVYYGVPV
485	00BW2087_2MRVTGM	WKNC.QQWWI	WG.ILGFWML	MICS.VLGNL	WVTVYYGVPV
486	00BW2127_2MRVRGI	PRNW.QQWWI	WG.ILGFW..	MIYS.MMGNL	WVTVYYGVPV
487	00BW2128_3MRVRGI	LKNC.QQWWI	WI.ILGFWLL	IITN.VVGKL	WVTVYYGVPV
488	00BW2276_7MRVRGI	LRNW.QQWWI	WG.ILGFWMV	MICS.VWGNL	WVTVYYGVPV
489	00BW3819_3MRVRGI	LRNW.QQWWI	WG.ILSFWVL	MICS.RGEDR	WVTVYYGVPV
490	00BW3842_8MRVRGI	LRNW.QQWWI	WV.ILGFW..	.IYS.VAGNL	WVTVYYGVPV
491	00BW3871_3MRVRGI	QRNW.QQWWI	WG.SLGFWML	MIYN.VMGSL	WVTVYYGVPV
492	00BW3876_9MRVREI	LRNW.QQLWT	WG.ILGFWVL	IICS.AGGNL	WVTVYYGVPV
493	00BW3886_8MRVRGI	LRIW.QQWWI	WA.SLGFWML	IICN.EKGKL	WVTVYYGVPV
494	00BW3891_6MRVRGI	LRNY.QQWWI	WG.ILGFWML	MMCN.VMGDL	WVTVYYGVPV
495	00BW3970_2MRVKGI	MRNC.QQWWI	WG.ILGFWML	LICN.GEGNL	WVTVYYGVPV
496	00BW5031_1MRVMGT	QRNC.QQWWI	WG.ILGFWML	MIYN.VGGNL	WVTVYYGVPV
497	96BW01B21MRVRGI	LRNY.PQWWI	WG.ILGFWMI	MLCN.VMGNL	WVTVYYGVPV
498	96BW0407MRVMGI	QRNC.QQWWI	WG.ILGFWMI	FNGM.GSW..	VT.VYYGVPV
499	96BW0502MRVMGI	LKNY.QQWWM	WG.ILGFWML	IISS.VVGNL	WVTVYYGVPV
500	96BW06_J4MRVKGI	PRNW.QQWWI	WG.SLGFWII	C..S.VMGNL	WVTVYYGVPV
501	96BW11_06MRVMEI	MRNC.QQWWI	WG.ILGFWML	MICN.VMGKS	WVTVYYGVPV
502	96BW1210MRVRGI	LRNY.LQWWI	WG.ILGFWML	MVCS.K.ENM	WVTVYG.VPV
503	96BW15B03MRVRGI	LRSW.QQWWI	WG.TLGFW..	.ICS.GLGNL	WVTVDGVPV
504	96BW16_26MIVRGI	LKTC.QQWWI	WI.ILGFWIL	IINN.VVGHL	WVTVDGVPV
505	96BW17A09MRVMGI	LRNC.QQWWI	WG.ILGFWML	MICS.VLGNL	WVTVYYGVPV
506	96BWM01_5MRVMGI	KKNW.QPWWI	WG.VLGFWTL	MICS.VMGNL	WVTVYYGVPV
507	96BWM03_2MRVRGT	QRNW.QRWWI	WS.ILAFWIL	INCN.GEEKL	WVTVYYGVPV
508	98BWMC12_2MRVMGI	QKNC.QRWWI	WG.ILGFWMI	MSYS.VLGNL	WVTVYYGVPV
509	98BWMC13_4MRVMGI	KMNW.QQWWI	WG.ILGFWML	MICS.VMGNL	WVTVYYGVPV
510	98BWMC14_aMRVKGI	LRNW.LQWWI	WG.SLGFWML	C..S.VMGNM	WVTVYYGVPV
511	98BWM014_1MRVMGT	LRNC.QQWWT	WG.ILGFWML	MICS.VGGNL	WVTVYYGVPV
512	98BWM018_dMRVMGI	QKNC.QHWWI	WG.ILGFWML	MICN.GK.DL	WVTVYYGVPV
513	98BWM036_aMRVRGI	LRNC.PQWWI	WG.ILGFWML	MTCN.MEGNL	WVTVYYGVPV
514	98BWM037_dMRVRGI	LRNY.QQWWI	WG.ILGFWML	MICN.VVGNL	WVTVYYGVPV
515	99BW3932_1MRVRGI	PRNW.QQWWI	WS.ILG....	.FCS.VVGQL	WVTVYYGVPV
516	99BW4642_4MRVKGI	LRNW.QQWWI	WG.ILGFWML	MICN.VVGNL	WVTVYYGVPV
517	99BW4745_8MRVRGI	LRDY.QQWWI	WS.ILGFWM.	.ICN.GMGNL	WVTVYYGVPV
518	99BW4754_7MRVMGI	KRNC.QQWWI	WG.ILGFWML	MI...CNGNL	WVTVYYGVPV
519	99BWMC16_8MRVMEI	WRNC.PPWWI	WG.ILGFWML	MICN.GG.NR	WVTVYYGVPV
520	A2_CD_97CDTRVMGT	QRNC.QKWE	WG.ILVFGMI	MMCK.AAD.L	WVTVYYGVPV
521	A2_CY_94CYMRVMGT	QRNY.QHLWR	GG.ILILGML	IMCK.ATD.L	WVTVYYGVPV
522	A2D_97KRMRVRGI	QRNY.QHLWK	WG.ILILGML	MISK.ATEDL	WVTVYYGVPV
523	A2G_CD_97CMRVKGM	QRNW.QNLWK	WG.ALILGLV	IICS.ASNL	WVTVYYGVPV
524	A_BY_97BL0MKARGM	XRNY.QHLWR	XG.TMLFWM	IMCK.AAEDL	VX.VYXXVPV
525	A_KE_Q23_AMRVMGI	QRNC.QHLLT	WG.IMILGTI	IFCS.AVENL	WVTVYYGVPV
526	A_SE_SE659MRVMGI	QRNC.QHLLR	WG.TIILGLI	IICS.VADKL	WVTVYYGVPV
527	A_SE_SE725MRVMGT	QMNW.QHLLR	WG.TIILGMI	MICS.TADNL	WVTVYYGVPV
528	A_SE_SE753MRAMGI	QRNC.QHLLR	WG.TMILGLV	IICS.VAGNL	WVTVYYGVPV
529	A_SE_SE853MRVKGI	QRNS.QHLLR	WG.TMILGMI	IICS.TADKL	WVTVYYGVPV
530	A_SE_SE889MRVMGT	QMNW.QNLWR	WG.TMILGII	IICS.AAENL	WVTVYYGIPV
531	A_SE_UGSE8MRVMGT	QRNC.QHLLN	WG.IMILGMI	IICS.TAENL	WVTVYYGVPV
532	A_UG_92UG0MRVMGI	ERNY.PCWWT	WG.IMILGMI	IICN.TAENL	WVTVYYGVPI
533	A_UG_U455_MRVMGI	QRNY.PCLWR	WG.TMILGLI	IICN..AQQL	WVTVYYGVPV
534	AC_IN_2130MRVRGI	LRNY.QQWWI	WG.SLGFWML	MVCN.VVGNL	WVTVYYGVPV
535	AC_RW_92RWMRVMGT	LMNY.QNLWG	WG.TMILGML	TICS.AANNL	WVTVYYGVPV
536	AC_SE_SE94MRVTGT	QRSC.QPWWI	WG.ILGFWML	IICS.ATDKL	WVTVYYGVPV
537	ACD_SE_SE8MRVMGI	QRNW.QHLLR	WG.TMILGMI	LICS.AVDKL	WVTVYYGVPV
538	ACG_BE_VI1MRVKGI	QRNY.QQWWT	WG.SLGLWML	LICN.VMGNL	WVTVYYGVPV
539	AD_SE_SE69MRVRGI	EMN.YQNLWR	WG.TLLLGML	MT.CSVTGRL	WVTVYYGVPV

540	AD_SE_SE71	...MRVMGI	QRNC.QNLLT	WG.TMILGMI	IICS.VAENL	WVTVYYGVPV
541	ADHK_NO_97	...MKVMGT	QRN.YPNWWR	WG.VLILGML	LICS.TTGNL	WVTVYYGVPV
542	ADK_CD_MAL	...MRVREI	QRN.YQNWWR	WG.MMLLGML	MT.CSIAEDL	WVTVYYGVPV
543	AG_BE_VI11	...MRVREGT	QMSWP.HLWN	GG.ILILGLV	IICS.ASNNL	WVTVYYGVPV
544	AG_NG_92NG	...MRVKGT	QRNWQ.HLWT	WW.TLILGLV	IICS.ASNNL	WVTVYYGVPV
545	AGHU_GA_VI	...MRVMET	QRN.YPRLWR	WG.TIILGML	MICN.AKENL	WITVYYGVPV
546	AGU_CD_Z32	...MKVKGI	QRNC.QHLWK	WG.TFILGLV	IICS.AAENL	WVTVYYGVPV
547	AJ_BW_BW21	...MRVMET	LMNCT.NLWR	WG.LMIFGML	MTCS.ATGNM	WVTVYYGVPV
548	B_AU_VH_AF	...MKVKET	KRN.WQRLWR	WG.IMLLGML	MICS.ATEKL	WVTVYYGVPV
549	B_CN_RL42_	...MRVTGI	RKN.YQHLWR	WG.TMLLGML	MICN.AAENL	WVTVYYGVPV
550	B_DE_D31_U	...MKVKEI	RKN.YQHLWR	WG.TMLLGML	MICS.ATEKL	WVTVYYGVPV
551	B_DE_HAN_U	...MKVKET	RKN.YQRLWR	GG.TLLLGML	MISS.VAGNL	WVTVYYGVPV
552	B_FR_HXB2_	...MRVKEK	YQHLWRWGW	WG.TMLLGML	MICS.ATEKL	WVTVYYGVPV
553	B_GA_OYI_	...MTARGET	RKN.YQRLWR	WG.TMLLGML	MICS.AAENL	WVTVYYGVPV
554	B_GB_CAM1_	...MRAKGI	RKN.CQRLWR	WG.TMLLGML	MICS.AADKL	WVTVYYGVPV
555	B_GB_GB8_C	...MKAKGT	RKN.YQHLWK	WG.IMLLGML	MICS.ATEKL	WVTVYYGVPV
556	B_GB_MANC_	...MKVKEI	RKN.YQNLWR	WG.TLFLGML	MICS.AEEKL	WVTVYYGVPV
557	B_KR_WK_AF	...MRVKGI	RKN.YQHWWR	WG.IMLLGMW	MICS.AAEKL	WVTVYYGVPV
558	B_NL_3202A	...MKVKET	RKN.YQHLWR	WG.TMLLGML	MICS.AAEQL	WVTVYYGVPV
559	B_TW_TWCYS	...MRVRGT	RMN.CQHLWR	WG.TMLLGML	MISS.AAENL	WVTVYYGVPV
560	B_US_BC_L0	...MRVKEI	RKN.YQHLWR	WG.TMLFGIL	MIYS.AAGNL	WVTVYYGVPV
561	B_US_DH123	...MRVMGI	RKN.YQHLWK	GG.TLLLGIL	MICS.AAEQL	WVTVYYGVPV
562	B_US_JRCSF	...MRVKGI	RKN.YQHLWK	GG.ILLLGTL	MICS.AVEKL	WVTVYYGVPV
563	B_US_MNCG_	...MRVKGI	RRN.YQHWGW	WG.TMLLGLL	MICS.ATEKL	WVTVYYGVPV
564	B_US_P896_	...MRVKEI	RKN.WQHLR.	GG.ILLLGML	MICSAAKEKT	WVTIYYGVPV
565	B_US_RF_M1	...MRVMEM	RKN.CQHLWK	WG.TMLLGML	MICS.AAEDL	WVTVYYGVPV
566	B_US_SF2_K	...MKVKGT	RRN.YQHLWR	WG.TLLLGML	MICS.ATEKL	WVTVYYGVPV
567	B_US_WEAU1	...MRVKGI	RKN.YQHLWK	WG.IMLLGIL	MICS.AAENL	WVTVYYGVPV
568	B_US_WR27_	...MRVKGI	RKN.CQHLWR	WG.IMLLGML	MICN.ATEQL	WVTVYYGVPV
569	B_US_YU2_M	...MRATEI	RKN.YQHLWK	GG.TLLLGML	MICS.AAEQL	WVTVYYGVPV
570	BF1_BR_93B	...MRVRGM	QRN.WQHLGK	WG.LLFLGIL	IICN.AENL	WVTVYYGVPV
571	C_BR_92BR0	...MRVEGI	QRNW.QQWWI	WG.ILGFWMV	MIYN.VGSNL	WVTVYYGVPV
572	C_BW_96BW0	...MRVMGI	QRNC.QQWWI	WG.ILGFWMI	INGM.GSW..	VT.VYYGVPV
573	C_BW_96BW1	...MRVMGI	MRNC.QPWWI	WG.ILGFWML	MICN.VMGKS	WVTVYYGVPV
574	C_BW_96BW1	...MRVRGI	LRNY.LQWWI	WG.ILGFWML	MVCS.K.ENM	WVTVYG.VPV
575	C_BW_96BW1	...MRVRGI	LRSW.QQWWI	WG.TLGFW..	IICS.GLGNL	WVTVDGVPV
576	C_ET_ETH22	...MKVMGI	QRNC.QQWWI	WG.ILGFWML	MICN.GMGNL	WVTVYYGVPV
577	C_IN_93IN1	...MRVRGT	LRNY.QQWWI	WG.VLGFWML	MICN.GGGNL	WVTVYYGVPV
578	C_IN_93IN9	...MRVRGT	LRNY.QQWWI	WG.VLGFWML	MICN.VGGNL	WVTVYYGVPV
579	C_IN_93IN9	...MRVRGI	LRNY.QQWWI	WG.ILGFWML	MICN.VVGNL	WVTVYYGVPV
580	C_IN_94IN1	...MRVRGT	LRNY.QQWWI	WG.VLGFWML	MICN.GGKDL	WVTVYYGVPV
581	C_IN_95IN2	...MRVRGI	LRNY.QQWWI	WG.VLGFWML	MICN.VGKDL	WVTVYYGVPV
582	CRF01_AE_C	...MGVKGT	QMNW.PHLWK	WG.TLILGLV	IICS.ASDTL	WVTVYYGVPV
583	CRF01_AE_C	...MRVKGT	RRNW.PNLWK	WG.TLILGLV	IICS.ASDNL	WVTVYYGVPV
584	CRF01_AE_C	...MRVKGT	QMNW.PNLWK	WG.TLILGLV	IMCS.ASDNL	WVTVYG.VPV
585	CRF01_AE_T	...MRVKET	QMNW.PNLWK	WG.TLILGLV	IICS.ASDNL	WVTVYYGVPV
586	CRF01_AE_T	...MRVKET	QMN..PNLWK	WG.TLILGLV	IICS.ASDDL	WVTVYYGVPV
587	CRF01_AE_T	...MRVKET	QINW.PNLWK	WG.TLILGLV	IMCS.ASNNL	WVTVYYGVPV
588	CRF01_AE_T	...MRVKET	QMSW.PNLWK	WR.TLILGLV	IICS.ASDNL	WVTVYYGVPV
589	CRF01_AE_T	...MRVKET	QMNW.PNLWK	WG.TLILGLV	IICS.ASDNL	WVTVYYGVPV
590	CRF01_AE_T	...MRVKET	QMNW.PNLWK	WG.TLILGLV	IICS.ASENL	WVTVYYGVPV
591	CRF02_AG_F	...MRVMGM	QRNY.PLLWK	WG.TIIFWIM	IICN.AEKL	WVTVYYGVPV
592	CRF02_AG_F	...MRVMGI	QRNY.PLFWK	WG.MIIFWIM	IICN.AEKL	WVTVYYGVPV
593	CRF02_AG_G	...MRVRGM	QRNC.QNLWR	WA..HDFWIL	IICN.AAENL	WVTVYYGVPV
594	CRF02_AG_N	...MRVMGI	QKNY.PLLWR	WG.TNIFWIM	IICN.AEQL	WVTVYYGVPV
595	CRF02_AG_S	...MRVMGI	QKNY.PLLWR	WG.MIIFWIM	TICS.AGNL	WVTVYYGVPV
596	CRF02_AG_S	...MRVMGI	LKSC.PPFWR	WGMIMLLWIL	IICN.AENL	WVTVYYGVPV
597	CRF03_AB_R	...MRVKEI	RKH...LWR	WG.TLFLGML	MICS.ATENL	WVTVYYGVPV
598	CRF03_AB_R	...MRVKEI	RKH...LWR	WG.TLLLGML	MICS.ATENL	WVTVYYGVPV
599	CRF04_cpx_	...MRVMGM	QRN.YPHLWE	WG.TLILGLV	IICS.ASNNL	WVTVYYGVPV
600	CRF04_cpx_	...MRVMGI	QRN.YPHLWE	WG.TLILGLV	IMCS.ASKDM	WVTVYYGVPV

182

00BW0762_1	WREAKTTTLFC	ASDAKAYDRE	VHNVWATHAC	VPTDPNPQEL	VLENVTFNFN
00BW0768_2	WKEAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	VLGNVTENFN
00BW0874_2	WKEAKTTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPDPQEM	VLENVTFNFN
00BW1471_2	WREAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEM	YLVNVTENFN
00BW1616_2	WKEAKTTTLFC	ASDAKAYDRE	VHNVWATHAC	VPTDPNPQEI	GLENVTFNFN
00BW1686_8	WKEAKTTTLFC	ASDAKAYEKE	VHNIWATHAC	VPTDPNPQEI	VLENVTFNFN
00BW1759_3	WRETKTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEL	VLGNVTESFN
00BW1773_2	WKEAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	PLKNVTENFN
00BW1783_5	WKEAKTTTLFC	ASDAKAYEKE	AHNIWATHAC	VPTDPNPQEM	FLENVTQNFN
00BW1795_6	WREAKAPLFC	ASDAKAYDRE	VHNVWATHAC	VPTDPNPQEM	VLKNVTENFN
00BW1811_3	WKEAKTTTLFC	ASDAKGYDRE	VHNVWATHAC	VPTDPNPQEL	VLGNVTENFN
00BW1859_5	WKEAKTTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
00BW1880_2	WKEAKATLFC	ASEAKAYESE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
00BW1921_1	WKEAKTTTLFC	ASDAKAYETE	VHNVWATHAC	VPTDPNPQEM	ALENVTENFN
00BW2036_1	WREAKTTTLFC	ASDAKAYETE	VHNIWATHAC	VPTDPNPQEI	VLGNVTENFN
00BW2063_6	WREAKATLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
00BW2087_2	WKEAKTTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEM	ELKNVTENFN
00BW2127_2	WKEAKAPLFC	ASDAKAYEKE	AHNVWATHAC	VPTDPNPQEI	ELKNVTENFN
00BW2128_3	WKEAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
00BW2276_7	WKEAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEL	VLENVTFNFN
00BW3819_3	WREAKATLFC	ASDAKAHERE	VHNVWATHAC	VPTDPNPQEM	VMENVTENFN
00BW3842_8	WKEAKTTTLFC	ASDAKGYETE	VHNVWATHAC	VPTDPDPQEM	VLGNVTENFN
00BW3871_3	WREAKTTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEM	LLKNVTENFN
00BW3876_9	WKEAKTTTLFC	ASDAKVYEKE	VHNVWATHAC	VPTDPNPQEM	VLDNVTENFN
00BW3886_8	WKEAKTTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEI	VLGGVTENFN
00BW3891_6	WREAKTTTLFC	ASDAKGYEKE	VHNVWATHAC	VPTDPDPQEM	VLENVTFNFN
00BW3970_2	WKEAKTTTLFC	ASDAKGYERE	VHNIWATHAC	VPTDPNPQEM	FLHNVTFNFN
00BW5031_1	WKEAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPSPQEI	VLENVTFNFN
96BW01B21	WKEAKTTTLFC	ASDAKAYEKG	VHNVWATHAC	VPTDPNPQEV	FLENVTENFN
96BW0407	WKEAKATLFC	ASDARAYDRE	VHNVWATHAC	VPTDPNPQEV	ILENVTENFN
96BW0502	WKEAKTTTLFC	TSDAKAYETE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
96BW06_J4	WKEAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPSPQEI	VLGNVTENFN
96BW11_06	WREAKATLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEV	VLENVTFNFN
96BW1210	WKEAKTTTLFC	ASDAKAYEGE	VHNVWATHAC	VPTDPNPQEL	VLGNVTENFN
96BW15B03	WREASNTLFC	ASYAKAYEKE	VHNVWATHAC	VPTDPNPQEI	ELDNVTENFN
96BW16_26	WKEAKTTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEI	ILKNVTENFN
96BW17A09	WREAKTTTLFC	ASDAKAFESE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
96BWM01_5	WREAKTTTLFC	ASDAKAYEAE	VHNVWATHAC	VPTDPNPQEI	ELKNVTENFN
96BWM03_2	WKEAKTTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
98BWMC12_2	WREAKTTTLFC	ASDAKAYERE	VHNIWATHAC	VPTDPNPQEM	VLENVTFNFN
98BWMC13_4	WKEAKAPLFC	ASDAKVYEKE	VHNVWATHAC	VPTDPNPQEL	VLENVTFNFN
98BWMC14_a	WREATTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	VLGNVTENFN
98BWM014_1	WKEAKTTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPSPQEM	FLANVTENFN
98BWM018_d	WREAKATLFC	ASNAKAYEKE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
98BWM036_a	WKEAKATLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPDPQEI	VLENVTFESFN
98BWM037_d	WKEAKTTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
99BW3932_1	WKEAKATLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQKL	VLGNVTENFN
99BW4642_4	WKEAKTTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
99BW4745_8	WREAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEL	VLKNVTENFN
99BW4754_7	WREAKTTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
99BWMC16_8	WREAKATLFC	ASDAKAYERE	VHNVWATHAC	VPTDPDPQEI	ALENVTENFN
A2_CD_97CD	WRDADTTTLFC	ASDAKAYATE	KHNVWATHAC	VPTDPNPQEV	NLANVTEDFN
A2_CY_94CY	WKDADTTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	NLENVTENFN
A2D_97KR	WRDAETTLFC	ASDAKAYDTE	AHNVWATHAC	VPTDPNPQEI	NLENVTENFN
A2G_CD_97C	WEDANTPLFC	ASDAKSYSTE	RHNVWATHAC	VPTDPNPQEM	ILENVTESFN
A_BY_97BL0	XXDAATTLFC	ASDAKAXDKE	VHNVWATHAC	VPTDPDPQEI	ILGNVTEKFD
A_KE_Q23_A	WRDADTTTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEI	HLDNVTEKFN
A_SE_SE659	WKDAETTLFC	ASDAKAYDPE	VHNVWATHAC	VPTDPNPQEM	HLENVTEESN
A_SE_SE725	WKDAETTLFC	ASDAQAYKTE	MHNVWATHAC	VPTDPNPQEL	HLKNVTEEFN
A_SE_SE753	WKDAETTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEI	HLKNVTEKFN

A_SE_SE853	WKDAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEL	HLANVTEEFN
A_SE_SE889	WRDAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	NLENVTEEFN
A_SE_UGSE8	WKDAETTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEL	YLENVTEDFN
A_UG_92UG0	WKDANTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPSPQEL	KMENVTTEEFN
A_UG_U455_	WKDAVTTLFC	ASDAKAYDAE	VHNVWATHAC	VPTDPNPQEI	DLVNVTEEFN
AC_IN_2130	WKDAETTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEI	HLENVTEDFN
AC_RW_92RW	WKDAETTLFC	ASDAKAYDPE	KHNVWATHAC	VPIDPDPQEI	HLENVTEEFN
AC_SE_SE94	WKEAKTTLFC	ASDAKAYEAE	VHNVWATHAC	VPTDPNPHEI	NLENVTENFN
ACD_SE_SE8	WKDAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	LLGNVTEDFN
ACG_BE_VI1	WKEAKTTLFC	ASDAKAYETE	AHNVWATHAC	VPTDPSPQEI	ELKNVTENFN
AD_SE_SE69	WRDAETTLFC	ASDAKAYDAE	VHNVWATHAC	VPTDPNPQEI	NLENVTEEFN
AD_SE_SE71	WKDAETTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEI	HLENVTENFN
ADHK_NO_97	WKEAKTTLFC	ASDAKAYDTE	MHNVWATHAC	VPTDPSPQEI	VLENVTENFN
ADK_CD_MAL	WKEATTTLFC	ASDAKSYETE	VHNIWATHAC	VPTDPNPQEI	ELENVTEGFM
AG_BE_VI11	WEDADTTLFC	ASDAKAYSTE	SHNVWATHAC	VPTDSNPQEI	PLENVTENFN
AG_NG_92NG	WEDADTPLFC	ASDAKAYSTE	RHNVWATHAC	VPTDPNPQEI	TLENVTETFN
AGHU_GA_VI	WRDAKTSLFC	ASDAKSYSTE	SHNVWATHAC	VPTDPNPQEI	NLENVTENFN
AGU_CD_Z32	WKDAETTLFC	ASDAKAYDTE	KHNVWATHAC	VPTDPNPQEL	SLGNVTEKFN
AJ_BW_BW21	WKEAKTTLFC	ASNAKAYSTE	GHNIWATHAC	VPTDPNPQEI	ILENVTENFN
B_AU_VH_AF	WKEATTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEI	LLENVTEEFN
B_CN_RL42	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
B_DE_D31_U	WKEATTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPPDPQEV	VLENVTEDFN
B_DE_HAN_U	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VMGNVTENFN
B_FR_HXB2_	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLVNVTENFN
B_GA_OYI_	WKEATTTLFC	ASDARAYATE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFD
B_GB_CAM1_	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLENVTENFN
B_GB_GB8_C	WKEATTTLFC	ASDAKAYDTE	KHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
B_GB_MANC_	WKEATTTLFC	ASDAKAHYTE	VHNVWATHAC	VPTDPNPQEI	VLENVTEYFD
B_KR_WK_AF	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPIDPNPQEV	FLENVTENFN
B_NL_3202A	WKEATTTLFC	ASDAKASDTE	VHNVWATHAC	VPTDPNPQEV	ALENVTEDFD
B_TW_TWCYS	WKEATTTLFC	ASDAKTYDTE	VHNVWATHAC	VPTDPNPQEV	TLGNVTENFN
B_US_BC_L0	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	IPTDPNPQEI	VLENVTEDFN
B_US_DH123	WKEANTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	LLENVTEDFN
B_US_JRCSF	WKETTTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLENVTEDFN
B_US_MNCG_	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	ELVNVTENFN
B_US_P896_	WREATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
B_US_RF_M1	WKEATTTLFC	ASEAKAYKTE	VHNVWATHAC	VPTDPNPQEV	LLENVTENFN
B_US_SF2_K	WKEATTTLFC	ASDARAYDTE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
B_US_WEAU1	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLENVTENFN
B_US_WR27_	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	RLENVTEDFN
B_US_YU2_M	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	KLENVTENFN
BF1_BR_93B	WKEATTTLFC	ASDAKAYEKE	AHNVWATHAC	VPTDPNPQEV	VLENVTEDFD
C_BR_92BR0	WKEAKTTLFC	ASDAKAYDAE	VHNVWATHAC	VPTDPNPQEM	VLENVTENFN
C_BW_96BW0	WKEAKATLFC	ASDARAYDRE	VHNVWATHAC	VPTDPNPQEV	NLENVTENFN
C_BW_96BW1	WREAKATLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEV	VLENVTENFN
C_BW_96BW1	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEL	VLGNVTENFN
C_BW_96BW1	WREASNTLFC	ASYAKAYEKE	VHNVWATHAC	VPTDPNPQEI	ELDNVTENFN
C_ET_ETH22	WKDASPTLFC	ASDAKAYDTE	VHNVWGTFAC	VPTDPSPQEL	GLENVTENFN
C_IN_93IN1	WKEAKTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEI	VLGNVTENFN
C_IN_93IN9	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	PLGNVTENFN
C_IN_93IN9	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEM	VLENVTENFN
C_IN_94IN1	WKEAKTTLFC	ASDAKAYGKE	VHNVWATHAC	VPTDPNPQEI	SLENVTENFN
C_IN_95IN2	WKEANTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	VMENVTENFN
CRF01_AE_C	WRDADTTLFC	ASDANAQETE	VHNVWATHVC	VPTDPNPQEI	HLENVTENFD
CRF01_AE_C	WRDADTILFC	ASDAKAHVTE	VHNVWATHAC	VPTDPNPQEI	YLENVTENFD
CRF01_AE_C	WRDADTTLFC	ASDAKAHETE	VHNIWATHAC	VPTDPNPQEI	DLENVTENFN
CRF01_AE_T	WKDADTTLFC	ASDAKAHETE	VHNVWTTTHAC	VPTDP . PQEI	HLENVTENFN
CRF01_AE_T	WRDADTTLFC	ASDAKAHETE	VHNVWATHAC	VPTDPNPQEI	HLENVTENFN
CRF01_AE_T	WRDADTTLFC	ASDAKAHETE	VHNVWATHAC	IPTDPNPQEM	HLENVTENFN
CRF01_AE_T	WRDADTTLFC	ASDAKAHEAE	VHNVWATHAC	VPTDPNPQEI	HLENVTENFN
CRF01_AE_T	WRDADTTLFC	ASDAKAHETE	VHNVWATHAC	VPTDPNPQEI	HLENVTENFN

CRF01_AE_T	WRDADTTLFC	ASDAKAHETE	VHNVWATHAC	VPTDPNPQEI	HMENVTENFN
CRF02_AG_F	WRNAETTLFC	ASDAKAYDAE	VHNVWATHAC	VPTDPNPQEI	HLKNVTEKFN
CRF02_AG_F	WRDAETTLFC	ASDAKAYDVE	VHNVWATHAC	VPTDPNPQEI	HLKNVTEKFN
CRF02_AG_G	WKTADTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	HLENVTEEFN
CRF02_AG_N	WKTAEETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	HLENVTEKFN
CRF02_AG_S	WRDAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	HLGNVTEDFN
CRF02_AG_S	RRDAETTLFC	ASDAKAYETE	VHNVWATHAC	VPTDPS PQEM	HLENVTENFN
CRF03_AB_R	WKEATTTLFC	ASDAKAYSKE	VHNVWATYAC	VPTDPS PQEI	PLKNVTENFN
CRF03_AB_R	WKEATTTLFC	ASDAKAYSKE	VHNVWATYAC	VPTDPS PQEI	PLENVTENFN
CRF04_cpx_	WRDAETTLFC	ASEAKAYEKE	VHNIWATHAC	VPTDPNPQEV	ALINVTENFN
CRF04_cpx_	WRDAETKPXC	ASDAKAYDKE	IHNIWATHAC	VPTDPNPQEL	ALTNVTENFN
CRF04_cpx_	WRDAETSPFC	ASDAKAYDKE	VHNIWATHAC	VPTDPNPQEI	FLKNVTEDFN
CRF05_DF_B	WREAKTTLFC	ASDAKGYDKE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
CRF05_DF_B	WKEATTTLFC	ASDAKGYEKE	AHNVWATHAC	VPTDPNPQEL	ALENVTENFN
CRF06_cpx_	WEDADTILFC	ASDAKAYSPD	KHNVWATHAC	VPTDPNPQEI	SLKNVTENFN
CRF06_cpx_	WEDADTILFC	ASDAKAYS AE	KHNVWATHAC	VPTDPNPQEI	PLKNVTENFN
CRF06_cpx_	WEDADTILFC	ASDAKAYS AE	KHNVWATHAC	VPTDPNPQEI	PLENVTENFN
CRF06_cpx_	WEDADTILFC	ASDAKAYS AE	KHNVWATHAC	VPTDPNPQEI	KLENVTENFN
CRF11_cpx_	WKDANTTLFC	ASDAQAYSPE	KHNVWATHYC	VPTDPNPQEI	LLGNVTENFN
CRF11_cpx_	WRDADTILFC	ASDARTYSTE	KHNVWATHSC	VPTDPNPREL	SLENVTENFN
D_CD_84ZR0	WKEATTTLFC	ASDAKS YKTE	AHNIWATHAC	VPTDPNPQEI	ELKNVTENFN
D_CD_ELI_K	WKEATTTLFC	ASDAKS YETE	AHNIWATHAC	VPTDPNPQEI	ALENVTENFN
D_CD_NDK_M	WKEATTTLFC	ASDAKAYKKE	AHNIWATHAC	VPTDPNPQEI	ELENVTENFN
D_UG_94UG1	WKEATTTLFC	ASDAKAYKAE	AHNIWATHAC	VPTDPNPQEI	KLENVTENFN
F1_BE_VI85	WKEATTTLFC	ASDAKAYERE	AHNVWATHAC	VPTDPNPQEV	FLKNVTENFD
F1_BR_93BR	WKEATTTLFC	ASDAKS YEKE	AHNVWATHAC	VPTDPNPQEV	VLENVTERFN
F1_FI_FIN9	WKEANTTLFC	ASDAKS YEKE	VHNVWATHAC	VPTDPNPQEV	ALN.VTENFN
F1_FR_MP41	WKEATTTLFC	ASDAKGYERE	VHNVWATHAC	VPTDPNPQEI	WLKNVTENFD
F2_CM_MP25	WKEATTTLFC	ASDAKAYERE	VHNVWATYAC	VPTDPS PQEL	VLGNVSEKFN
F2KU_BE_VI	WKEANTTLFC	ASDAKPYDTE	VHNVWVTHAC	VPTDPNPQEV	FLQNVTENFN
G_BE_DRCBL	WEDANAPLFC	ASDAKAHSTE	SHNIWATHAC	VPTDPS PQEI	NMRNVTENFN
G_NG_92NG0	WEDADTPLFC	ASDAKSYSSE	KHNVWATHAC	VPTDPNPQEI	AIENVTENFN
G_SE_SE616	WEDADTTLFC	ASDAKSYS AE	SHNVWATHAC	VPTDPNPQEI	IMENVTEYFN
H_BE_VI991	WKEAKTTLFC	ASDAKAYDTE	RHNVWATHAC	VPTDPNPQEM	VLENVTETFN
H_BE_VI997	WKEAKTTLFC	ASDAKAYEPE	KHNVWATHAC	VPTDPS PQEM	VLANVTENFN
H_CF_90CF0	WKEAKTTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEM	VMENVTESFN
J_SE_SE702	WRDAKTTLFC	ASDAKAYSTE	KHNVWATHAC	VPTDPNPQEM	SLPNVTENFN
J_SE_SE788	WKDAKTTLFC	ASDAKAYSTE	KHNVWATHAC	VPTDPS PQEM	NLPNVTENFN
K_CD_EQTB1	WKEATTTLFC	ASDAKAYETE	VHNVWATHAC	VPTDPNPQEV	VLENVTENFN
K_CM_MP535	WKEATPTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEV	EMENVTENFN
N_CM_YBF30	WREAETTLFC	ASDAKAHSTE	AHNIWATQAC	VPTDPNPQEV	LLPNVTEKFN
O_CM_ANT70	WEDATPVLFC	ASDANLTSTE	KHNIWASQAC	VPTDPTPYEY	PLHNVTDNFD
O_CM_MVP51	WEEAAPVLFC	ASDANLTSTE	QHNIWASQAC	VPTDPNPHEF	PLGNVTDNFD
O_SN_99SE_	WEEATPVLFC	ASDANLTSTE	QHNIWASQAC	VPTDPS PYEY	PLTKVTDNFN
O_SN_99SE_	WEEATPVLFC	ASDVNLTSTE	QHNIWASQAC	VPTDPS PYEY	PLKNVTDNFN
U_CD_83C	WKDAETTLFC	ASDAKAYEKE	SHNVWATHAC	VPTDPS PQEL	VLGNVTENFN

00BW0762_1	MWKNYMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCINV	TN.....
00BW0768_2	MWKNDMVDQM	HEDVISLWDQ	SLKPCVKLTP	LCITLNCTSI	NG.....
00BW0874_2	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNY	NN.....
00BW1471_2	MWKNDMVDQM	HEDIISIWDQ	SLKPCVKLTP	LCVTLYCTNV	TKR.....
00BW1616_2	MWKNDMVNQM	HEDIISLWDQ	SLKPCVRLTP	LCVTLNCNNV	TT.....
00BW1686_8	MWKNDVVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLQCSNV	S.....
00BW1759_3	MWKNDMVDQM	HEDIISLWDQ	SLNPCVKLTP	LCVTLKCSNV	N.....
00BW1773_2	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLECEDA	N.....
00BW1783_5	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLTCSNL	NI.....
00BW1795_6	MWKNDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCTNA	TI.....
00BW1811_3	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCINA	TN.....
00BW1859_5	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLTCKDY	N.....
00BW1880_2	MWENGMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCSNA	KA.....
00BW1921_1	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCSDA	K.....
00BW2036_1	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNA	NV.....
00BW2063_6	MWENDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCRNA	NN.....
00BW2087_2	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCVTV	NCT.....
00BW2127_2	MWKNDMVEQM	HEDIIRLWDE	SLKPCVRLTP	LCVTLRCSNA	GSG.....
00BW2128_3	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLSCNAT	N.....
00BW2276_7	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCSIV	N.....
00BW3819_3	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTQ	LCVTLECSNV	N.....
00BW3842_8	MWENDMVDQM	HEDVISLWDE	SLKPCVKLTP	LCVTLNCTNY	NG.....
00BW3871_3	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLMCSNV	T.....
00BW3876_9	MWENDMVDQM	HEDIISLWDQ	SPKPCVKLTP	LCVTLKCTDA	T.....
00BW3886_8	MWKNDMVDQM	HEDVISLWDE	SLKPCVKLTP	LCVTLKCGNV	NN.....
00BW3891_6	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCVSI	N.....
00BW3970_2	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLECKNV	TTN.....
00BW5031_1	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCSAA	NN.....
96BW01B21	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCASTY	N.....
96BW0407	MWKNDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTKV	NGT.....
96BW0502	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCRNV	N.....
96BW06_J4	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTS	LCVTLHCSNV	N.....
96BW11_06	MWENDMVNQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCT..
96BW1210	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCSNN	VTR.....
96BW15B03	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCTNY	ST.....
96BW16_26	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCTNV	T.....
96BW17A09	MWKNDMVDQM	HEDIISLRDQ	SLKPCVKLTP	LCVTLNCTNA	TN.....
96BWM01_5	MWENDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCKNV	TS.....
96BWM03_2	MWKNDMADQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTEA	KV.....
98BWMC12_2	MWKNDMVDQM	HEDIIRLWDQ	SLKPCVKMTP	LCVTLNCANF	NAS.....
98BWMC13_4	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCSNV	TV.....
98BWMC14_a	MWRNDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCTNV	T.....
98BWM014_1	MWENDMVDQM	HQDIISLWDE	SLKPCVKLTP	LCVTLNCRNA	NLN.....
98BWM018_d	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLTCTNA	TKNVTN....
98BWM036_a	MWKNDMVDQM	HEDVISIWDQ	SLKPCVKLTP	LCVTLNCSNV	N.....
98BWM037_d	MRDNDMVDQM	HEDIINLWDQ	SLKPCVRLTP	LCVTLNCKDA	SVN.....
99BW3932_1	MWKNDMVDQM	HEDMIRLWDQ	SLKPCVKLTP	LCVTLKCREV	N.....
99BW4642_4	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCTNV	N.....
99BW4745_8	MWKNDMVDQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLICSNV	I.....
99BW4754_7	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCNKV	TV.....
99BWMC16_8	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCVNV	TKNVTK....
A2_CD_97CD	MWKNNMVEQM	HADIISLWDQ	SLKPCVKLTP	LCVTLNCSNA	NTNT.....
A2_CY_94CY	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVILNCSNA	NTSTH.....
A2D___97KR	MWKNGMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCSRNV	KNTIS.....
A2G_CD_97C	MWKNDMVEQM	HVDIISLWDQ	SLKPCVKLTP	FCVTLNCTNA	TFPNA.....
A_BY_97BL0	MXKNNXVEQM	QTDIISL.DQ	SLKPCVKLTP	LCVTLNCAEP	NSTRS.....
A_KE_Q23_A	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLHCTNV	TSV.....
A_SE_SE659	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV
A_SE_SE725	MWKNSMVEQM	HTDIISLWDE	SLKPCVKLTP	LCVTLNCTNA
A_SE_SE753	MWKNYMVEQM	HTDIISLWDQ	SLEPCVKLTP	LCVTLECHYN	ITV.....

A_SE_SE853	MWKNSMVEQM	HTDIISLWDQ	SLIPCVKLTP	LCVTLECN DY	NYN.....
A_SE_SE889	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCSSV	TN.....
A_SE_UGSE8	MWKNNMVEQM	HTDIISLWDQ	SLKPCVQLTP	LCVTLNCSSN	VTA.....
A_UG_92UG0	MWKNNMVEQM	HTDIISLWDQ	SLKPCVQLTP	LCVTLDCSYN	ITN.....
A_UG_U455_	MWKNNMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNI	TIN.....
AC_IN_2130	MWKNSMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCSSV	NG.....
AC_RW_92RW	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLECN NI	TNVNN.....
AC_SE_SE94	IWKNYMVEQM	HQDIISLWDQ	SLKPCVKLTP	LCVTLNCRDA	TV.....
ACD_SE_SE8	MWKNNMVEQM	HTDIISLWDQ	SLQPCVKLTP	LCVTLNCTNV	TIT.....
ACG_BE_VI1	MWKNDMVDQM	HQDIISLWDE	SLKPCVKLTP	LCVTLNCSSV	TAIN.....
AD_SE_SE69	MWKNNMVEQM	HTDIISLWDQ	SLKPCVQLTP	LCVTLNCNNV	TNKN.....
AD_SE_SE71	MWKNNMVKQM	HTDIISLWDQ	SLQPCVKLTP	LCVTLHCNDT	.N.....
ADHK_NO_97	MWENNMDVQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCTDP	AN.....
ADK_CD_MAL	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV	NGTAVNG.TN
AG_BE_VI11	MWKNNMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLTCTNV	NCTNN.....
AG_NG_92NG	MWKNNMVEQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTNV	NCNSN...VT
AGHU_GA_VI	MWKNNMVEQM	HTDIISLWDQ	SLKPCVQITP	LCVTLECSKI	N.....
AGU_CD_Z32	MWKNNMVEQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLSCSDI	R.....
AJ_BW_BW21	IWKNDMVEQM	QEDIISVWDE	SLKPCVKLTP	LCVTLNCTNA	TVSNT.....
B_AU_VH_AF	MWKNNMVEQM	HEDIISLWDQ	SLKPCVQLTP	LCVTLNCTDE	LT.....
B_CN_RL42_	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNL	K.....
B_DE_D31_U	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	K.....
B_DE_HAN_U	MWKNDMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLKCTDY	N.....
B_FR_HXB2_	MWKNDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVSLKCTDL	K.....
B_GA_OYI_	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLDCTDV	NTTSSS....
B_GB_CAM1_	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLICITNV	NN.....
B_GB_GB8_C	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	R.....
B_GB_MANC_	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLDCTDY	VG.....
B_KR_WK_AF	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCTDL	NDTNTN....
B_NL_3202A	MWKNNMVEQM	HEDIINLWDQ	SLKPCVKLTP	LCVTLNCTDF	G.....
B_TW_TWCYS	MWKNNMADQM	QEDIISLWDE	SLKPCVELTP	LCVTLKCN DT
B_US_BC_L0	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDE	LKNA.....
B_US_DH123	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLHCTDL	K.....
B_US_JRCSF	MWKNNMVEQM	QEDVINLWDQ	SLKPCVKLTP	LCVTLNCKDV
B_US_MNCG_	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	R.....
B_US_P896_	MWKNNMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTNL
B_US_RF_M1	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDA	NLN.....
B_US_SF2_K	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	G.....
B_US_WEAU1	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV	NVTN.....
B_US_WR27_	MWKNNMXEQM	HEDIIXLWDQ	SLKPCVKLTP	LCVTLNCTDV
B_US_YU2_M	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL
BF1_BR_93B	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLRCSNA	TT.....
C_BR_92BR0	MWENDMVEQM	HQDIISLWDQ	SLKPCVKLTP	LCVTLHCSNR	T.....
C_BW_96BW0	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTEV	NGTSDSS...
C_BW_96BW1	MWENDMVNQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV	TV.....
C_BW_96BW1	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCSSN	VTR.....
C_BW_96BW1	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCTNY	ST.....
C_ET_ETH22	MWKNDMVEQM	HQDIISLWDQ	GLKPCVKLTP	LCVTLNCNAI	KNNTKVT...
C_IN_93IN1	MWKNDMVDQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECRNV	S.....
C_IN_93IN9	MWKNDMVNQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECKNV	K.....
C_IN_93IN9	MWKNDMVNQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECSY	NGTSKAN...
C_IN_94IN1	MWKSDMVNQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECGNV	T.....
C_IN_95IN2	MWKNDMVNQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECRNV	NST.....
CRF01_AE_C	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLHCTKA	KLNDTYN...
CRF01_AE_C	MWKNNMVEQM	QEDVISLWDQ	SLQPCVKLTP	LCVTLHCTKA	SFTNATS...
CRF01_AE_C	MWKNNMVEQM	QEDVISL.DQ	SLKPCVKLTP	LCVTLDCTKA	DFYTTFK...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLQPCVKLTP	LCVTLHCTTA	KLTNVTN...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTNA	NLTNVNN...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTNA	NWTNANV...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTTA	NFTNFNL...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTNA	NLTNGSS...

CRF01_AE_T	MWKNKMAEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTNV	NATNVSN...
CRF02_AG_F	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	NSS.....
CRF02_AG_F	MWKNNMVEQM	HEDIISLWDQ	SLKPCVELTP	LCVTLDYCNV	SS.....
CRF02_AG_G	MWKNNMVEQM	HVDIISLWDQ	SLKPCVKLTP	LCVTLDQCNF	KN.....
CRF02_AG_N	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNF	NN.....
CRF02_AG_S	MWKNSMVEQM	HEDIISLWDQ	SLKPCVQLTP	LCVTLHCQDN	LT.....
CRF02_AG_S	MWKNNMVEQM	HVDIISLWDQ	SLKPCVKLTP	LCVTLECHNY	NYT.....
CRF03_AB_R	MGKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	KK.....
CRF03_AB_R	MGKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTEV	KT.....
CRF04_cpx_	MWKNDMVEQM	HEDIISLWNE	GLKPCAKLTS	LCVTFTCINA	T.....
CRF04_cpx_	MWENSTVEQM	HEDIISLWDE	GLKPCVKLTP	LCVALNCSNA	TIIINS....
CRF04_cpx_	MWKNNMVEQM	HEDIISLWEE	GLKPCVKLTP	LCVALNCGDA	TIK.....
CRF05_DF_B	MWKNDMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCTDF	KA.....
CRF05_DF_B	MWKNNMVEQM	HADIISLWDQ	SLKSCVKLTP	LCVTLNCTDA	TS.....
CRF06_cpx_	MWKNNMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLTCTNA	TLGNKTLGNN
CRF06_cpx_	MWENHMVEQM	HEDIISLWDE	SLKPCVKLTP	LCVTLICITNI	NITSTNS...
CRF06_cpx_	MWKNNMVEQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTNV	TDHGIN....
CRF06_cpx_	MWKNNMVEQM	HEDIISLWEE	SLKPCVKLTP	LCVTLNCTNV	NAT.....K
CRF11_cpx_	MWKNNMVEQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCAEV	TS.....
CRF11_cpx_	MWKNNMVEQM	HEDVISLWDE	SLKPCVKLTP	LCVALNCTDA	R.....
D_CD_84ZR0	MWKNNMVDQM	HEDIISLWDQ	SLKPCVKLTP	RCVTLNCTDA	SRN.....S
D_CD_ELI_K	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCSDE	LRNNG....T
D_CD_NDK_M	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDE	LRN.....S
D_UG_94UG1	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNW	VTD.....
F1_BE_VI85	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCTNA	TN.....
F1_BR_93BR	MWENNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLDICRNI	AT.....
F1_FI_FIN9	MWENDMVEQM	HKDIISLWDQ	SLKPCVKLTP	LCVTLNCTNA	TT.....
F1_FR_MP41	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLHCSDV	NI.....
F2_CM_MP25	MWKNNMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTKA	II.....
F2KU_BE_VI	MWKNNMVEQM	HADIISLWDQ	GLQPCVKLTP	LCVTLNCSEK	IN.....
G_BE_DRCBL	MWKNNMVEQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTEI	N...N....
G_UG_92NG0	MWKNNMVEQM	QEDIISLWEE	SLKPCVKLTP	LCITLNCTNV	N.....
G_SE_SE616	MWKNNMVEQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTDV	TNKGKNR.NN
H_BE_VI991	MWVNDMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLDICSSV	NA.....
H_BE_VI997	MWDNDMVEQM	QTDIISLWDQ	SLKPCVKLTP	LCVTLDICSN	TR.....
H_CF_90CF0	MWENNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV	RN.....
J_SE_SE702	MWKNDMVDQM	QEDIISVWDE	SLKPCVKITP	LCVTLNCSDV	NSNNS.....
J_SE_SE788	MWKNDMVDQM	QEDIISVWDE	SLKPCVKITP	LCVTLNCSNI	TSNSN.....
K_CD_EQTB1	MWKNNMVEQM	HTDIISLWDE	SLKPCVKLTP	LCVTLTCTNV	TN.....
K_CM_MP535	MWKNNMVEQM	HTDIISLWDE	SLKPCVELTP	LCVTLNCTDY	KG.....
N_CM_YBF30	MWENKMADQM	QEDIISLWEQ	SLKPCVKLTP	LCVTMLCNSD	YGEER.....
O_CM_ANT70	IWKNYMVEQM	QEDIISLWDQ	SLKPCVQMTF	LCVQMECTN.
O_CM_MVP51	IWKNYMVDQM	HEDIISLWEQ	SLKPCCEKMTF	LCVQMNCVD.
O_SN_99SE_	IWKNYMVEQM	QEDIISLWEQ	SLKPCVQMTF	LCVQMNCCTNY	VQ.....
O_SN_99SE_	IWENYMVEQM	QEDIISLWEQ	SLKPCVQMTF	LCVQMNCCTN.
U_CD_83C	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTF	LCVTLNCIDV	KN.....

00BW0762_1ATNVT	N.....	A.....	DYKNCSFNIT	TELRDKRKE
00BW0768_2THK	V.....	TNDTLYG...	EIKNCSFNVT	TEIRDKRRKE
00BW0874_2T	E.....	GNTTYGG...	EMRNCSFNIT	TELRDKKRQE
00BW1471_2VI	T.....	YNNNMTE...	EMKNCSFNIT	TELRDKKTKE
00BW1616_2YNGTY	S.....	D.....	GMKSCSFNIT	TELRDKRRKE
00BW1686_8	..RDATSSSS	E.....	GMREGMR...	EIKNCSFNVT	TELRDKRKNV
00BW1759_3KT.NFT	D.....	TTNG.....	EIKNCSFNIT	TEVRDRKKNE
00BW1773_2NGS...VTQG...	EIKNCSFNVT	TELRDKIQKV
00BW1783_5	.TNSTAFNTT	I.....	K.....E...	EMKNCSFNMT	TEIRDRKRKE
00BW1795_6	.TDNTIDEGM	G.....	N.....	EIKNCSFNIT	TELRDKKKRE
00BW1811_3SN	T.....	YNSIKE...	EMKNCSFNIT	TEIRDKKKQV
00BW1859_5KN	I.....	TYD..NN...	EIKNCSFNIT	TELRDKRKNV
00BW1880_2NSNAS	M.....	EG.....	EIENCSFNIT	TELRDKRKQE
00BW1921_1	..GNGN....RTG...	EIKNCSFNVT	TELRDKRQV
00BW2036_1	.TYHNVTY..NNTD...	EVKNCSFNMT	TELRDKKQV
00BW2063_6	.NASNTYQVT	T.....	PT..PPD...	IMKNCSFNIP	TELRDKSKKE
00BW2087_2	...NNVTSC	L.....	CNNTICE...	QMRNCSFNAT	TEIRDKKQV
00BW2127_2	...NATANR	A.....	THNPMEG...	EIKNCSFNAT	TEIKDRKKQV
00BW2128_3	...KSNSTN	V.....	TSENKEG...	EMKNCSFNIT	TEINKKKQRE
00BW2276_7GT	DMTNCTFNAT	TEIKDKKRKV
00BW3819_3VTSSV	N.....	ITKNMMD...	EIKNCSFNVT	TEVRDKKKQV
00BW3842_8	.TKNNDTK..	I.....	YNDTMYG...	EIKNCSFNMT	TELRDKKEKM
00BW3871_3	..RNQTKNQ	N.....	YTYEGIG...	EIKNCSFNMT	TELRDKKKNV
00BW3876_9VND	T.....	VNHSMEKE...	ETKNCSFNAT	TEIRDKKRKV
00BW3886_8	.DTEN.....MKE...	EMRNCTFNIT	TEIRDKEKQM
00BW3891_6AT.SNG	T.....	VTIN..G...	EIKNCSFNVT	TELRDKRKE
00BW3970_2VTINN	V.....	TANNNTS...	DMKNCSFNAT	TEVTDKIRKE
00BW5031_1	TVAEMKG...	EIKNCSFNIT	TEMRDKRQE
96BW01B21G..TYT	D.....	N...YQE...	KIKNCSFNIT	TEIRDKKQSG
96BW0407NGTSN	N.....	SSVPMEE...	EMKNCSFNIT	TELRDKKQV
96BW0502ATNNIM	I.....	D..NSNKG...	EMKNCSFNVT	TELRDKKQEV
96BW06_J4	..GSNN.ANS	S.....	YSNDMKE...	EIKNCSFNMT	TELRDKKQV
96BW11_06	.NDTLHQNL	T.....MKNCSFNVT	TELRDKRKE
96BW1210N.....	YNNKNNG...	EIKNCSFNAT	TEIRDKKQV
96BW15B03	.NYSNTMN..	S.....	YNNNTTE...	EIKNCTFNMT	TELRDKKQV
96BW16_26SNATMG	N.....	TLENGGG...	EMKNCSFNMT	TEIRDKKKQV
96BW17A09TN	N.....	VTSSMIG...	GMKNCSFNIT	TELRDKRKE
96BWM01_5	.KDINTSNAE	M.....	K.....A...	EMKNCSFNIT	TELRDKKKQE
96BWM03_2	.NMKKDT...MKE...	EIKNCSFKVN	TELRDKKKHE
98BWMC12_2STS	T.....	GTNSMNG...	QIKNCSFNIT	TELRDKRKE
98BWMC13_4	.NTTYNNAID	G.....	ET..IDK...	EMKNCSFNIT	TELRDKKKQE
98BWMC14_a	..VDANSTYV	I.....	HVGNIIT...	EMKNCSFNMT	TELRDKNKNV
98BWM014_1STRKS.NPSMQG...	EIKNCSFNIT	TEIRDKRRKV
98BWM018_dN	N.....	DTTYNIE...	EMRNCSFNIT	TEIRDKRRQE
98BWM036_aN.	T.....	IDGAMKE...	GMKNCSFNIT	TEVRDKKNQ
98BWM037_dYT NAT	G.....	WPTED...	KLQNCNFVT	TVIRDKKHKE
99BW3932_1ATK	N.....	GNITMKG...	EIKNCSFNAT	TEIKHKKKEM
99BW4642_4AT	N.....	VNRTMTE...	EIKNCSFNIT	MELDRKQV
99BW4745_8TI.TNT	T.....	IYKYTTS...	DIRNCPFNVT	TELRDKRRKE
99BW4754_7NTTVT	V.....	TNNTMDT...	VMKNCSFNVT	TELRDKRKE
99BWMC16_8N	LNNNMKE...	EIKNCSFNIT	TELRDKKQV
A2_CD_97CD	..NS.....TE	EIKNCSYNMP	TELRDKTKQV
A2_CY_94CY	...SNSSSTQ	S.....PINE	EIKNCSYNIT	TELRDKTKQV
A2D_97KR	...STQS...PDSN	NTMNCSETT	TELRDKKQV
A2G_CD_97C	...TGNN...	S.....IFTE	EMKNCSYNIT	TELRDKTKTV
A_BY_97BL0	...NNSSVNS	N.....	SSDSLFX...	XMKNCSFNMT	TELRDKRKT
A_KE_Q23_A	...NTTGDR.E	GLKNCSFNMT	TELRDKRQV
A_SE_SE659	...NS..TRV	V.....	NITDKE...	EIKNCSFNMT	TELRDKKQV
A_SE_SE725	...NG..TON	V.....	NITN.V...	GMRNCSFNMT	TELRDKKQV
A_SE_SE753	...KNITVSS	N.....	NNISISNSTE	DMRNCSFNMT	TELRDKKQV

A_SE_SE853	...VTNSSHS	Y.....	NVTNMQ....	EMKNCSFNVT	TELDRDKRQKV
A_SE_SE889SSVT	N.....	ITSDMAG...	EIKNCSFNMT	TEIRDKRQKV
A_SE_UGSE8	...NTNSTSA	N.....	LTDSVKG...	EMRNCSFNIT	TELDRDKKKKV
A_UG_92UG0	...NITNSIT	N.....	SSVNMRE...	EIKNCSFNMT	TELDRDKNRKV
A_UG_U455_	...NTN.NNT	N.....	ITDGVRE...	EMKNCSFNMT	TELDRDKKQKV
AC_IN_2130	...NSTGWGKE	EIKNCSFNIT	TELDRDKRQKV
AC_RW_92RW	...TVN....	ITDDMKG...	EIKNCSFNMT	TELDRDKKQRV
AC_SE_SE94	...TPNNATH	N.....	DSM..V...G	DMKNCPFNMT	TELDRDKRRKE
ACD_SE_SE8	...TNATDSN	N.....	..ASLQDMAK	EMTNCSFNMT	TELDRDKKQRV
ACG_BE_VI1SNGTAI	N.....	ITESIKG...	EMKNCSFKAT	TEIKDKKKKE
AD_SE_SE69ETSMN	G.....	EIKNCSFNMT	TELDRKEQQV
AD_SE_SE71	...VTNATNI	T.....	NANTITG...	EMKNCSFNMT	TEIMDKKRRKV
ADHK_NO_97	...HTDTTNNTSIQPSQ	PSANCSFNVT	TAIRDKQKQV
ADK_CD_MAL	AGSNRTNAEL	KM.....EIG	EVKNCSFNIT	PVGSDKR.QE
AG_BE_VI11	.STREIRGKN	CSLD.....TEVG	ELKNCSFNIT	TELDRDKKKTE
AG_NG_92NG	STGNSAGTNA	TCNI.....EEAN	NLKNCSFNIT	TEIRDKKKTE
AGHU_GA_VI	...ITNNSTD	KANV.....	...TNN..DA	EMRNCSFNIT	TEIRDKRRKE
AGU_CD_Z32NSTES	N.....	ITAEMQG...	EIKNCSFNMT	TELDRDKQKI
AJ_BW_BW21GCTNN	NCT.....VS	EMKECHFNT	GGGR..RKKE
B_AU_VH_AF	...NVTFTNS	RHVTNS...	.SYVGSMEKG	EMKNCSFNIT	TSIRDKRHKE
B_CN_RL42	...NATNTSS	T.....MEGG	EIKNCSFNIT	TSIKTKVK.D
B_DE_D31_U	...NATNTNN	SSWT.....	...MTGEMKG	EIKNCSFNIT	TSIRDKVQKE
B_DE_HAN_U	...NATNSS.WGRMEKG	EIQNCSFKVT	TNIRDKVQKE
B_FR_HXB2_	...NDTNTNS	SS.G.....	...RMIMEKG	EIKNCSFNIS	TSIRGKVQKE
B_GA_OYI_	.LRNATNTTS	SS.....	...WETMEKG	ELKNCSFNIT	TSIRDKMQEQ
B_GB_CAM1_	...TRTNSSD	WDRR.....	...EGEKMKG	EIKNCSFNVT	TSIRNKVRKE
B_GB_GB8_C	...NDTNTNN	SIME.....GG	EMKNCSFNIT	TSIRDKMQKE
B_GB_MANC_	...NATNTTS	TNNTAS...	.GSWGAMR.G	EIKNCSFNIT	TNIRDKVHKE
B_KR_WK_AF	.N.SSTSENN	TNPTIS...	..GGEGMGEG	EMKNCSFNVT	TNIRDKVQKE
B_NL_3202A	...NATNTTS	S..S.....	...GVIEIEG	EIKNCSFKIN	TNMKDQAQIE
B_TW_TWCYS	...TMSKND	N.....	...TLTMEKG	EIKNCSFNVT	TSIRDKVQKE
B_US_BC_L0	.TNTTSTNTP	SGS.....	...WKKMERG	EIKNCSFNVL	G...DKKQKA
B_US_DH123	...NGTNLKN	GTK.....	...IIGKSMRG	EIKNCSFNVT	KNIIDKVQKE
B_US_JRCSF	...NATNTTSSSEGMMERG	EIKNCSFNIT	KSIRDKVQKE
B_US_MNCG_	...NTTNTNN	STANN.NS..	.NSEGTIKGG	EMKNCSFNIT	TSIRDKMQKE
B_US_P896_	...NITKNTT	N....PTS..	..SSWGMMEKG	EIKNCSFYIT	TSIRNKVKKE
B_US_RF_M1GTNVTS	SSG.....	...GTMMENG	EIKNCSFQVT	TSRRDKTQKK
B_US_SF2_K	...KATNTNS	SN.....	...WKEEIKG	EIKNCSFNIT	TSIRDKIQKE
B_US_WEAU1	.LKNETNTNS	SSG.....	...GEKMEEG	EMKNCSFNVT	TLIRNKRRKE
B_US_WR27_	...WNATSTS	KNTTITNS..	.SNERPMEKG	EMKNCSFSIT	TSIRDKVQKE
B_US_YU2_M	.R.NATNTTS	SS.....	...WETMEKG	EIKNCSFNIT	TSIRDKVQKE
BF1_BR_93B	...NST....	.QND.....	...TLKEEPG	AIQNCSFNMT	TEVRDKQLKV
C_BR_92BR0IDYN..	N.....	RTDNMGG...	EIKNCSFNMT	TEVRDKREKV
C_BW_96BW0	V..PANGTSN	SSVSMKE...	EMRNCSFNIT	TELDRDKNQKE
C_BW_96BW1	.NDTLHQNFT	D.....MKNCSFNVT	TELDRDKRHE
C_BW_96BW1NS..NA	T.....	YNNKNNG...	EIKNCSFNAT	TEIRDKQKQV
C_BW_96BW1	.NYSNTMNAT	S.....	YNNNTTE...	EIKNCTFNMT	TELDRDKKQV
C_ET_ETH22N	N.....	SINSAND...	EMKNCSFNIT	TELDRDKRKA
C_IN_93IN1RNVSSY	N.....	TYNGSVE...	EIKNCSFNAT	PEVRDRKQRM
C_IN_93IN9NDSTHN	E.....	TYTESVK...	EIKNCSFNAT	TEIRDKQTV
C_IN_93IN9	ATNNVNATSN	G.....	NATSNGE...	EIQQCFFNVT	TEMRDKKQRV
C_IN_94IN1QNGTYN	D.....	...ESNK...	EITNCTFNMT	TEIRGRKQKV
C_IN_95IN2GNGTHS	K.....	TYNESMK...	EIKNCSFNAT	TVIKDKKQTV
CRF01_AE_C	GTAKL....NDTIGD	EVNCSFNVT	TELDRDKQEV
CRF01_AE_C	DRIK.....MED	AVRNCSFNMT	TELQDKKQEV
CRF01_AE_C	NTTEK....P	E.....	..IEISEMQK	EVSNCPFNIT	TELDRKEQEV
CRF01_AE_T	I.....TNVP	N.....	..IG..NITD	EVNCSFNMT	TEIRDKQKV
CRF01_AE_TNVS	N.....	..IIG.NITD	EVNCSFNMT	TELDRDKQV
CRF01_AE_T	TNVN..NNVT	N.....	..IVG.NITE	EVNCSFNMT	TELIDKKQKV
CRF01_AE_T	TKADNMTNVS	N.....	..ITIGNITD	EVNCTFNMT	TDLIDKKQKV
CRF01_AE_T	K.....TNVS	N.....	..IIG.NITD	EVNCTFNMT	TELTDKKQKV

CRF01_AE_T	T.....TEAP	N.....	..IV...GTD	EVKNCSFNVT	TELRDKTQQV
CRF02_AG_F	...NSSTSNS	SNSSTPINRT	IDSDMQE...	EIKNCSFNMT	TELRDKKQKV
CRF02_AG_F	...NSSISVK	S.....	ISRDMQG...	EIKNCSFNMT	TELRDKKQKV
CRF02_AG_G	ISDGSNS...	EIKNCSFNMT	TELRDKKQKV
CRF02_AG_N	...SYSNSS	N.....	LTSDMNG...	EIKNCSFNIT	TEVRDKKKKM
CRF02_AG_S	...SS.GN.	ISENMQG...	EIKNCSFNMT	TELRDKKQKV
CRF02_AG_S	...RNN....	SKINEVQ...	EMKNCSFNMT	TVLKDKKKKM
CRF03_AB_R	...EVTSTNT	S.....SIKMM	EMKNCSFNIT	TDLRDKVKKE
CRF03_AB_R	...NDTSTNA	S.....GIEMM	KN..CSFNIT	TDLRDKVKKE
CRF04_cpx_	...TTNSTN	GTVI.....	...K....E	GIKNCSFDIT	TEIRDKKKKE
CRF04_cpx_	TNNSTTNSTG	NSTV.....	...KS...TA	EIKNCSFNIT	TEVRDKQKKE
CRF04_cpx_	...STNSTP	NVTT.....	...T.....N	EMKNCSFNIT	TEIRDKKKKA
CRF05_DF_B	...NSTANST	TNST.....	...TLKEETG	AVQNCSFNMT	TEVNDKKLV
CRF05_DF_B	...ATTTSKN	ISATPTSN..	PNDTLKEEQG	AIQNCTFNIT	TEVKDKNKR
CRF06_cpx_	STNSTLGNNS	TIVD.....DISK	EIKNCSFNIT	TEIRDKTKKE
CRF06_cpx_T.KNI	TVES.....GE	EIKNCSFNVT	TEIRDKQKEE
CRF06_cpx_NNN	TVEG.....KE	EIKNCSFNVT	TEIKDKKKKE
CRF06_cpx_	YSNETVGKSL	TVKD.....RE	EIKNCSFNIT	TEVRDQKKTE
CRF11_cpx_YNTT	EMKNCSFNVT	TELIDRRKQE
CRF11_cpx_DNAT	DIKNCTFNIT	TELEDKKKNE
D_CD_84ZR0	TDNNSTLPTV	KP.....GE.	.MKNCSFNIT	TVVTDKRKQV
D_CD_ELI_K	MGNNVTTEEK	G.....MKNCSFNVT	TVLKDKKQV
D_CD_NDK_M	KGNGKVEEEE	K.....RKNCSFNVRDKREQV
D_UG_94UG1	...TTNTT	G.....MANCSFNIT	TEIRDKKKQV
F1_BE_VI85	...NSQ....EK...PG	AMQNCSFNMT	TEVRDKKLKL
F1_BR_93BR	...NGTNDTI	AIND.....	...TLKEDPE	AIQNCSFNIT	TEIRDKQLKV
F1_FI_FIN9	...TNDTLS.	DQSS.....	...TLKEEPG	AIQNCSFNMT	TEVEDKKQKV
F1_FR_MP41	...TSNATTT	NDTS.....	...TP.EESG	AIQNCSFNMT	TEVKDKKLRV
F2_CM_MP25	...NVTSSNN	TTLA.....	...PNVTISE	EMKNCSFNIT	TEIRDKQKKE
F2KU_BE_VI	...INSTDLT	NWANKTNNWA	NETTLLNITT	GMRNCSFNIT	TMLKDKKKKQ
G_BE_DRCBLNS	TRNI.....TEEY	RMTNCSFNMT	TELRDKKKAE
G_NG_92NG0	.SANHTEANN	..TV.....ENKE	EIKNCSFKIT	TERGGKKKEE
G_SE_SE616	STDNSTETNN	S.TV.....DNPG	EIKNCSFNVT	TEIRDKKKKE
H_BE_VI991	...TNVTKSN	NSTD.....	...INIGEIQ	EQRNCSFNVT	TAIRDKNQKV
H_BE_VI997	...NDTNSSS	TVNA.....	...TSSPSAN	ELTNCSFNVT	TVIRDKQQRV
H_CF_90CF0	...NTSNSTS	SMEA.....	...GG.....	ELTNCSFNVT	TVLRDKQKQV
J_SE_SE702	...TDSNS	SASN.....NSPE	IMKNCSFNVT	TEIRNKRKQE
J_SE_SE788	...TTSNS	SVS.....SPD	IMTNCSFNIT	TEIRNKRKQE
K_CD_EQTB1	...NRTNANK	NDT.....	NINATVTSTD	EIKNCSFNIT	TELKDKKKRV
K_CM_MP535	...TNSTN..	NATSTVVSPA	EIKNCSFNIT	TEIKDKKKKE
N_CM_YBF30	...NNTNMTT	R.....	...EPDIGYK	QMKNCSFNAT	TELTDKKKQV
O_CM_ANT70	...IAG...TTNEN	LMKKCEFNV	TVIKDKKEKK
O_CM_MVP51	...LQTNKTG	LLN...ETIN	EMRNCSFNVT	TVLTDKKEQK
O_SN_99SE_	..GNYTNSSS	INNDTSSPEN	LVKQCEFNV	TVVKDKKEKK
O_SN_99SE_	..VNDETSSS	VKNDTSSSEN	LMKKCEFNV	TVLKDKEQK
U_CD_83CSTNN	N.....TEEA	TITNCSFKVP	TELKDKTETV

	201			250
00BW0762_1	YALFYRLDIV	QLGE.....NNAN	SE.....YRLI
00BW0768_2	HALFYRLDIV	PLDEKDK...SSN	SN.....YRLI
00BW0874_2	SALFYRLDIV	PLNGS.....ERNK	SE.....YRLI
00BW1471_2	RALFYRLDIV	PLNESDN...NSY	RE.....YRLI
00BW1616_2	YALFYRLDIV	PLEN.....SEN	SE.....YRLI
00BW1686_8	YALFYKLDIV	PLEE.....NDI	ST.....YRLI
00BW1759_3	HALFYRLDIV	PLEGE.....NNTN	NE.....YRLI
00BW1773_2	HALFYRLDIV	QLD.....N	SS.....YRLI
00BW1783_5	YALFYKLDIV	PLEGNNS...E..YRLI
00BW1795_6	YALFYRLDIV	SLDNENN...KT.	AE.....YRLI
00BW1811_3	YALFYKPDIV	PLDGS.....NS	SE.....YRLI
00BW1859_5	YALFYKIDIV	PLND.....N.NSN.N	SM.....YRLI
00BW1880_2	YALFYRLDIV	PLDSPS....NATN	SR.....YRLI
00BW1921_1	YALFYRLDIV	QLN.....	SE.....YRLI
00BW2036_1	YALFYKLDIV	PLNGNSG...	SE.....YRLI
00BW2063_6	YALFYKLDIV	PLGNTNG...T..	.E.....YRLI
00BW2087_2	YALFYKLDIV	SLDD.....NN	S.....YRLI
00BW2127_2	YALFYRLDIV	PLDND.....SA	TN.....YRLI
00BW2128_3	YALFYKLDIV	PLNNS.....SDNSS	GE.....YRLI
00BW2276_7	QALFYKLDIV	PLNSTGE...NNN	TE.....YRLI
00BW3819_3	YALFYRLDIV	PLNGK.....NS	SS.....YRLI
00BW3842_8	HALFYRLDIV	PLEDNSG...NSS	SN.....YRLI
00BW3871_3	YALFYKLDIV	PLND.....N..	NE.....YRLI
00BW3876_9	NALFYKLDIV	PLHE.....GN	S.....YRLI
00BW3886_8	YALFYRLDIV	PLHDSSS...DG.	SE.....YVLI
00BW3891_6	HALFYRLDIV	PLNG.....KNQS	NE.....YRLI
00BW3970_2	NALFYTLDIV	PLDENQ....N.....YRLI
00BW5031_1	FALFNILDIV	PLNNEN....NTKN	SD.....YRLI
96BW01B21	YALFYKFDIV	PLN.....GNNT	SE.....YILI
96BW0407	RALFYSLDIV	QPNN.....S	TE.....YRLI
96BW0502	HALFYRLDIV	PLQG.....NN	NE.....YRLI
96BW06_J4	YALFYRLDIV	PLGD.....N..	SS.....YRLI
96BW11_06	YALFYRLDIV	PLNNKNE...S..	SE.....YRLI
96BW1210	YALFYRLDIV	PLDN.....NS	SE.....YRLI
96BW15B03	YALFYKLDIV	PLNSNS....	SE.....YRLI
96BW16_26	YALFYRLDIV	PLNGE.....NSNSS	GE.....YRLI
96BW17A09	SALFYRLDIV	PLNENNS...SSN	SE.....YRLI
96BWMO1_5	YALFYKLDIV	PLTNDAS...EN.	SE.....YRLI
96BWMO3_2	YALFYKLDIV	PLDGNNE...DGN	KQ.....YRWI
98BWMC12_2	SALFYRLDIV	PLK.....ENS	SE.....YRLI
98BWMC13_4	QALFYRLDIV	PLDNANG...T..	SE.....YRLI
98BWMC14_a	YALFYRLDIV	PLGE.....D..	SS.....YRLI
98BWMO14_1	YALFYKLDIV	ELDG.....NS	SN.....YVLI
98BWMO18_d	SALFYKLDIV	PLD.....NSS	SK.....YILI
98BWMO36_a	YVLFYKLDIV	PLNGNG....SN	SE.....YRLI
98BWMO37_d	YALFYRPDIV	PLNEG.....N.....YRLI
99BW3932_1	YALFYRLDIV	PLKN.....S	SE.....YRLI
99BW4642_4	NALFYKLDIV	PLNE.....K.ANNSSY	SY.....YRLI
99BW4745_8	YALFYRIDIV	PLDE.....NNNS	SE.....YRLI
99BW4754_7	HALFYRLDIV	PLETK.....NSNE	SA.....YRLI
99BWMC16_8	YALFYKVVIV	PLSE.....NST	SE.....YRLI
A2_CD_97CD	YSLFYELDIV	LLNRSKN...SSY	ST.....YRLI
A2_CY_94CY	YSLFYRLDIV	QLDESENKNTSGSN	TL.....YRLI
A2D___97KR	QALFYELDIV	QLNSSDSND.TLN	RQ.....YRLI
A2G_CD_97C	RSLFYTLDIV	QINKDNN...T.....YRLI
A_BY_97BL0	HSLFYKLDIV	STSNNDXS..Q.....YRLI
A_KE_Q23_A	YSLFYRLDIV	PINEN.....QG.....	SE.....YRLI
A_SE_SE659	HSLFYRLDIV	QMNE.....RGNSSNSSY	NE.....YRLI
A_SE_SE725	YSLFYKLDIV	QINDN.....GNNSNNS..	SE.....YRLI
A_SE_SE753	YSLFYRLDIV	KIDEN.....KSN...SSN	SK.....YRLI

A_SE_SE853	TSLFYKLDVV	PIGGN.....DTNS	TQ.....YRLI
A_SE_SE889	HALFYRLDVV	PMDN.....NNS	.L.....YRLI
A_SE_UGSE8	YSLFYKLDIV	KINKNKSFRG	.KNSSGNSSS	DR.....YRLI
A_UG_92UG0	YSLFYKLDVV	QINNG.....NNSS	NL.....YRLI
A_UG_U455	YSLFYRLDIV	QINKTD.....N	NS.....YRLI
AC_IN_2130	YSLFYRLDVV	PIEEGQGNSSNSGY	KE.....YRLI
AC_RW_92RW	YSLFYRLDIV	QINSNSN...NSSH	NQ.....YRLI
AC_SE_SE94	HALFYRLDIV	PLDEGNSNSNESNNNY	SD.....YRLI
ACD_SE_SE8	YSLFYKLDVV	QINSN.....QNNS	SQ.....YRLI
ACG_BE_VI1	YALFYRLDIL	PLNKENK...GSS	GK.....YRLI
AD_SE_SE69	HSLFYKLDVV	QMGNSNS...	SQ.....YRLI
AD_SE_SE71	YSLFYKLDVV	QINENQ.....	..YNSSNNSN	KE.....YRLI
ADHK_NO_97	HALFYRVDLV	SIDN.....NDNN	TQ.....YRLI
ADK_CD_MAL	YATFYNLDLV	QIDDSN...S	S.....YRLI
AG_BE_VI11	HALFYRPDVV	PINNDN...SSYMLI
AG_NG_92NG	YALFYRLDVV	PIDGNNNV..S.....NNYRLI
AGHU_GA_VI	YALFYKHDLV	PITN.....ET	KT.....FILI
AGU_CD_Z32	YSLFYRLDIV	PIEENSNG.N..S	SE.....YRLI
AJ_BW_BW21	YALFYKEDIA	LIKDRPN...NS	NY.....SEYILV
B_AU_VH_AF	FALFYKLDVV	QIDGS.....N	TS.....YRLI
B_CN_RL42	YALFYKVDVV	PIGND.....S	TS.....YRLI
B_DE_D31_U	YAHFYKLDVV	PIDND.....N	TS.....YRLI
B_DE_HAN_U	SALFYKTDVV	PIDNNKTS..NRDNT	TS.....YMLI
B_FR_HXB2	YAFFYKLDII	PIDND.....T	TS.....YKLT
B_GA_OYI	YALFYKLDVL	PIDKN.....D	TK.....FRLI
B_GB_CAM1	YALFYKLDVV	PIDKAN....	TS.....YTLI
B_GB_GB8_C	YALLYKLDIV	SIGSD.....N	TS.....YILT
B_GB_MANC	YALFYKLDVV	PIEKK.....N	TS.....FRLI
B_KR_WK_AF	YALFYKLDII	PIDN.....	TS.....YALR
B_NL_3202A	YALFYKLDVV	PIDNN..N..TNTSY	TS.....YRLI
B_TW_TWCYS	YASFYRLDLV	QTDEN.....S	TS.....YRLI
B_US_BC_L0	YALFYKLDVV	PIDNDKNS..	TK.....YRLI
B_US_DH123	YALFYRHDVV	PIDRN.....I	TS.....YRLI
B_US_JRCSF	YALFYKLDVV	PID.....NKNN	TK.....YRLI
B_US_MNCG	YALLYKLDIV	SIDND.....S	TS.....YRLI
B_US_P896	YALFNRLDVV	PIE.....NTNN	TK.....YRLI
B_US_RF_M1	YALFYKLDVV	PIEKGNI SPK	N.NTSNNTSY	GN.....YTLI
B_US_SF2_K	NALFRNLDVV	PIDN..AS..TTNY	TN.....YRLI
B_US_WEAU1	YALFYKLDVM	PIDHDNTS..YTLI
B_US_WR27	HALFYRLDVV	PIDK.....NNTN	TS.....YRLI
B_US_YU2_M	YALFYNLDVV	PIDN.....	AS.....YRLI
BF1_BR_93B	HALFYRLDIV	PISNDNSSNDNSS	RE.....YRLI
C_BR_92BR0	HALFYRLDIV	PLKNE.....SSNTS	GD.....YRLI
C_BW_96BW0	RARFYRLDIV	QLNNN.....SNS	NE.....YRLI
C_BW_96BW1	YALFYRLDIV	PLNNKNE...SN	SE.....YRLI
C_BW_96BW1	YALFYRLDIV	PLDN.....NS	SE.....YRLI
C_BW_96BW1	YALFYKLDIV	PLNSNS....	SE.....YRLI
C_ET_ETH22	YALFYKLDIV	PLN.....NGS	TD.....YRLI
C_IN_93IN1	YALFYGLDIV	PLN...KKNSSENS	SE.....YRLI
C_IN_93IN9	YALFYRLDIV	QLN...SDDKKNSS	EY.....YRLI
C_IN_93IN9	HALFYRLDLV	PLDNEKNSSFSNSS	KT.....YRLI
C_IN_94IN1	YALFYKLDIV	PIS...ETSNQS..RLI
C_IN_95IN2	YALFYKLDIV	PLDNEEQENDSNSS	GY.....YRLI
CRF01_AE_C	HALFYVPDIV	RIG....EK	..NKNSSGNS	SE.....YILI
CRF01_AE_C	HALFYTSDDV	QISSSVQNNN	NSNTSGQNNS	HK.....FRLI
CRF01_AE_C	YALFYRSDLV	PIE.....	..RNSGENNG	SS.....YRLI
CRF01_AE_T	HALFYKLDIV	QIEDK.....NDS	SK.....YGLI
CRF01_AE_T	HALFYKLDIV	QMN.....KNS	SE.....YRLI
CRF01_AE_T	YALFYKLDIV	QMN.....SNS	SE.....YRLI
CRF01_AE_T	YALFYKLDIV	PIG.....NNN	NM.....YRLI
CRF01_AE_T	HALFYKLDIV	QIEDK.....KTS	SE.....YRLI

CRF01_AE_T	QALFYKLDIV	QMGG.....NDS	GE.....YRLI
CRF02_AG_F	SALFYRLDVV	QINES.....GN	SQ.....YRLI
CRF02_AG_F	SALFYRLDVV	QINES.....SN	SQ.....YRLI
CRF02_AG_G	NALFYRVDVV	QMNS.....Q.....YRLI
CRF02_AG_N	HALFYRLDVV	QINEN.....NG	SQ.....YRLI
CRF02_AG_S	YALFYRYDVV	QINETG....DN	IQ.....YRLI
CRF02_AG_S	AALFYKIDIV	PIDKN.....A	TY.....YRLI
CRF03_AB_R	YALFYKLDVV	QIDND.....S.....YRLI
CRF03_AB_R	HALFYKLDVV	QIDND.....S.....YRLI
CRF04_cpx_	YALFYRIDIV	PINARVPING	...SNRNNST	EE.....YMLI
CRF04_cpx_	HALFYRLDVV	PINNNVPINN	...TSNTSEY	RE.....YRLM
CRF04_cpx_	YALFYRLDIV	PINDNNSTN.	...SRRSSNT	SD.....YMLI
CRF05_DF_B	HALFYRLDIV	PISSD....DSSN	SS.....YRLI
CRF05_DF_B	HALFYRLDIV	SINS.....SRK	E.....YRLI
CRF06_cpx_	YALFYRPDIV	PIGDD.....S	NN.....SDYRLI
CRF06_cpx_	YALFYRLDVV	PINDG.....S	NN.....NSYRLI
CRF06_cpx_	RALFYTLDVV	PINDN.....G	NN.....STYRLI
CRF06_cpx_	YALFYRPDVM	QVDG.....K	NS.....STYRLI
CRF11_cpx_	YALFYKLDIV	PINDNNN...SS	NV.....SDYRLI
CRF11_cpx_	RALFYRLDVV	PINDS.....SS	NI.....GQYRLI
D_CD_84ZR0	HALFYRLDVV	QIDNEGKNE.INDTY	GT.....YRLI
D_CD_ELI_K	YALFYRLDIV	PIDNDSS...TNS	TN.....YRLI
D_CD_NDK_M	YALFYKLDIV	PIDNNNR...TNS	TN.....YRLI
D_UG_94UG1	QALFYKLDVV	KINDNDS...DN	TS.....YRLI
F1_BE_VI85	SALFYRLDIV	PIGNN...N.S	SE.....YRLI
F1_BR_93BR	HALFYKLDIV	QINKD...DN.	RT.....YRLI
F1_FI_FIN9	HALFYRLDIE	PISNN...N.SR	EE.....YRLI
F1_FR_MP41	NALFYKLDII	PINNS.....SS	SD.....YRLI
F2_CM_MP25	YALFYKLDVV	QINNS.....	NTS.....YRLI
F2KU_BE_VI	YALFYREDIV	PINIKKNNKTNSN	SKKNNNTSNN	SIENSKYRLI
G_BE_DRCBL	YALFYRTDVV	PINEMNNENNGT	NS.....TWYRLT
G_NG_92NG0	YALFYKLDVV	PISNGN....K.....TSYRLI
G_SE_SE616	YAFFYRLDVV	PINN.....A.....TNYRLT
H_BE_VI991	HALFYRADIV	QIDEGER...NKSD	NH.....YRLI
H_BE_VI997	HALFYRLDVV	PIDETSNNN.NSNS	TK.....YRLI
H_CF_90CF0	HALFYRLDVV	PIDNNS....	TQ.....YRLI
J_SE_SE702	YALFYRQDVV	PIN.....S	DN.....KSYILI
J_SE_SE788	YALFYRQDVV	PID.....S	NN.....KNYILI
K_CD_EQTB1	SALFYKLDIV	QIKQSEINQSESEDRLI
K_CM_MP535	SALFYRLDVL	PLN.GEGNNSSTEYRLI
N_CM_YBF30	YSLFYVEDVV	PINAYN....KTYRLI
O_CM_ANT70	QALFYVSDLM	ELNETSSTNKT	NS.....KMYTLT
O_CM_MVP51	QALFYVSDLS	KVNDNAVN.G.....TTYMLT
O_SN_99SE_	QALFYVSDLM	KINEANDT..K.....DMYTLI
O_SN_99SE_	QALFYVSDLM	KVNENND...TMYTLI
U_CD___83C	HTLFYKLDVV	PLNVTN....N	SS.....	..ISSTYRLI

00BW0762_1	NCNTSTITQA	CPKVNFDPIP	IHYCAPAGYA	ILKCNTKTFD	GTGPCTNVST
00BW0768_2	NCNTSAVTQA	CPKVSFEPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCHNVST
00BW0874_2	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW1471_2	NCNTSTITQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW1616_2	KCNTSTITQA	CPKVNFDPIP	IHYCAPAGYA	ILKCRNKTFN	GTGPCNNVST
00BW1686_8	NCNTSSISQA	CPKVSFGPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
00BW1759_3	NCNTSAVTQA	CPKVTFDPIP	VHYCAPAGYA	ILKCNNKTFN	GAGPCNNVST
00BW1773_2	NCNTSAITQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNNQTFN	GTGPCNDVSS
00BW1783_5	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW1795_6	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GKGPCNNVST
00BW1811_3	NCNTSALTQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCTNVST
00BW1859_5	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNDKTFN	GTGPCQNVST
00BW1880_2	NCNTSAITQA	CPKINFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW1921_1	NCNTSAITQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW2036_1	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
00BW2063_6	NCNTSTITQS	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW2087_2	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVSI
00BW2127_2	NCNTSAITQA	CPKISFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW2128_3	NCNTSALTQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW2276_7	NCNTSAITQA	CPKITFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVSP
00BW3819_3	NCNTSAVTQS	CPKISFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW3842_8	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GIGPCQNISI
00BW3871_3	NCNTSAISQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
00BW3876_9	HCNTSTITQA	CPKVSFEPIP	IHYCAPAGYA	ILKCNDKTFN	GTGPCLVNST
00BW3886_8	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNKTFN	GTGPCQNVST
00BW3891_6	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW3970_2	NCNTSKVTQA	CPKVSFDPIP	LHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW5031_1	SCNTSTITQA	CPKVSFDPPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
96BW01B21	NCNTSAISQA	CPKVSFDPIP	IHYCTPAGFA	ILKCNNKTFN	GTGPCNNVST
96BW0407	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GLGPRNVST
96BW0502	NCNTSAITQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNNQTFN	GTGPCNNVSS
96BW06_J4	NCNTSTISQA	CPKISFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
96BW11_06	NCNTSTITQS	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
96BW1210	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCTNVST
96BW15B03	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCKNNKTFN	GTGPCQNVST
96BW16_26	NCNTSALTQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
96BW17A09	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILECNNKTFN	GTGPCTNVST
96BWM01_5	NCDTSTITQS	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
96BWM03_2	NCNTSSITQA	CPKVSFDPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCQNVST
98BWMC12_2	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
98BWMC13_4	NCNTSTITQS	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GIGPCNNVST
98BWMC14_a	NCNTSAISQA	CPKISFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
98BWM014_1	NCNTSTVKQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
98BWM018_d	NCNTSVITQA	CPKVTFEPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
98BWM036_a	NCNTSTLTQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
98BWM037_d	NCNTSTVTQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNNKTFN	GKGPCNNVST
99BW3932_1	NCYTSAIAQT	CPKISFDPIP	IHYCAPAGYA	ILKCYNKTFN	GTGPCKNVST
99BW4642_4	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
99BW4745_8	NCNTSAVTQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
99BW4754_7	NCNTSAITQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTRPCNNVST
99BWMC16_8	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNDVST
A2_CD_97CD	SCNTSVITQA	CPKVSFEPIP	IHYCAPAGYA	ILKCKDKEFN	GKGSCSNVSS
A2_CY_94CY	NCNTSTITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCKDPRFN	GTGSCKNVSS
A2D___97KR	HCDTSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDPEFN	GTGPCKNVSS
A2G_CD_97C	KCNTSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDPKFN	GTGPCENVSS
A_BY_97BL0	NCNTSAMTQA	CPXVTFEPIP	IYYCAPAGFA	ILKCDTNTFT	RTXPCKNVST
A_KE_Q23_A	NCNTSAITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCKDEGFN	GTGLCKNVST
A_SE_SE659	NCNTSAITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCKDDAFN	GTGRCKNVST
A_SE_SE725	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKEFN	GTGPCNNVST
A_SE_SE753	NCNTSAITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCDNKEFN	GTGLCNNVST

A_SE_SE853	NCNTSAITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCRDENFN	GTGPCKNVST
A_SE_SE889	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDEKFN	GTGPCKNVSS
A_SE_UGSE8	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNEDEFN	GTGTCRNVST
A_UG_92UG0	NCNTSALTQA	RPKVTFEPIP	IHYCAPAGYA	ILKCNDEKFN	GTGLCKNVST
A_UG_U455	NCNTSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDPEFN	GKGPCRNVST
AC_IN_2130	NCNTSAITQA	CPKVTFNPIP	IHYCTPAGYA	ILKCNEETFN	GTGPCKNVST
AC_RW_92RW	NCNTSAITQA	CPKVSFEPIP	INYCAPAGFA	ILKCKDKKFN	GTGPCKNVST
AC_SE_SE94	NCNTSAITQA	CPKVSFDPIP	IHYCAPPGFA	ILKCKDAKFN	GIGPCNNVST
ACD_SE_SE8	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKEFN	GTGPCKNVST
ACG_BE_VI1	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCCNVST
AD_SE_SE69	NCNTSAIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCKDTEFN	GTGPCKNVST
AD_SE_SE71	NCNTSAITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCKDEKFN	GTGPCKNVST
ADHK_NO_97	NCNTSVITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCNNKTFS	GTGPCKNVST
ADK_CD_MAL	NCNTSVITQA	CPKVTFDPIP	IHYCAPAGFA	ILKCNDDKFN	GTEICKNVST
AG_BE_VI11	NCNSSTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILRCRDKKFN	GTEPCKNVST
AG_NG_92NG	NCNVSTIKQA	CPKVSFDPLP	IHYCAPAGFA	ILKCRGKNFT	GTGQCKNVSS
AGHU_GA_VI	HCNTSTITQA	CPKVSFDPIP	IHYCAPAGFA	ILKCKDKAFN	GTGPCKNVST
AGU_CD_Z32	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDEEFE	GKGPCRNVST
AJ_BW_BW21	KCNTTVIKQA	CPKVSFQPIP	IHYCAPAGFA	ILQCNDKKFN	GTGPCKNVST
B_AU_VH_AF	NCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKTFN	GKGPCANIST
B_CN_RL42	NCNTSVITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNNKKFN	GTGPCTNVST
B_DE_D31_U	SCNTSVITQA	CPKVSFEPIP	IHYCTPAGFA	MLKCKDKRFN	GKGQCKNVST
B_DE_HAN_U	HCNRSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDDKFN	GKGPCRNVST
B_FR_HXB2	SCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCTNVST
B_GA_OYI	HCNTSTITQA	CPKISFEPIP	MHYCTPAGFA	ILKCNDDKFN	GTGPCTNVST
B_GB_CAM1	HCNTSVITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNDDKFN	GKGPCCTNVST
B_GB_GB8_C	ECNASVITQA	CPKISFEPIP	IHFCAAGFA	ILKCNNKTFD	GKGPCCTNVST
B_GB_MANC	SCNTSTITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNNKKFD	GKGQCTNVST
B_KR_WK_AF	HCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILQCNDKKFN	GTGPCCNVST
B_NL_3202A	SCNTSVITQA	CPKVSFEPIP	IHFCTPAGFA	LLKCNDDKFN	GTGPCKNVST
B_TW_TWCYS	SCNASVIKQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNNKTFN	GTGTCCTNVST
B_US_BC_L0	SCNTSVITQA	CPKISFEPIP	IHYCAPAGFA	ILKCKDKKFN	GTGSCCKNVST
B_US_DH123	SCNTSTLTQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDKKFN	GTGPCTNVST
B_US_JRCSF	SCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKTFN	GKGQCKNVST
B_US_MNCG	SCNTSVITQA	CPKISFEPIP	IHYCAPAGFA	ILKCNDDKFS	GKGSCCKNVST
B_US_P896	SCNTSVITQA	CPKVSFQPIP	IHYCVPAGFA	MLKCNNKTFN	GSGPCTNVST
B_US_RF_M1	HCNSSVITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNDDKFN	GTGPCKNVST
B_US_SF2_K	HCNRSVITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNNKTFN	GKGPCCTNVST
B_US_WEAU1	NCKSSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDDKFN	GKGPCRNVST
B_US_WR27	HCNTSTITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNDDKFN	GTGQCKNVST
B_US_YU2_M	SCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDDKFN	GTGPCTNVST
BF1_BR_93B	NCNTSTLTQA	CPKVSWDPIP	IHYCAPAGYA	ILKCNDDKFN	GTGPCRNVST
C_BR_92BR0	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCCNVST
C_BW_96BW0	NCNTSTITQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GSGPCNNVST
C_BW_96BW1	NCNTSTITQS	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCCNVST
C_BW_96BW1	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCTNVST
C_BW_96BW1	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCKNNTFN	GTGPCCNVST
C_ET_ETH22	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCRDKTFT	GTGPCHNVST
C_IN_93IN1	NCNTSAITQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCCNVST
C_IN_93IN9	NCNTSAITQA	CPKVTFDPIP	IHYCTPAGYA	ILKCKDKTFT	GTGPCHNVST
C_IN_93IN9	NCNTSAITQA	CPKVTFDPIP	IHYCTPAGYA	ILKCKDKTFT	GTGPCHNVST
C_IN_94IN1	SCNTSVITQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNDDKFN	GTGPCRNVST
C_IN_95IN2	NCNTSALTQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCHNVST
CRF01_AE_C	HCNTSVIKQA	CPKVTFDPIP	IHYCTPAGYA	ILKCKDKTFT	GTGPCKNVSS
CRF01_AE_C	HCNTSVIKQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNDDKFN	GTGPCKNVSS
CRF01_AE_C	HCNTSVIKQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNDDKFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKISFDPIP	IHYCTPAGYV	ILKCNDDKFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKISFDPIP	IHYCTPAGYA	ILKCNDDKFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNDDKFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKISFDPIP	IHYCTPAGYA	MLKCNDDKFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKISFDPIP	IHYCTPAGYA	ILKCNDDKFN	GTGPCKNVSS

CRF01_AE_T	NCNTSVIKQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNDKNFN	GTGPCKNVSS
CRF02_AG_F	NCHTSAITKA	CPRVTLEPIP	IHYCAPAGLA	ILKCNDKKFN	GTGLCKNVST
CRF02_AG_F	NCNTSAIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCKNVST
CRF02_AG_G	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDRNFN	GTGPCKNVST
CRF02_AG_N	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDKGFN	GTGPCKNVST
CRF02_AG_S	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKDFN	GTGPCKNVST
CRF02_AG_S	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNEKDFS	GTGSCKNVST
CRF03_AB_R	SCNTSVVTQA	CPKISFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCTNVST
CRF03_AB_R	SCNTSVVTQA	CPKISFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCTNVST
CRF04_cpx_	NCNASTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNEKNFT	GLGPCTNVSS
CRF04_cpx_	SCNTSNHKQA	CPKVTLEPNS	HTLLCPGWFC	DLKCNDKNSP	GLGSCTNVSP
CRF04_cpx_	NCNVSSITQA	CPKIKFEPIP	IHYCAPAGFA	ILQCNEKRFN	GS GPCKNVSS
CRF05_DF_B	NCNTSTIKQA	CPKVSWDPIP	IHYCAPAGYA	ILKCNEKKFS	GTGPCKNVST
CRF05_DF_B	NCNTSTIKQA	CPKVCWDPIP	IHYCAPAGYA	ILKCNEKRFN	GTGPCKNVST
CRF06_cpx_	NCNVSTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKDFN	GTGPCKNVST
CRF06_cpx_	NCNASTIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCRDKNFN	GTGPCKNVST
CRF06_cpx_	NCNTSTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKNFN	GTGPCKNVST
CRF06_cpx_	NCNASTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKNFN	GTGACKNVST
CRF11_cpx_	NCNVSTIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCRDKEFN	GTGPCKNVST
CRF11_cpx_	NCNVSAVKQA	CSKVTFEPIP	IHYCAPAGFA	ILKCRDKEFN	GTGPCKNVST
D_CD_84ZR0	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKRFN	GTGPCKNVSS
D_CD_ELI_K	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKKFN	GTGPCKNVST
D_CD_NDK_M	NCDTSTITQA	CPKISFEPIP	IHFCAAGFA	ILKCRDKKFN	GTGPCKNVST
D_UG_94UG1	NCNTSAITQA	CPKMTFEPIP	IHYCAPAGFA	ILKCNEKKFN	GTGPCKNVST
F1_BE_VI85	NCNTSTITQA	CPKVSWDPIP	IHYCAPAGYA	ILKCNDKRFN	GTGPCKNVST
F1_BR_93BR	NCDASTITQA	CPKVSWDPIP	IHYCAPAGYA	ILKCNEKNFT	GTGSCKNVST
F1_FI_FIN9	TCNTSTITQA	CPKVSWDPIP	IHYCAPAGYA	ILKCKDKRFN	GTGPCKNVST
F1_FR_MP41	NCNTSTIKQA	CPKVSWDPIP	IHYCAPAGYA	ILKCRDPRFN	GTGPCKNVST
F2_CM_MP25	NCNTSTLTQA	CPKVSFDPIP	IHYCAPAGFA	ILKCNNKTFN	GTGLCRNVST
F2KU_BE_VI	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNEKEFN	GTGPCKNVST
G_BE_DRCBL	NCNVSTIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCVDKKFN	GTGTCNNVST
G_NG_92NG0	HCVNSTIKQA	CPKVNFDPIP	IHYCAPAGFA	ILKCRDKEYN	GTGPCKNVST
G_SE_SE616	HCVNSTIKQA	CPKVTFDPIP	IHYCAPTGFA	ILKCRDKEFN	GTGPCKNVST
H_BE_VI991	NCNTSVIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNGKKFN	GTGPCTNVST
H_BE_VI997	NCNTSVITQA	CPKVSFDPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCTNVST
H_CF_90CF0	NCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKTFN	GTGLCTNVST
J_SE_SE702	NCNTSVIKQA	CPKVSFQPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCKNVST
J_SE_SE788	NCNTSVIKQA	CPKVSFQPIP	IHYCAPAGFA	ILKCNDKNFN	GTGSCKNVST
K_CD_EQTB1	NCNTSTVTQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNNTCN	GTGPCTNVST
K_CM_MP535	NCNTSTITQT	CPKVTFEPIP	IHYCAPAGFA	ILKCKDKRFN	GTGPCKNVST
N_CM_YBF30	NCNTTAVTQA	CPKTSFEPIP	IHYCAPAGFA	IMKCNEGNFS	GNGSCTNVST
O_CM_ANT70	NCNSTTITQA	CPKVSFEPIP	IHYCAPAGYA	IFKCNSTEFN	GTGTCRNITV
O_CM_MVP51	NCNSTTIKQA	CPKVSFEPIP	IHYCAPTGFA	IFKCNDDTFN	GTGLCHNISV
O_SN_99SE_	NCNSTTIKQA	CPKVSFEPIP	IHYCAPAGYA	IFKCNSTEFN	GTGPCKNITA
O_SN_99SE_	NCNSTTIKQT	CPKVSFEPIP	IHYCAPAGYA	IFKCNNTGFN	GTGPCTNVTV
U_CD_83C	NCNTSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCKNVST

00BW0762_1	VQCTHGIKPV	VSTQLLLLNGS	LSEE.GIVIR	SENITNNAKT	IIVHLNESVE
00BW0768_2	VQCTHGIKPV	VPTQLLLLNGS	LAEE.EIIIR	SEALTNNAKT	IIARLNKSV
00BW0874_2	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLAENDKT	IIVHLNESVE
00BW1471_2	VLCTHGIKPV	VSTQLLLLNGS	LSEG.EIMIR	SENLTDNAKT	IIVQLNKPVE
00BW1616_2	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIVIR	SENITNNAKI	IIVHLNETVD
00BW1686_8	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIIR	SENMTDNVVP	IIVHLNESVE
00BW1759_3	VQCTHEIKPV	VSTQLLLLNGS	LAEE.QIIIR	SENMTNNAKT	IIVHLKKPVQ
00BW1773_2	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIIIR	SENLTNNAKI	IIVHLKDPVN
00BW1783_5	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTNNVKT	IIVHLNESIQ
00BW1795_6	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIIR	SKNLTDNART	IIVHLNESVQ
00BW1811_3	VQCTHGIKPV	VSTQLLLLNGS	LAEE.DIIIR	SENLTNDVKT	IIVHLNESVE
00BW1859_5	VQCPHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENIEDNVKT	IIVHLNESIE
00BW1880_2	VQCTHGIKPV	VATQLLLLNGS	LAEE.EIVIR	FKNITNNAKI	IIVQLNTSVG
00BW1921_1	VQCTHGIKPV	VSTQLLLLNGS	LAEE.GIIIR	SENLTDNAKT	ITVQLDQAVE
00BW2036_1	VQCTHGIRPV	VSTQLLLLNGS	LAEG.EIIIR	SENLAENDKT	IIVHFNESVE
00BW2063_6	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIIIR	SKNITDNVKT	IIVHLNEAVE
00BW2087_2	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTNNAKT	IIVHLNDSVE
00BW2127_2	VQCTHGIKPL	VSTQLLLLNGS	LAQQ.QIMIT	SENLTNNAKI	IIVHLKEAIN
00BW2128_3	VQCTHGIKPV	VSTQLLLLNGS	LAEE.IIIR.	SENLTNNAKT	IIVQLKEPVK
00BW2276_7	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTNNVKT	IIVHLNKSVE
00BW3819_3	VQCTHGIKPV	VSTQLLLLNGG	LAEK.EIIIR	SENLTNNVKT	IIVHLNESVE
00BW3842_8	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIIR	SKNLSDNAKI	IIVHLNESVG
00BW3871_3	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIIR	SENLTNNAKT	IIVHLNESVK
00BW3876_9	IQCTHGIKPV	VSTQLLLLNGS	LAEK.DIIIR	SENLTNNIKT	IIVHLNDSVQ
00BW3886_8	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIIR	SENLTNNAKT	IIVHLNESIE
00BW3891_6	VQCTHGIKPV	VSTQLLSNGS	LSEK.EIIIR	SENLTNNVKT	IIVHLNESVE
00BW3970_2	IQCTHGIKPV	VSTQLLLLNGS	RAEK.EIIIR	SENMTNNAKT	IIVHLNESIE
00BW5031_1	VQCTHGIKPV	VSTQLLLLNGS	LA.E.EIVIR	SENISDNAKT	IIVHLNESVE
96BW01B21	VQCTHGIKPV	VSTQLLLLNGS	LAEE.DIIIR	SENLTNDVKT	IIVHLNESIE
96BW0407	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTDNAKI	IIVHLNESVR
96BW0502	VQCAHGIKPV	VSTQLLLLNGS	VAKG.EIIIR	SENLTNNAKI	IIVQLNKPVK
96BW06_J4	VQCTHGIKPV	VSTQLLLLNGS	LAEE.KIIIR	SGNVTNNAKT	IIVHLNESVE
96BW11_06	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIIIR	FKNITNNAKT	IIVHLNESVE
96BW1210	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENITDNVKT	IIVHLNKSVE
96BW15B03	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIIR	SKNLSNNAYT	IIVHLNDSVE
96BW16_26	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTNNAKT	IIVHLNESVE
96BW17A09	VQCTHGIKPV	VSTRLLLLNGS	LAEE.EIIIR	SENLTNNAKI	IMVQLNESIE
96BWM01_5	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIIIR	SKNITDNVKT	IIVHLNESVE
96BWM03_2	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTDNAKT	IIVHFNESVQ
98BWMC12_2	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTNNVKT	IIVHLNESVE
98BWMC13_4	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIVIR	SENLTNDVKT	IIVHLNQSVQ
98BWMC14_a	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EVVIR	SENLTNNAKT	IIVQLKEPVK
98BWM014_1	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIIIR	SENITNNIKT	IIVHLNEPVE
98BWM018_d	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SKNITNNANT	IIVQLKDPVD
98BWM036_a	IQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTNDVKT	IIVHLKDPID
98BWM037_d	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTNHFRT	IIVQLNQSIE
99BW3932_1	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIVIR	SENLTNNVKT	IIVHLNESIE
99BW4642_4	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIVR	SENLTNDVKT	IIVHLDKPVG
99BW4745_8	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIIVR	SENLTNNAKI	IIVQLKQSVG
99BW4754_7	VQCTHGIKPV	VSTQLLLLNGS	RAEK.EVVIR	AESLTDNAKV	IIVHLKDSVQ
99BWMC16_8	VQCTHGIKPV	VSTQLLLLNGS	LAEE.DIIIR	SKNLTDNAKT	IIVHLNESVN
A2_CD_97CD	VQCAHGIRPV	ASTQLLLLNGS	LAEG.KVMIR	SENITDNAKN	IIVQFNKPPV
A2_CY_94CY	VQCTHGIKPV	ASTQLLLLNGS	LAEGGKIMIR	SENITNNAKN	IIVQFTKPVV
A2D_97KR	VQCTHGIRPV	ASTQLLLLNGS	LAEGNKTIIR	SANITDNNTN	IIVQFTKPVQ
A2G_CD_97C	VQCTHGIRPV	VSTQLLLLNGS	LAEE.EVMIR	SENITDNAKN	IIVQFDKPVE
A_BY_97BL0	VQCTHXIKPV	VSTQLLLLNGS	LAEKX.VMIR	SENITDNVKI	IIVQLTEPVN
A_KE_Q23_A	VQCTHGIKPV	VSTQLLLLNGS	LAEKN.ITIR	SENITNNAKI	IIVQLVQPVV
A_SE_SE659	VQCTHGIKPV	VSTQLLLLNGS	LAKGG.IRIR	SENITNNVKT	ILVQLDKPVN
A_SE_SE725	VQCTHGIKPV	VSTQLLLLNGS	LAEEK.IMIR	SENISDNAKT	IIVQLTEPVT
A_SE_SE753	VQCTHGIKPV	VSTQLLLLNGS	LATK..IMIR	SENITNNAKT	IIVQLVEPVE

A_SE_SE853	VQCTHGIKPV	VSTQLLLLNGS	LAREK.VMIR	SENITNNVKN	IIVQLKEPVE
A_SE_SE889	VQCTHGIRPV	VSTQLLLLNGS	LAETE.VMIR	AENITNNIKN	IIVQFNKSVE
A_SE_UGSE8	VQCTHGIRPV	VSTQLLLLNGS	LAKEE.VRIR	SENISDNAKT	IIVQFTKPVE
A_UG_92UG0	VQCTHGIRPV	VSTQLLLLNGS	LAEGK.VMIR	SENITNNVKN	IIVQLNESVT
A_UG_U455_	VQCTHGIKPV	VSTQLLLLNGS	LAERE.IRIR	SENFTNNAKT	IIVQLVNPVK
AC_IN_2130	VQCTHGIKPV	VSTQLLLLNGS	LAEKE.VIIR	SENITNNVKN	IIVQLAEPVR
AC_RW_92RW	VQCTHGIKPV	VSTQLLLLNGS	LAEEE.IIIR	SENITNNAKT	IIVQLNETVQ
AC_SE_SE94	VQCTHGIKPV	ISTQLLLLNGS	LSETG.VKIR	SENITNNAKT	IIVQLDEAVE
ACD_SE_SE8	VQCTHGIKPV	VSTQLLLLNGS	LAEEE.IIVR	SENLTNNAKI	IIIQLNETVK
ACG_BE_VI1	VQCTHGIKPV	VSTQLLLLNGS	LAEK..VVIR	SENITNNAKT	IIVQFDSPVK
AD_SE_SE69	VQCTHGIKPV	VSTQLLLLNGS	LA.EGKVRIR	SENITDNNTKN	IIVQFTEPVT
AD_SE_SE71	VQCTHGIKPV	VSTQLLLLNGS	LAKEE.VIIR	SENITNNAKN	IIVQFVKPVT
ADHK_NO_97	VQCTHGIKPV	VSTQLLLLNGS	LA..EKVIIR	SKNITDNNTKN	IIVHFNESVQ
ADK_CD_MAL	VQCTHGIKPV	VSTQLLLLNGS	LA.EEEIMIR	SENLTDNNTKN	IIVQLNETVT
AG_BE_VI11	VQCTHGIKPV	VSTQLLLLNGS	LA.EEEIIVR	SENFTNNAKV	IIVQLKEPIE
AG_NG_92NG	VQCTHGIKPV	VSTQLLLLNGS	LA.EGEIVIR	SENLTDNAKV	IIVQLNKTIG
AGHU_GA_VI	VQCTHGIRPV	VTTQLLLLNGS	LA.EGEIIIIR	SENITENTKN	IIVQLNETVE
AGU_CD_Z32	VQCTHGIKPV	VSTQLLLLNGS	LAEKE.VRIR	SENFSDNAKI	IIVQLAKPVN
AJ_BW_BW21	VQCTHGIKPV	VSTQLLLLNGS	IA.EEEIIIIR	SENITNNAKT	IIVQLNNTVE
B_AU_VH_AF	VQCTHGIRPV	VSTQLLLLNGS	LA.EKEIVIR	SDNFTDNAKS	IIVQLNESVE
B_CN_RL42	VQCTHGIRPV	VSTQLLLLNGS	LA.EEEVVIK	FSNFTDNARV	IIVQLNESVE
B_DE_D31_U	VQCTHGIRPV	VSTQLLLLNGS	LA.EEEVVIR	SDNFTDNAKT	IIVQLKESVE
B_DE_HAN_U	VQCTHGIRPV	VSTQLLLLNGS	LA.EKEVVIR	SDNFTDNNTKT	IIVHLNESVE
B_FR_HXB2_	VQCTHGIRPV	VSTQLLLLNGS	LA.EEEVVIR	SVNFTDNAKT	IIVQLNTSVE
B_GA_OYI_	VQCTHGIKPV	VSTQLLLLNGS	LA.EEEVIIR	SSNFTNNAKI	IIVQLNKSVE
B_GB_CAM1_	VQCTHGIRPV	VSTQLLLLNGS	LA.EKEVVIR	SENFTNNAKT	IIVQLKEPVE
B_GB_GB8_C	VQCTHGIRPV	VSTQLLLLNGS	LA.EEKVVIR	SDNFTDNVKT	IIVQLKEAVE
B_GB_MANC_	IQCTHGIRPV	VSTQLLLLNGS	LA.EEEVVLIR	SDNFTDNAKT	IIVHLNESVE
B_KR_WK_AF	VQCTHGIRPV	VSTQLLLLNGS	LA.EEEIVLR	SENFTNNAKT	IIVQLNASVE
B_NL_3202A	VQCTHGIRPV	VSTQLLLLNGS	LA.EEEVVIR	SANFSNNAKT	IIVQLNESVA
B_TW_TWCYS	VQCTHGIRPV	VSTQLLLLNGS	IA.EEEILIK	SENITNNAKT	IIIQLNKSVK
B_US_BC_L0	VQCTHGIKPV	VSTQLLLLNGS	LA.EEEVVIR	SANFSDNAKT	IIVQLKEAVE
B_US_DH123	VQCTHGIRPV	VSTQLLLLNGS	LA.EEEVVIR	SSNFTDNAKI	IIVQLNETVE
B_US_JRCSF	VQCTHGIRPV	VSTQLLLLNGS	LA.EEKVVIR	SDNFTDNAKT	IIVQLNESVK
B_US_MNCG_	VQCTHGIRPV	VSTQLLLLNGS	LA.EEEVVIR	SENFTDNAKT	IIVHLNESVQ
B_US_P896_	VQCTHGIRPV	VSTQLLLLNGS	LA.EEDIVIR	SENFTDNAKT	IIVQLNESVV
B_US_RF_M1	VQCTHGIRPV	VSTQLLLLNGS	LA.EEEVVIR	SENFTDNVKT	IIVQLNASVQ
B_US_SF2_K	VQCTHGIRPI	VSTQLLLLNGS	LA.EEEVVIR	SDNFTNNAKT	IIVQLNESVA
B_US_WEAU1	VQCTHGIRPV	VSTQLLLLNGS	LA.EEDIVIR	SENFTDNAKN	IIVQLNVSIE
B_US_WR27_	VQCTHGIRPV	VSTQLLLLNGS	LA.EEEVVIR	SANFTNNAKT	IIVQLKESVE
B_US_YU2_M	VQCTHGIRPV	VSTQLLLLNGS	LA.EEEIVIR	SENFTNNAKT	IIVQLNESVV
BF1_BR_93B	VQCTHGIKPV	VSTQLLLLNGS	LA.EKDIIIR	SQNISDNAKT	IIVQLNVSPV
C_BR_92BR0	IQCTHGTGPV	VSTQLLLLNGS	LAE.EEIIIR	SKNLTDNVKT	IIVHLNESVE
C_BW_96BW0	VQCTHGIKPV	VSTQLLLLSGS	LAE.EEIVIR	SENLTNNAKI	IIVHLNKTVR
C_BW_96BW1	VQCIHGIKPV	VSTPLLLNGS	LAEK.EIIR	FKIITNNAKT	IIVHLNESVE
C_BW_96BW1	VQCTHGIKPV	VSTQLLLLNGS	LAE.EEIIIR	SENITDNVKT	IIVHLNKSVE
C_BW_96BW1	VQCTHGIKPV	VSTQLLLLNGS	LAEGGEIIIR	SKNLSNNAYT	IIVHLNDSVE
C_ET_ETH22	VQCTHGIKPV	VSTQLLLLNGS	IAEG.ETIIR	FENLTNNAKI	IIVQLNESVE
C_IN_93IN1	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIR	SENLTNNVKT	IIVHLNQSVQ
C_IN_93IN9	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIR	SENLTNNAKT	IIVHLNQSVQ
C_IN_93IN9	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIR	SENLTDNVKT	IIVHLNQSVQ
C_IN_94IN1	VQCTHGIKPV	VSTQLLLLNGS	LSEG.EIIR	SENLTNNVKT	IIVHLNKSVE
C_IN_95IN2	VQCTHGIKPV	VSTQLLLLNGS	LAEG.GIIR	SENLTNNVKT	IIVHLNQPVE
CRF01_AE_C	VQCTHGIKPV	VSTQLLLLNGS	LAE.EDIIIR	SENLTNNAKT	IIVHLNKSVE
CRF01_AE_C	VQCTHGIKPV	VSTQLLLLNGS	LAE.EEIIIR	SEDLTDNAKT	IIVHLNKSIE
CRF01_AE_C	VQCTHGIKPV	VSTQLLLLNGS	LAE.EEIIIR	SENLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKPV	VSTQLLLLNGS	LAE.EEIIIR	SENLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKPV	VSTQLLLLNGS	LAE.EEIIIR	FENLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKPV	VSTQLLLLNGS	LAE.EEIIIR	SENLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKPV	VSTQLLLLNGS	LAE.EEIIIR	SENLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKPV	VSTQLLLLNGS	LAE.EEIIIR	SEDLTNNAKT	IIVHLNKSVE

CRF01_AE_T	VQCTHGIKP	VSTQLLLNGS	LAKE.EIIIR	SENLTNNAKT	IIVHLNKSVK
CRF02_AG_F	VQCTHGIKP	VSTQLLLNGS	LAEEE.VVIR	SENITNNAKN	IIVQLVAPVR
CRF02_AG_F	VQCTHGIKP	VSTQLLLNGS	LAEEE.VVIR	SENITNNAKN	IIVQLVTPVR
CRF02_AG_G	VQCTHGIKP	VSTQLLLNGS	LAEEE.IVIR	SENITNNVKN	IIVQLAKPVR
CRF02_AG_N	VQCTHGIKP	VSTQLLLNGS	LAEGE.VVIR	SENITNNAKT	IIVQLANPVK
CRF02_AG_S	VQCTHGIKP	VSTQLLLNGS	LAEEE.IVIR	SENFTNNAKI	IIVQLHESVK
CRF02_AG_S	VQCTHGIKP	VSTQLLLNGS	LAEGD.IVIR	SENISNNAKT	IIVQLNKPVW
CRF03_AB_R	VQCTHGIKP	VSTQLLLNGS	LA.EEEVVIR	SVNFTDNTKT	IIVQLKEPVE
CRF03_AB_R	VQCTHGIKP	VSTQLLLNGS	LA.EEEVVIR	SVNFTDNTKT	IIVQLKEPVE
CRF04_cpx_	VRCTHGIKP	VSTQLLLNGS	LA.TEEVVIR	SKNITDNTKN	IIVQLAKAVK
CRF04_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.TGGVVIR	SKNFTDNPKN	IIVQLDKAVK
CRF04_cpx_	VQCTHGIKP	VSTQLLLNGS	LS.TEGVVL	SKNFTDNTKN	IIVQLAEAVK
CRF05_DF_B	VQCTHGIKP	VSTQLLLNGS	LA.KEGIIIR	SQNISDNAKN	IIVHLNESVH
CRF05_DF_B	VQCTHGIKP	VSTQLLLNGS	LA.EESIIIR	SQNILDNTKT	IIVHLNESVQ
CRF06_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EGNITIK	TENITDNTKN	IIVQLNQPVE
CRF06_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EEEIIIK	SKNLTNTKI	IIVQLNKSVE
CRF06_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EDEIIIK	SENHTNNAKI	IIVQLNKTVO
CRF06_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EEEIIIK	TENLTDNSKN	IIVQLNKSIE
CRF11_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EEKVKIR	SENFTNNAKT	IIVQFNNTVR
CRF11_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EGEVRIR	SENLTNNAKT	IIVQLNSTVR
D_CD_84ZR0	VQCTHGIRPV	VSTQLLLNGS	LA.EEEIVIR	SENLTNNAKI	IIVHLNQSVE
D_CD_ELI_K	VQCTHGIRPV	VSTQLLLNGS	LA.EEEVIIR	SENLTNNAKN	IIVHLNESVK
D_CD_NDK_M	VQCTHGIRPV	VSTQLLLNGS	LA.EEEIIIR	SENLTNNVKT	IIVQLNASIV
D_UG_94UG1	VQCTHGIKP	VSTQLLLNGS	LA.EEEIIIR	SENLTNNAKI	IIVQLNESVP
F1_BE_VI85	VQCTHGIKP	VSTQLLLNGS	LA.EEGIVIR	SQNISNNAKT	IIVHLNESVQ
F1_BR_93BR	VQCTHGIKP	VSTQLLLNGS	LA.EGEIVIR	SQNISDNAKT	IIVHLNESVQ
F1_FI_FIN9	VQCTHGIRPV	VSTQLLLNGS	LS.EGGIIIR	SQNLSDNAKT	IIVHLNESVQ
F1_FR_MP41	VQCTHGIRPV	VSTQLLLNGS	LA.EEDIIIR	SQNISDNAKT	IIVHLNESVQ
F2_CM_MP25	VQCTHGIKP	VSTQLLLNGS	LA.EEKMIIR	SENISDNTKT	IIVQFKNPVK
F2KU_BE_VI	VQCTHGIRPV	ISTQLLLNGS	LA.EKEIIIR	SGNISDNTKN	IIVQLNETVE
G_BE_DRCBL	VQCTHGIKP	VSTQLLLNGS	LA.EKDIIIS	SENISDNAKV	IIVHLNRSVE
G_NG_92NG0	VQCTHGIKP	VSTQLLLNGS	LA.EEDIRIR	SENFTDNTKV	IIVQLNNSIE
G_SE_SE616	VQCTHGIKP	VSTQLLLNGS	LA.EGKIKVR	SENFTDNTKV	IIVQLNKTVE
H_BE_VI991	VQCTHGIRPV	VSTQLLLNGS	LA.EVEEVIIR	SKNITDNTKN	IIVQLNEPVQ
H_BE_VI997	VQCTHGIKP	VSTQLLLNGS	LA.EGQVIIR	SKNISDNTKN	IIVQLDSPIE
H_CF_90CF0	VQCTHGIRPV	VSTQLLLNGS	LA.BEQIIIR	TKNISDNTKN	IIVQLKTPVN
J_SE_SE702	VQCTHGIKP	VSTQLLLNGS	VA.EGDIIIR	SENISDNAKN	IIVQLNDTVE
J_SE_SE788	VQCTHGIKP	VSTQLLLNGS	IA.EGDIIIR	SENISDNAKN	IIVQLNKTVE
K_CD_EQTB1	VQCTHGIKP	VSTQLLLNGS	LA.EEEIIIR	SEDITKNNTKN	IIVQLNEAVE
K_CM_MP535	VQCTHGIKP	VSTQLLLNGS	LA.EEEIIIR	SENITDNTKN	IIVQLNETVQ
N_CM_YBF30	VQCTHGIKP	ISTQLILNGS	LNTDGIVIR.	...NDSHSN	LLVQWNETVP
O_CM_ANT70	VTCTHGIRPT	VSTQLILNGT	LS.KGKIRMM	AKDILEGGKN	IIVTLNSTLN
O_CM_MVP51	VTCTHGIKPT	VSTQLILNGT	LS.REKIRIM	GKNITESAKN	IIVTLNTPIN
O_SN_99SE_	VTCTHGIKPT	VSTQLILNGT	LS.EGNIRIM	GKNISDNMKN	IIVTLNSTIN
O_SN_99SE_	VTCTHGIRPT	VSTQLILNGT	IS.EGKIRIM	GKNISDTGKN	IIVTINSTIN
U_CD___83C	VQCTHGIRPV	VSTQLLLNGS	LSEE.EVIIR	SENITNNAKT	IIVQLNETVK

00BW0762_1	IVCTRPNN.	.TRRSVRIG.	.PGQTFYATGDIIGN	IRQAHCNISK
00BW0768_2	IECTRPNN.	.TRKSIRIG.	.PGQTFYATGDIIGD	IREAHCNINK
00BW0874_2	IVCTRPNN.	.TRKSIRIG.	.PGQTFYATGDVIGD	IRQAHCNTSE
00BW1471_2	IVCTRPNN.	.TRKSVRIG.	.PGQTFYATGDIIGD	IRQAHCNISN
00BW1616_2	IVCTRPNN.	.TRKSMRIG.	.PGQTFYATGDIIGN	IREAHCNISK
00BW1686_8	INCTRPNN.	.TRKSIRIG.	.PGQTFYATGAIIGD	IRQAYCTVNA
00BW1759_3	IVCTRPNN.	.TRRSVRIG.	.PGQTFYARGDIIGN	IRQAHCNISR
00BW1773_2	ITCTRPNN.	.TRKSIRIG.	.PGQTFYATGDIIGD	IRQAHCNISA
00BW1783_5	INCTRPNN.	.TRKSVRIG.	.PGQTFYATGDIIGD	IRQAHCNISE
00BW1795_6	IVCTRPNN.	.TRKSVRLG.	.PGQAFYATGDIIGD	IRKAYCTINE
00BW1811_3	IVCTRPNN.	.TRKSIRIG.	.PGQAFFATGEIIGD	IRQAHCNISA
00BW1859_5	IVCIRPNN.	.TRKSIRIG.	.PGQTFYATGDIIGN	IREAHCNITR
00BW1880_2	IVCTRPNN.	.TKKSMRIG.	.PGQTFYATGDIIGD	IRQAHCNISE
00BW1921_1	IECTRPNN.	.TRKSIRIG.	.PGQTFYATGDIIGN	TRQAHCNVSA
00BW2036_1	IECIRPNN.	.TRKSIRIG.	.PGQVIFYATGDIIGD	IREAHCNITE
00BW2063_6	IVCTRPNN.	.TRKSVRIG.	.PGQTFYATGEVIGD	IREAHCNISE
00BW2087_2	IVCTRPNN.	.TRKSIRIG.	.PGQAFYATDAIIGD	IRQAHCNISR
00BW2127_2	IVCTRPNN.	.TRTSIRIG.	.PGHSFFATNGIIGD	IRQAHCSISK
00BW2128_3	INCTRPNN.	.TRKSIRIG.	.PGQAFYATGDIIGD	IRQAHCNISK
00BW2276_7	IVCVRPNN.	.TRKSVRIG.	.PGQTFYATGNIIGD	IREAHCNISE
00BW3819_3	IKCTRPNN.	.TRRSVRIG.	.PGQAFYTN.DIIGD	IRLAHCNISK
00BW3842_8	IVCTRPNN.	.TRKSIRIG.	.PGQTFYAAGDIIGN	IRQAHCNISE
00BW3871_3	ITCTRPNN.	.TRESIRIG.	.PGQTFYATGDIIGD	IRKAYCNISI
00BW3876_9	IVCTRPNN.	.IRKSVRIG.	.PGQAFYATGDIIGD	IREAYCNING
00BW3886_8	IVCVRPNN.	.TRKSIRIG.	.PGQTFYATGEIIGN	IRQAYCSISG
00BW3891_6	IECTRPNN.	.TRRSIRIG.	.PGQTFYATGEIIGD	IRQAYCTINE
00BW3970_2	IECIRPNN.	.TRKSIRIG.	.PGQTFYATNGMIGD	IRQAHCNISG
00BW5031_1	IECRRPNN.	.TGKSVRIG.	.PGQTFYATGGIIGE	IRRAHCDING
96BW01B21	INCTRPNN.	.TRKSIRIG.	.PGQTFYAAGEIIGK	IRLAYCNISE
96BW0407	IECTGPNN.	.TRKSMRIG.	.PGQTFYATGEIVGD	IRQAHCNISE
96BW0502	IVCVRPNN.	.TRKSVRIG.	.PGQTFYATGEIIGD	IRQAYCIINK
96BW06_J4	IVCTRPNN.	.TRKSIRIG.	.PGQTFYAT.DIIGD	IRQAYCNVSK
96BW11_06	IVCIRPNN.	.TRKSVRIG.	.PGQTFYATEAIIGN	IREAHCNISE
96BW1210	IVCTRPNN.	.TRKSIRIG.	.PGQTFYATGDIIGD	IRQAHCNISK
96BW15B03	IVCTRPNN.	.TRKGIRIG.	.PGQTFYATENIIGD	IRQAHCNISA
96BW16_26	IVCIRPNN.	.TRKSIRIG.	.PGQTFYATGDIIGD	IRQAHCIING
96BW17A09	IVCTRPNN.	.TRKSTRIG.	.RGQTFYAMGRIIGD	IRQAHCNISG
96BWM01_5	IECTRPNN.	.TRRSVRIG.	.PGQAFYATGDIIGD	IRAAHCNISE
96BWM03_2	INCTRPNN.	.TRKSVRIG.	.PGQAFYATGDIIGD	IRKAYCNISK
98BWMC12_2	IVCTRPNN.	.TRKSMRIG.	.PGQIFYATGDIIGD	IREAHCNISK
98BWMC13_4	IECTRPNN.	.TRKSMRIG.	.PGQAFYATGEIIGN	IRQAYCNINE
98BWMC14_a	IVCTRPNN.	.TRKSIRIG.	.PGQTFYATGDIIGD	IRQAHCNISE
98BWM014_1	IVCTRPNN.	.TRTSIRIG.	.PGQTFYATGDIIGD	IRQAHCNISE
98BWM018_d	ILCVRPSNN.	.TRKSVRIG.	.PGQTFYATGDIIGD	IRQAHCNISA
98BWM036_a	IVCTRPNN.	.TRKSVRIG.	.PGQTFYATGDIIGD	IRQAHCNISK
98BWM037_d	INCTRPNN.	.TRKSIRIG.	.PGQAFYATNDIIGD	IRQAHCNISE
99BW3932_1	IVCIRPNN.	.TRKSIRIG.	.PGQTFYATGAIIGN	IREAYCNISG
99BW4642_4	IVCIRPNN.	.TRKSIRIG.	.PGQTFYATGDIIGN	IKEAYCNIKE
99BW4745_8	IECIRPNN.	.TRKSIRIG.	.PGQTFYATGEIIGD	IRKAHCTINK
99BW4754_7	INCTRPNN.	.TRKSMRIG.	.PGQTFYATGEIIGD	IRQAHCNISR
99BWMC16_8	ITCTRPNN.	.TRKSIRIG.	.PGQTFYATGDIIGD	IRQAHCSINK
A2_CD_97CD	INCTRPNN.	.TRKSIRIFG.	.PGQAFYTNNIIGD	IRQAHCNISI
A2_CY_94CY	ITCIRPNN.	.TRKSIRIFG.	.PGQAFYTN.EIIGD	IRQAHCNINK
A2D_97KR	INCTRPNN.	.QRRSVRIG.	.PGRAFYTRQ	TYTR.QAKGD	IRQAQCNISS
A2G_CD_97C	ITCIRPNN.	.TRKSIRIFG.	.PGQAFYTN.SIIGD	IRQAYCNISK
A_BY_97BL0	ITCIRPNN.	.TRTSIRIG.	.PGQTFYATGDVIXD	IRKAYCNVSR
A_KE_Q23_A	IKCIRPNN.	.TRKSIRIG.	.PGQAFYATGDIIGD	IRQAHCNVTR
A_SE_SE659	ITCIRPYHN.	.TRTRIHIH.	.PG.RSFYTGDIIGD	IRQAHCTVNR
A_SE_SE725	INCTRPNN.	.TRTSIRIG.	.PGQAFYATGDITGD	IRQAHCTVSR
A_SE_SE753	INCTRPNN.	.TRTSVPIG.	.PGKVIFYATGEIIGD	IRQAHCNVSK

A_SE_SE853	INCTRPNN.	.TRKSIRIG.	.PGQAFYATG	EVIGD	IRQAHCNVSR
A_SE_SE889	IICIRPNN.	.TRKSIRIG.	.PGQAFYATG	DIIGD	IRQAYCDVNR
A_SE_UGSE8	IICTRPNN.	.TRKSIRIG.	.PGQAFYGMG	DIIGD	IRKAHCNVSR
A_UG_92UG0	INCTRPNN.	.TRRSVRIG.	.PGQTFYATG	DIIGD	IRQAHCNVSG
A_UG_U455	INCSRPNYTR	KNIRRSYIG.	.SGQAFYVTG	KIIGD	IRQAHCNVSR
AC_IN_2130	INCTRPNN.	.TRTSIRIG.	.PGQTFYTS.	NIIGD	IRQAHCNVSR
AC_RW_92RW	INCSRPNNN.	.TRKSVHIG.	.PGQAFYATG	DVIGD	IRQAYCTVNG
AC_SE_SE94	INCTRPNN.	.TRRSVHIG.	.PGQAFYATG	DITGD	IRKAHCIVNG
ACD_SE_SE8	INCTRPNN.	.TRNSIRIG.	.PGQAFYATG	AITGD	IRQAHCNVSR
ACG_BE_VI1	INCTRPNN.	.TRKSVRIG.	.PGQTFYATG	DIIGD	IRQAHCNISG
AD_SE_SE69	INCTRPNNNT	.RK.SVRIG.	.PGQALYVTG	GII..G...D		IRQAFCEVNR
AD_SE_SE71	INCTRPNN.	.TRKSVHMG.	.PGKVFYATG	DIIGD	IRQAHCNVSK
ADHK_NO_97	INCTRIANNT	RKS..IHIG.	.PGQAFYAAE	PVI..G...D		IRQAHCNISE
ADK_CD_MAL	INCTRPNNNT	.RR.GIHFG.	.PGQALYTTG	IVG.....D		IRRAYCTINE
AG_BE_VI11	INCTRPNNNT	RKSIGLPGG.	...QAFYATG	DII..GD...		IRQAHCNVSG
AG_NG_92NG	INCTRPNNNT	RKSIRIGPG.	...QAFYATG	EII..G....	
AGHU_GA_VI	INCTRPNNNT	RKG..IRIG.	.PGRVIYATS	AIT..G...D		IRQAHCNISK
AGU_CD_Z32	ITCMRPNNY.	.TRKSIHIG.	.PGRALYPEG	DIIGD	IRQAHCNVSR
AJ_BW_BW21	IKCVRPANNT	RKGIHTGPG.	...QVLYATG	AVV..GD...		IRQAHCNVSR
B_AU_VH_AF	IHCMRPNNNT	.RK.GIYVG.	.PGRHIYATE	KIV..G...D		IRQAHCNISR
B_CN_RL42	IKCIRPNNNT	.RK.SIHLG.	.PGKAWYTTG	QII..G...D		IRQAHCNLSS
B_DE_D31_U	INCTRPNNYT	.SK.RIRIG.	.ARRAFYTKG	KII..G...D		IRQAHCNISG
B_DE_HAN_U	INCTRPNNNT	.RK.GIHIG.	.PGRAVYTTG	RIV..G...D		IRLAHCNISR
B_FR_HXB2	INCTRPNNNT	.RK.RIRIQR	GPGRAFTIG	KIG.....N		MRQAHCNISR
B_GA_OYI	INCTRPNNNT	.RN.RISIG.	.PGRAFHTTK	QII..G...D		IRQAHCNLSR
B_GB_CAM1	INCTRLNNNT	.RK.SIAIG.	.PGRTVYATD	RII..G...D		IRQAHCNLSS
B_GB_GB8_C	INCTRPNNNT	.RK.GIYMG.	.PGRRFYTTG	RII..G...D		IRQAHCNISK
B_GB_MANC	INCTRPNNNS	.RK.SIYIG.	.PGRRFHVTR	AVT..G...D		IRQAHCNISK
B_KR_WK_AF	INCTRLNNNT	.RK.SIRIG.	.PGSTFYATG	AII..G...D		IRQAHCNISR
B_NL_3202A	INCTRPNNNT	.RK.GIHIG.	.PGKAFYATG	QII..G...D		IRQAHCNLSR
B_TW_TWCYS	INCTRPNNIS	KRR.SMHIG.	.TGRVFTYTQ	..I..G...N		IRQAHCNLSK
B_US_BC_L0	INCTRPNNKT	.RK.RITTG.	.PGRVYTTG	EIV..G...D		IRQAHCNLSR
B_US_DH123	INCTRPNNNT	.RK.GITLG.	.PGRVFTYTG	EIV..G...D		IRKAHCNISK
B_US_JRCSE	INCTRPNNNT	.RK.SIHIG.	.PGRAFYTTG	EII..G...D		IRQAHCNISR
B_US_MNCG	INCTRPNNYK	.RK.RIHIG.	.PGRAFYTTK	NII..G...T		IRQAHCNISR
B_US_P896	INCTRPNNNT	.RR.RLSIG.	.PGRAFYARR	NII..G...D		IRQAHCNISR
B_US_RF_M1	INCTRPNNNT	.RK.SITKG.	.PGRVIYATG	QII..G...D		IRKAHCNLSR
B_US_SF2_K	INCTRPNNNT	.RK.SIYIG.	.PGRAFHTTG	RII..G...D		IRKAHCNISR
B_US_WEAU1	INCTRPNNNT	.RK.KITLG.	.PGRVLYTTG	EII..G...D		IRRAHCNLSR
B_US_WR27	INCTRPNNKI	.RR.RIHIG.	.PGRAFYTDR	..V..G...D		IRQAYCNISG
B_US_YU2_M	INCTRPNNNT	.RK.SINIG.	.PGRALYTTG	EII..G...D		IRQAHCNLSK
BF1_BR_93B	INCTRPNNNT	RKS..IPIG.	.PGRAFYTTG	EII..G...D		IRKAHCNVSG
C_BR_92BR0	INCTRPNN.	.TRKSIRIG.	.PGQAFYATG	EIIGD	IRQAHCNISR
C_BW_96BW0	IVCTRPNN.	.TRRSVRIG.	.PGQTFYATG	EIIGD	IR.AHCNISE
C_BW_96BW1	IVCIRPNN.	.TRKSVRIG.	.PGQTFYATE	AIIGN	ISEAHCNISE
C_BW_96BW1	IVCTRPNN.	.TRKSIRIG.	.PGQTFYATG	DIIGD	IRQAHCNISK
C_BW_96BW1	IVCTRPNN.	.TRKGIRIG.	.PGQTFYATE	NIIGD	IRQAHCNISA
C_ET_ETH22	ITCTRPNN.	.TRESIRIG.	.PGQTFYATG	DIIGD	IRQAHCNISE
C_IN_93IN1	IVCTRPNN.	.TRKSIRIG.	.PGQTFYATG	DIIGD	IRQAHCNISR
C_IN_93IN9	IVCTRPNN.	.TRKSIRIG.	.PGQTFYATG	EIIGD	IRQAHCNISK
C_IN_93IN9	IECVRPNN.	.TRESIRIG.	.PGQTFYATG	EIIGD	IRQAHCNISA
C_IN_94IN1	IVCTRPNN.	.TRKSIRIG.	.PGQTFYATG	EIVGN	IRQAHCNISK
C_IN_95IN2	IMCTRPDNN.	.TRKSIRIG.	.PGQTFYATG	DIIGD	IRQAHCNISE
CRF01_AE_C	INCTRPFFKN.	.MRTSARIG.	.PGQVFKYTG	SITGD	IRKAYCEING
CRF01_AE_C	INCTRPFFKK.	.VRISARIG.	.PGRVFHTTG	NINGD	IRKAYCEINK
CRF01_AE_C	INCTRPFFKK.	.MRTSVRIG.	.PGRVFKYTG	SITGD	IRKAYCEING
CRF01_AE_T	INCTRPNN.	.MRTSMRIG.	.PGQVFKYTG	SITGD	IRKAYCEING
CRF01_AE_T	INCTRPNN.	.TRTSITMG.	.PGQVFKYTG	DIIGD	IRKAYCEING
CRF01_AE_T	INCTRPFFYN.	.KRTRTSIG.	.QGRVLYRTG	DITGN	IGKPYCEING
CRF01_AE_T	INCTRPSPGK.	.EEKRMTIG.	.PGKVFYSTG	KITGD	IRKAYCVING
CRF01_AE_T	INCTRPNN.	.TRTSITIG.	.PGRVFKYTG	DIIGN	IRKAYCEING

203

00BW0762_1	TKWNKTLRSRI	GEKLKEHFPN	...KTIRFN.	.SSAGGDLEI	TTHSFNCRGE
00BW0768_2	EKWNSTLQGV	REKLEKHFPN	...KNITFE.	.PSSGGDLEI	TTHSFNCRGE
00BW0874_2	QKWNKTLQV	GKKLAEHFPN	...KTIIFN.	.SSSGGDLEI	TTHSFNCGGE
00BW1471_2	SNWNSTLQV	ARKLEKYFPN	...KTIKFO.	.PSSGGDLEI	TTHSFNCRGE
00BW1616_2	TKWENTLHMV	SEKLKENFPN	...KTIVFN.	.SSAGGDLEI	TTHSFNCRGE
00BW1686_8	SKWNETLQKV	KKKLGEHFPD	...KNITFE.	.SPSGGDLEI	TTHTFNCRGE
00BW1759_3	GEWNETLMEV	SKELRKYFPN	...KNITFA.	.PSSGGDLEI	TTHSFNCRGE
00BW1773_2	AQWNKTLQEV	GAKLEEHPN	...KTIKFN.	.QSSGGDLEI	TTHSFICRGE
00BW1783_5	KAWNKTLLHRV	SEXLKEHFPN	...KTIKFT.	.SPSGGDLEI	IQHTFNCGGE
00BW1795_6	SKWITTLHRV	SEKLKEHFPN	...KAINFT.	.QPKGGDLEI	TTHSFNCRGE
00BW1811_3	TNWNKTLQMV	SEKLQOHFPN	...KTIKFD.	.KHSGGDLEI	TTHSFNCRGE
00BW1859_5	EEWNKTLQGV	EEKLKEHFPN	...KKITFK.	.PSSGGDLEV	TTHSFNCGGE
00BW1880_2	DVWRKTLFNV	SNKLKEYFPK	...RNITFN.	.SSTGGDLEI	TTHSFNCRGE
00BW1921_1	GAWNKTLLQKV	GEELRKHFPN	...KTIQFN.	.SSSGGDLEI	TTHTFNCRGE
00BW2036_1	SAWNRTLHRV	SKKLREHFPN	...TTIKFO.	.PASGGDLEI	TTHSFNCRGE
00BW2063_6	EKWNKTLYRV	SEKLKEYFPN	...KTIKFD.	.QPTGGDLEI	TKHSFNCRGE
00BW2087_2	DKWNKTLQV	GEKLAEHFPN	...KTIKFA.	.PSSGGDLGI	TTHSFNCRGE
00BW2127_2	DAWNKTLQV	GKKLEEFYFPN	...KTIKFA.	.NSSGGDLEI	TTHSFNCGGE
00BW2128_3	EEWNKTLREV	KGKLGKHFN.	...KTIMFA.	.PSSGGDLEI	TAHSFNCRGE
00BW2276_7	NQWNKTLQV	GKKLKEHFN.	...KTIKFE.	.QSSGGDLEI	TMHSFNCRGE
00BW3819_3	KAWNKTLLQV	VKKLKEHFPN	...RTIKFT.	.PPPGGNLEI	TTHSFNCRGE
00BW3842_8	GNWTKTLQV	SRKLRQIFNK	...SNIEFK.	.PHSGGDPEI	TTHSFNCRGE
00BW3871_3	HEWNKTLQV	KKKLGEHFPN	...KTIKFO.	.PSSGGDLEI	ATHTFNCRGE
00BW3876_9	SDWNRTLQV	KNKLGEHFPN	...TVIKFE.	.PSSGGDLEI	TTHSFNCRGE
00BW3886_8	GNWTETLRRV	KNKLGEHFPN	...KTITFG.	.PSSGGDLEI	TTHSFNCRGE
00BW3891_6	STWNRTLQEV	SRKLVERFPN	...KTIRFO.	.PPSGGDLEI	TTHSFNCRGE
00BW3970_2	ADWNRTLQV	GRKLAGYFPN	...KTISFO.	.PSSGGDLEI	TTHSFNCGGE
00BW5031_1	TKWTETLQKI	SEKLRGYFK.	...KTIIFA.	.PSSGGDPEI	TTHSFNCRGE
96BW01B21	EVWKKTLQV	GRKLKEHFPN	...KTIQFO.	.PPSGGDLEV	TTHSFNCRGE
96BW0407	KDWNKTLHRV	RKKLAEHFS.	...KNITFK.	.PSSGGDLEI	TTHSFNCGGE
96BW0502	TEWNSTLQV	SKKLEEHFSK	...KAIKCE.	.PSSGGDLEI	TTHSFNCRGE
96BW06_J4	TNWNKTLQV	KGELRKHFH.	...KNITFO.	.PASGGDLEI	TTHTFNCRGE
96BW11_06	SQWNKTLHRV	IEKLKEHFPN	...KTIGFS.	.QAAGGDLEI	TTHSFNCGGE
96BW1210	GAWNKTLQV	GKKLKEHFPN	...KTIRFK.	.ESSGGDLEI	TTHSFNCGGE
96BW15B03	GEWNKAVQV	SAKLREHFPN	...KTIEFO.	.PSSGGDLEI	TTHSFNCRGE
96BW16_26	SEWKRTLQV	SEKLGKHFN	...KTIKFA.	.PHSGGDLEI	TTHVLNCRGE
96BW17A09	..WNNTLQV	VKKLRKHFPN	...KTITFA.	.PPSGGDLEI	TTHSFNCGGE
96BWM01_5	SKWNKILYRV	SEKLKEHFPN	...KTIQFG.	.QPIGGDLEI	TTHSFNCRGE
96BWM03_2	GEWAKVMQV	TGKLKEHFP.	...KNITFO.	.PPSGGDLEI	TTHSFNCRGE
98BWMC12_2	QKWNKTLQV	GKKLAEYFPN	...RTIAFN.	.SSARGDLEI	ATHSFNCRGE
98BWMC13_4	SLWNETLYKV	SEKLKEYFN.	...TTIEFO.	.QPAGGDLEI	TTHSFNCRGE
98BWMC14_a	EEWNNSLQV	AKKLREHFPN	...KTIAFN.	.SSSGGDLEI	TTHTFNCRGE
98BWM014_1	GNWTKTLHRV	GEKLKEHFPN	...KTIKFA.	.PPSGGDLEI	IMHSFNCGGE
98BWM018_d	DDWKSTLQNV	SEKLRRHFPN	...KTIVFN.	.SPSGGDLEI	ITHSFNCEGE
98BWM036_a	ERWNKTLQEV	GEKLERHFPN	...KTIEFK.	.PSSGGDLEI	TTHSFNCRGE
98BWM037_d	KKWYKALHGV	REKLKVLFPN	...KNISFO.	.PAAGGDLEV	TTHSFNCKGE
99BW3932_1	DAWNKTLQV	GRKLKEYFPG	...STIRFA.	.PHSGGDLEI	TTHSFNCRGE
99BW4642_4	SEWNRTLQV	GEKLGKYFPS	...KTIKFN.	.SSSGGDLEI	TTHSFNCRGE
99BW4745_8	KAWNNTLQEV	GRKLAEHFPN	...KTIKFO.	.PHSGGDPEI	TMHSFTCGGE
99BW4754_7	SQWNKTLYEV	SEKLREKFPN	...KTIQFN.	.SSTGGDLEI	TTHSFNCGGE
99BWMC16_8	EAWNKTLLRV	SKKLREHFPN	...KTIIFD.	.KSSGGDLEI	TTHSFNCGGE
A2_CD_97CD	TEWNATLKKV	VEQLREHFPN	...KTIIFN.	.SSSGGDLEI	TTHSFNCGGE
A2_CY_94CY	TLWNTLQKV	AEQLREKFPK	...KTIIFT.	.NSSGGDPEI	TTLFSNFCAGE
A2D_97KR	RQWNTLQKV	AEQLRKYFSN	...KTIIFT.	.NSSGGDIEI	TTHSVNCGGE
A2G_CD_97C	AGWNDILQV	AEQLGKHFSG	...KNITFA.	.NSSGGDLEI	TTHSFNCGGE
A_BY_97BL0	AAXNSTLQKI	STQLRKYFNN	...KTIIFK.	.SSTGXDLEV	TTHSFNCGGE
A_KE_Q23_A	SRWNKTLQEV	AEKLRTYFGN	...KTIIFA.	.NSSGGDLEI	TTHSFNCGGE
A_SE_SE659	SEWNNTLQV	AKQLRTYFGN	...KTIIFT.	.NSSGGDLEI	TTHSFNCKGE
A_SE_SE725	SSWNKTLQDI	VTQLRVYWN.	...RTIIFN.	.SSSGGDLEI	TTHSFNCGGE
A_SE_SE753	SKWNATLQKV	AIKLREYFDD	...KTIIFT.	.KPSGGDLEI	TTHSFNCGGE

A_SE_SE853	AKWNKTLHEV	AKQLRTYFNN	...KTIIFT.	.NSSGGDLEI	TTHTVNCGGE
A_SE_SE889	TEWNEALQKV	VNQLKTHFKN	...KTIIFN.	.SSSGGDLEI	TTHSFNCGGE
A_SE_UGSE8	SKWNETLKKV	AIQLRKYWN.	...TTIIFT.	.NSSGGDLEI	TTHSFNCGGE
A_UG_92UG0	SQWNKTLHQV	VEQLRKYWNN	...NTIIFN.	.SSSGGDLEI	TTHSFNCAGE
A_UG_U455_	RDWNRTIQQV	AEQLKKKFNN	...KTIIFA.	.SSSGGDIEI	TTHSFNCGGE
AC_IN_2130	AEWNKALNKI	GKQLRKYFVN	...KTIKFA.	.NSSGGDLEI	TTHSFNCEGE
AC_RW_92RW	TKWNRTLQKV	AEKLSHYFEN	..ITTIIFK.	.NSSGGDLEI	TTHSFNCGGE
AC_SE_SE94	TKWNKTLHKV	VTQLRKYFVN	...KPIIFT.	.PSSGGDVEV	TTHSFNCRGE
ACD_SE_SE8	SEWNKTLQQV	AKKLGDP LNK	...TEIIFK.	.PPSGGDLEI	TTHSFNCGGE
ACG_BE_VI1	KEWNKTLQAV	GKKLAEYYPN	...KTINFT.	.QASGGDLEI	VTHSFNCGGE
AD_SE_SE69	TKWDKTLREV	AIQLKHYYG.	..NKTIVIFAN	.SS.GGDIEI	TTHSFNCRGE
AD_SE_SE71	SAWNNTLQQV	VIQLRRYFNN	...KTIIFT.	.NSSGGDLEI	TTHSFNCGGE
ADHK_NO_97	GSWMKTLHKV	ATQLXQHFS.	..NKTIIFNA	.SA.GGDIEI	TTHSFNCAGE
ADK_CD_MAL	TEWDKTLQQV	AVKLGSLLN.	..KTKIIFNS	.SS.GGDPEI	TTHSFNCRGE
AG_BE_VI11	KDWGKMLQEV	SRQLKKFFNN	...KTIFFNS	.SA.GGDLEI	TTHSFNCRGE
AG_NG_92NG	QEWQEMLQKV	QAQLEQVFN.	...KSITFNS	.SA.GGDLEI	TTHSFNCRGE
AGHU_GA_VI	EQWNRTLERV	KEKLGRHFK.	..NKTITFKP	.AS.GGDPEV	TMHIFNCRGE
AGU_CD_Z32	KEWSETLSKV	AAQLRKHFVN	T.RTDIIFA.	.NSSGGDVEI	TTHSFNCGGE
AJ_BW_BW21	KNWTDTLHKV	TAKLKEYFN.	...TTIEFQP	.AS.AGDLEI	MTHTFNCGGE
B_AU_VH_AF	TNWTSLVRQI	AVKLRRERFK.	..NKTIVFNH	.SS.GGDPEI	VRHSFNCGGE
B_CN_RL42	TKWNNTLKQI	TKKLREQFG.	..NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
B_DE_D31_U	AKWDSTLRQI	VKKLRERFG.	..NKTIVFNQ	.SS.GGDPEI	VTHSFNCGGE
B_DE_HAN_U	ARWNKTLNQI	FRKLREIRQF	.ENKTIVFNR	.SS.GGDPEI	VMHSFNCGGE
B_FR_HXB2	AKWNNTLKQI	ASKLREQFG.	..NNKTIIFKQ	.SS.GGDPEI	VTHSFNCGGE
B_GA_OYI_	ATWEKTLQI	ATKLRLKQFR.	.N.KTIAFDR	.SS.GGDPEI	VMHSFNCGGE
B_GB_CAM1	TKWNNTLKQI	VTKLKEQFG.	..NKTIIFNQ	.SS.GGDPEI	VMHSFNCGGE
B_GB_GB8_C	EKWNNTLHQI	VIELRKQFR.	..NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
B_GB_MANC_	AKWEKTLKQI	VEKLREKFG.	..NKTIIFNQ	.SS.GGDPEI	VTHSFNCGGE
B_KR_WK_AF	EKWNDTLKQL	VIKLGEQFG.	.NSNIIVFKQ	.SS.GGDPEI	VMHSFICGGE
B_NL_3202A	AKWNNTLKQI	VSKLRKQFG.	..NKTIVFSQ	.PL.GGDPEI	VMHSFNCGGE
B_TW_TWCYS	AEWNNTLPQI	VKKFREQFG.	..NKTIVFNQ	.SS.GGDLEI	VMHSFNCGGE
B_US_BC_L0	AKWNDTLRQI	VIKLRL.EQF	.ENKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
B_US_DH123	VKWHNTLKR	VEKLREKFE.	..NKTIVFNK	.SS.GGDPEI	VMHSFNCGGE
B_US_JRCSE	AQWNNTLKQI	VEKLRL.EQF	.NNKTIVFTH	.SS.GGDPEI	VMHSFNCGGE
B_US_MNCG_	AKWNDTLRQI	VSKLKEQFK.	..NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
B_US_P896_	AKWNNTLQOI	VIKLRL.EKF	.RNKTIAFNQ	.SS.GGDPEI	VMHSFNCGGE
B_US_RF_M1	AQWNNTLKQV	VTKLRL.EQF	.DNKTIVFTH	.SS.GGDPEI	VLHSFNCGGE
B_US_SF2_K	AQWNNTLEQI	VKKLREQFG.	..NNKTIVFNQ	.SS.GGDPEI	VMHSFNCRGE
B_US_WEAU1	TSWNNTLKQI	VEKLREIKQF	.KNKTIVFKQ	.SS.GGDPEI	VMHSFNCGGE
B_US_WR27_	TKWKNTLEKI	VAKIREIKQF	.KNKTIVFNH	.SS.GGDPEI	VMHSFNCGGE
B_US_YU2_M	TQWENTLEQI	AIKLKEQFG.	..NNKTIIFNP	.SS.GGDPEI	VTHSFNCGGE
BF1_BR_93B	TKWNETLEKV	RAKLKPHFPN	...ATIKFNS	.SS.GGDLEI	TMHSFNCRGE
C_BR_92BR0	TAWNKTLEQV	GKKLAEHFPN	...KAIFKA.	.KHSGGDLEI	TTHSFNCRGE
C_BW_96BW0	RDWNTLNRV	SKKLAEHFPN	...KTIEFK.	.PSSGGDLEI	TTHSFNCRGE
C_BW_96BW1	SQWNNTLQRV	SEKLKEHFPN	...KTIKFN.	.QPAGGDLEI	TTHSFNCGGE
C_BW_96BW1	GAWNNTLQV	GKKLKEHFPN	...KTIRFK.	.ESSGGDLEI	TTHSFNCGGE
C_BW_96BW1	GEWNKAVQV	SAKLREHFPN	...KTIEFQ.	.PSSGGDLEI	TTHSFNCRGE
C_ET_ETH22	EKWNKTLQKV	KEKLQKHFPN	...KTIEFK.	.PSSGGDLEI	TTHSFNCGGE
C_IN_93IN1	DKWNETLQV	GKKLAEHFHN	...KTIKFA.	.SSSGGDLEI	TTHSFNCRGE
C_IN_93IN9	ENWTDTLQV	SKKLAEHFPN	...KTIKFD.	.SPSGGDLEI	TTHSFNCRGE
C_IN_93IN9	DRWNETLQV	GEKLAEHFPN	...KTIKFA.	.PSSGGDLEI	TTHSFNCRGE
C_IN_94IN1	RDWNETLQV	SEKLAKHFPN	...KTIKFA.	.PSSGGDLEI	TTHSFNCRGE
C_IN_95IN2	DKWNETLQV	SKKLAEHFPN	...KTIIFN.	.SSSGGDLEI	TTHSFNCRGE
CRF01_AE_C	TKWNETLKQV	TKKLREHFPN	...KTIIFQ.	.PSSGGDPEI	TMHHFNCRGE
CRF01_AE_C	TKWKETLKQV	TRKLREHLNG	...TMTISFR	.PSSGGDPEI	TMHHFNCRGE
CRF01_AE_C	TKWNETLQOI	IRKLEEHFPN	...KTIQFKP	.PSSGGDLEI	TMHHFNCRGE
CRF01_AE_T	TKWNKVLKQV	TEKLKEHFPN	...KTIIFQ.	.PPSGGDLEI	TMHHFNCRGE
CRF01_AE_T	TKWNEVLKQV	AGKLKEHFPN	...KTIIFK.	.PPSGGDLEI	TMHHFNCRGE
CRF01_AE_T	TKWNKVLNQV	TEKLKEHFPN	...RNISFQ.	.PPSGGDLEI	TMHHFICRGE
CRF01_AE_T	TKWNETLKQV	AGKLREHFPN	...KTIIFQ.	.PPSGGDLEI	TMHHFNCRGE
CRF01_AE_T	TKWNKVLKQV	TEKLKEHFN.	...KTIIFQ.	.PPSGGDLEI	TMHHFNCRGE

CRF01_AE_T	TKWNKVLKQV	TEKLKEHFN.	...KTIIFQ.	.PPSGGDLEI	TMHFNCRGGE
CRF02_AG_F	SEWNRTLQQV	ATQLRKHFN.	...KTIIFA.	.NSSGGDIEI	TTHSFNCGGE
CRF02_AG_F	SKWNNTLQQV	AIQLRKHFN.	...TTIIFA.	.NPSGGDIEI	TTHSFNCGGE
CRF02_AG_G	TDWNNTLQQV	ATQLGKYFRD	T...TRIKFD.	.NPSGGDLEI	MTHSFNCGGE
CRF02_AG_N	TEWNKTLHQV	VTQLKTYFKN	...TTIIFA.	.NPLGGDVEI	TTHSFNCGGE
CRF02_AG_S	QQWNKTLHDV	ATKLREYFNN	...TTIIFD.	.EPSGGDLEI	TTHSFNCGGE
CRF02_AG_S	EKWNSTLQKV	VTKLKGHFNS	...SKIIFT.	.NSSGGDLEI	TTHSFNCGGE
CRF03_AB_R	TKWNNTLKQI	VIKLRKQFG.	..NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
CRF03_AB_R	TKWNNTLEQI	VSKLRKQFR.	..NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
CRF04_cpx_	NDWNTLKV	SEELKRLFP.	..NKTIKFAP	.PV.GGDLEI	TTHSFNCKGE
CRF04_cpx_	SDWNEALQKV	VVKLREHFP.	..NKTIIFNQ	.SS.GGDLEI	TTHSFNCGGE
CRF04_cpx_	KDWNNTLQKI	VDELKRFHP.	..NKNITFAP	.SA.GGDVEI	TTHSFRLGGE
CRF05_DF_B	EQWNKTLIQV	AKELQSHFP.	..NKTIKFNS	.SS.GGDLEI	TMHSFNCRGE
CRF05_DF_B	AQWNKTLQV	KEELRAHIKD	IGNKTIVFNS	.SA.GGDLEI	TSHIFNCRGE
CRF06_cpx_	ANWTDILGEV	KVKLEEVFNN	...THITFKS	.SA.GGDLEI	TTHSFNCGGE
CRF06_cpx_	KAWNSMLQNV	TAKLKELFNN	...KNITFNS	.SA.GGDLEV	TTHSFNCGGE
CRF06_cpx_	TAWKETLQNV	TEKLKQLLN.	...TNITFNP	.SA.GGDLEI	TTHSFNCRGE
CRF06_cpx_	TDWNMLKNV	TTKLIEVFK.	...KNITFNS	.SA.GGDLEI	TTHSFNCGGE
CRF11_cpx_	AEWLNTLQQV	ATQLRGKFN.	...KTIIFDN	.PSPGGDIEI	TSHSFNCRGE
CRF11_cpx_	ADWNNTLQQV	AEQLHNNFN.	...KTIVFNE	.HS.GGDLEV	TTHSFNCGGE
D_CD_84ZR0	VKWNNTLRQV	ARKLGNLLN.	..QTKIIFKP	.SS.GGDPEI	TTHSFNCGGE
D_CD_ELI_K	AQWSKTLQQV	ARKLGTLLN.	..KTIIFKP	.SS.GGDPEI	TTHSFNCGGE
D_CD_NDK_M	AEWNKALQQV	ATKLGNLLN.	..KTTITFKP	.SS.GGDPEI	TSHMLNCGGD
D_UG_94UG1	AGWNKTLQQV	AEKLGNNLN.	..QTTIIFKP	.SS.GGDPEI	TTHSFNCGGE
F1_BE_VI85	TQWNNTLEYV	KAELKSHFPN	N...TAIKFNQ	.SS.GGDLEI	TMHSFNCRGE
F1_BR_93BR	TQWRNTLAKV	KAKLGSYFPN	...ATIKFNS	.SS.GGDLEI	TRHNFNCMGE
F1_FI_FIN9	EQWNKTLDRV	KAELKLHFNK	...TIQFNS	.SS.GGDLEI	TMHSFNCRGE
F1_FR_MP41	TQWSKTKTQV	QEKLRALFNK	...TIKFNQ	.SS.GGDLEI	TMHSFNCRGE
F2_CM_MP25	KQWYDTLIKI	ATEFKDQYN.	...KTVGFQP	.SA.GGDLEI	TTHSFNCRGE
F2KU_BE_VI	ENWNKTLEGV	KAKLHGFFTN	...KTIIIFKP	.HS.GGDPEV	VMHTFNCGGE
G_BE_DRCBL	TKWNETLRDV	QAKLQEYFIN	...KSIEFNS	.SS.GGDLEI	TTHSFNCGGE
G_NG_92NG0	IKWREMLKNV	TAQLRKIYN.	..NKNITFNS	.SA.GGDLEI	TTHSFNCRGE
G_SE_SE616	RKWKEALQNV	AAELGKIFNK	S.SENITFNS	.SA.GGDLEI	TTHSFICRGE
H_BE_VI991	KQWNETLHKV	ITKLGSYFD.	..NKTIIILQP	.PA.GGDIEI	ITHSFNCGGE
H_BE_VI997	EKWNKTLQOI	ATQLSKYFV.	..NRTLIFKP	.HS.GGDLEV	TTHSFNCRGE
H_CF_90CF0	TDWNKTLHQV	VTQLGIHLN.	..NRTISFKP	.NS.GGDMEV	RTHSFNCRGE
J_SE_SE702	KDWNNTLRRV	AKKLREHFN.	...KTIDFTS	.PS.GGDIEI	TTHSFNCGGE
J_SE_SE788	RDWSNTLRRV	ATKLREHFN.	...KTINFTS	.PS.GGDIEI	VTHSFNCGGE
K_CD_EQTB1	GQWNKTVNQV	KKELGKHFN.	...KTIIIFQP	.SS.GGDPQV	TRHIFNCRGE
K_CM_MP535	EKWNMTLSRV	KEKLKEHFKN	...GTITFKP	.PNPGGDPEI	LTHMFNCAGE
N_CM_YBF30	ELWEPMNRT	REEIKKILGK	...NNITFRA	RERNEGDLEV	THLMFNCRGE
O_CM_ANT70	TDWGKILKQT	AERYLELVNN	TGSINMTFN.	.HSSGGDLEV	THLHFNCHGE
O_CM_MVP51	TVWENALQQT	AIRYLNLVNQ	TENVTIIFS.	.RTSGGDAEV	SHLHFNCHGE
O_SN_99SE_	SDWEKALKQT	AERYLDRNN	TNTVNITFE.	.RSIGGDSEV	THLHFNCHGE
O_SN_99SE_	SVWEEALKQT	AERYLELMNN	TNTVNITFN.	.HSTGGDPEV	THLHFNCHGE
U_CD_83C	GEWRNTLQQV	AIALRRQFNN	...KSIIFN.	.SSSGGDIEI	TTHTFNCGGE

	451			500
00BW0762_1	FFYCNTTRLF	NGTYN.....STGD	TNS.....TN STITLQCRIK
00BW0768_2	FFYCDTSNLF	NKTRR.....DN..AN ETITLPCRIK
00BW0874_2	FFYCNTSRLF	NSTYN.....PNST	YIEGR...SN ATITLQCRIK
00BW1471_2	FFYCYTTKLF	NSTYN.....STYT	GSESN..... .ITIPCRIK
00BW1616_2	FFYCNTSKLF	NGTYN.....SNNN	TA..... .DITLQCRIK
00BW1686_8	FFYCNTSNLS	NETYL.....ANLT	SNVTK....N ATITLPCRIK
00BW1759_3	FFYCNTSNLF	NNTYR.....ADNN	ITNDNSN... .ITLQCRIK
00BW1773_2	FFYCNTSALF	NSTYN.....STNT	SGHN....DT RIITLPCRIK
00BW1783_5	FFYCNTSKLF	NGTYN.....GTS.	...ISS...N SSITLQCRIK
00BW1795_6	FFYCNTSELF	NGTYN.....STG.	...DSN...S NLITLQCRIK
00BW1811_3	FFYCNTSQLF	NGTYM.....PNTY	MS....SSDN RNITIPCRIK
00BW1859_5	FFYCNTTHLF	NGNG.....ESD INITLPCRIK
00BW1880_2	FFYCDTTKLF	NGTYN.....STEQ	TN..... STITLQCRIK
00BW1921_1	FFYCNTSQLF	NGTYN.....DT.Y	ESNSG....N STITLPCRIK
00BW2036_1	FFYCDTSKLF	NSSYN.....DTEL	YSYNS....T ANITLPCRLK
00BW2063_6	FFYCNTSQLF	NSSYS.....RHN.	...NTS...N STITLPCNIK
00BW2087_2	FFYCNTSGLF	N.....GTF	NGT...HSTN TNITLPCRIK
00BW2127_2	FFYCNTTILF	NSTYY.....P...	NTK...SDTT ETITLPCRIK
00BW2128_3	FFYCNTSLLF	DETQL.....SKE.N NTINIQCRIK
00BW2276_7	FFYCNTSKLF	NGTYM.....PNYN	TSN...SSNN SNITLPCRIK
00BW3819_3	FFYCNTSGLF	NGTYN.....G...	TND...NDTD SDITLPCRIK
00BW3842_8	FFYCNTSLLF	NSSYN.....GNSS	YNDTGS...N STITLQCRIK
00BW3871_3	FFYCNTSILF	NDTYW.....FNGT	ANDTG....S NNITIPCRIK
00BW3876_9	FFYCNTSGLF	NNNLI.....NNG.AE DTIRLPCRIK
00BW3886_8	FFYCNTSKLF	NSTNN.....NTE.	..SES....N ATITLPCRIK
00BW3891_6	FFYCNISRLF	NRPNM.....TKNM	TSDIKNN... STITLPCRIK
00BW3970_2	FFYCNTSSLF	NNTYR.....PTYW	PGTE....SN STITLQCRIK
00BW5031_1	FFYCNTSQLF	NSTYR.....ANTS	NS..... .NITLPCRIK
96BW01B21	FFYCDTSELF	NSTYM.....SNGG	NISS.....S TIIMLPCRIE
96BW0407	FFYCNTSRLF	NESYN.....FDES	YWN.N...TN KTIMLPCRIK
96BW0502	FFYCDTSQLF	NSTYS.....PSNG	TENK...LN GTITITCRIK
96BW06_J4	FFYCNTSRLF	DETYL.....S...	GTDED....N GTITLPCRIK
96BW11_06	FFYCNTSKLF	NSTYI.....QLN.	.STETP...N STITLPCRIK
96BW1210	FFYCNTSQLF	NSTYN.....Y	MPS...NNTG TNITLQCRIK
96BW15B03	FFYCNSSKLL	NSSYN.....GTSY	RGTESN...S SIITLPCRIK
96BW16_26	FFYCNTSKLF	NSTYN.....STDR	SNN.....T DNITIQCRIK
96BW17A09	FFYCNTSILF	NSTYN.....STYT	GSDSNS.... .TITIPCRIK
96BWM01_5	FIYCNTSKLF	NGTYN.....STG.TS...N STITLSCRIK
96BWM03_2	FFYCNTSELF	NGTYN.....GTD.	..NNS....N KTITLLCRIK
98BWMC12_2	FFYCNTSGLF	NSTYN.....PNST	YTESK...AN SNITLHCRIK
98BWMC13_4	FFYCNTTKLF	NGTYS.....QPN.	.STGTP...H SNITLPCRIK
98BWMC14_a	FFYCNTSQLF	NSTYN.....G...	RNSTT....N ATITLPCRIK
98BWM014_1	FFYCNTSKLF	NSTYN.....ATY	NST...DTSN STITIPCRIK
98BWM018_d	FFYCNTSGLF	NS.....AFNDN...	SG GTITLQCRIE
98BWM036_a	FFYCNTSGLF	NSTYY.....SNKT	SSN...MTN EIITIPCKIK
98BWM037_d	FFYCNTSKLF	NTSWL.....DSYI	SNTG....NN SIITLPCRIK
99BW3932_1	FFYCNTSRLF	NSTYN.....P...	NTK...SNTG SWIILPCRIK
99BW4642_4	FFYCNTSKLF	TYQSN.....TY..VAN STITLPCRIK
99BW4745_8	FFYCNTSELF	NSTYN.....ANTY	NTATGNNS.. TTITLPCRIK
99BW4754_7	FFYCNTSKLF	NSTFN.....SNGH	DST....GN DPLTIPCRIK
99BWMC16_8	FFYCNTSNLF	NNTYY.....PNMT	NTDTK...SN LTITLPCRIK
A2_CD_97CD	FFYCNTTGLF	NSTWEN....GTNK	QNYTE...SN DTITLQCRIK
A2_CY_94CY	FFYCNTTGLF	NGTWNN...GTWN	GPYTPNN.TN GSIILPCRIK
A2D_97KR	FFYCDTSGLF	NSTWPAN...ASRE	NEEKD...R. .NVTLPCRIK
A2G_CD_97C	FFYCNTTNLF	NSTFNTT...SLFN	STGRNGTNDN TTITIPCRIK
A_BY_97BL0	FFYCNTTDLF	NSTX.....DGTVT	NSTKAN.... GTITLPCRIK
A_KE_Q23_A	FFYCNTSGLF	NSTWY.....VNSTW	NDTDSTQESN DTITLPCRIK
A_SE_SE659	FFYCNTSSLF	NSTWS.....NDNNT	QGSNSTET.K DTITLPCRIK
A_SE_SE725	FFYCNTSGLF	NSTWS.....Q.NDT	GVSNSTES.N GTIILPCRIK
A_SE_SE753	FFYCNTSGLF	NSTIL.....NSTKM	NDNASRESYD DTITLQCRIK

A_SE_SE853	FFYCNTSGLF	NSTWS.....SNASE	PMSNSTES.N	DTITLQCRIK
A_SE_SE889	FFYCNTSGLF	NSTWN.....GTDSM	QKLNST....	GNITLPCRIK
A_SE_UGSE8	FFYCNTSGLF	NSSWN.....END.T	KVNYNTES.N	DTITLQCRIK
A_UG_92UG0	FFYCNTSGLF	NSTWV.....NGTTS	STSN.....	GTITLPCRIK
A_UG_U455_	FFYCNTSGLF	NSIWN.....GSMSN	DMGP.....N	GTITLQCRIK
AC_IN_2130	FFYCNTSGLF	NGTWNASMQ.ES	NSTESN....	ETIILPCRIK
AC_RW_92RW	FFYCNTSGLF	NSTWS.....KR	NGTWQSNNGTE	LNITLPCRIK
AC_SE_SE94	FFYCDTSGLF	NSTWPFNS..T	NSTGPN....	GTITLQCRIK
ACD_SE_SE8	FFYCNTSGLF	NSTWV.....NGSRE	SNSTDN....	DTITLPCRIK
ACG_BE_VI1	FFYCNTSGLF	NSTYN.....PSYN	STESVN...E	TTIILPCKIK
AD_SE_SE69	FFYCNTTGLF	NSTWNDDTAT.EQKPN..	DTIRLQCRIK
AD_SE_SE71	FFYCNTSGLF	NSTWN.....NTDSM	QESHSTET.N	DTITLPCRIK
ADHK_NO_97	FFYCNTSQLF	NSTWNHTST.YNST	EN.....	GTITLPCRIK
ADK_CD_MAL	FFYCNTSKLF	NSTWQNNGA.RLSN	S..TE.ST..	GSITLPCRIK
AG_BE_VI11	FFYCNTSALF	NFSSETNST.FP.N.....		TTLTLPCRIK
AG_NG_92NG	FFYCNTSGLF	NESGGNDT..TITLPCRIK
AGHU_GA_VI	FFYCNTTKLF	NDTENKN...NDAEN...	KTITLPCRIK
AGU_CD_Z32	FFYCNTSGLF	NSTWK.....NSTSI	NDTVSN....	GTITLPCRIK
AJ_BW_BW21	FFYCNTSGLF	NKSLNETS.NETT	DGAN.....	NTITLTCRIK
B_AU_VH_AF	FFYCNTSQLF	NSTWFNSTG.NDTE	RATNN..T..	ENITLPCRIK
B_CN_RL42	FFYCNTSQLF	NSTWNDTG..T	WNDTTGNS..	.TITLPCRIK
B_DE_D31_U	FFYCNSAQLF	NSTWNDTK..ES	NNTNG.....	.TITLPCRIK
B_DE_HAN_U	FFYCNTTKLF	NSTWNNTST.WN..	DNGND.....	.TITLPCRIK
B_FR_HXB2_	FFYCNTSQLF	NSTWFNSTW.STEG	SNNTEGSD..	.TITLPCRIK
B_GA_OYI_	FFYCNTSQLF	NSTWNDTTR.AN..	.STEV.....	.TITLPCRIK
B_GB_CAM1_	FFYCNTTQLF	NTTWLFNGT.WNDT	EGLNNTER..	.NITLPCRIK
B_GB_GB8_C	FFYCKTAQLF	NSTWNSTGN.GTIK	SNTTE.....	.IITLPCRIK
B_GB_MANC_	FFYCNTSQLF	NSTWNTGND.TRES	NDTNN..T..	GNITLPCRIK
B_KR_WK_AF	FFYCNTTQLS	NSTWQRSDG.TWNR	TGGLNETK..	ENITLPCRIK
B_NL_3202A	FFYCNTSQLF	NSTWNDTGN.VTER	SNNNE.....	.NITLPCRIK
B_TW_TWCYS	FFYCNTATPLF	NSTWNATST.LNAT	NEENE.....	.NITLLCRIK
B_US_BC_L0	FFYCKSTQLF	NSTWAGNNT.WNSS	AERSDDTG..	GNITLPCRIK
B_US_DH123	FFYCNTKKLF	NSTWNGTEG.SYNI	EGND.....	.TITLPCRIK
B_US_JRCSF	FFYCNTSQLF	NSTWNDTEK.SSG.	TEGND.....	.TIILPCRIK
B_US_MNCG_	FFYCNTSPLF	NSTWNGNNT.WNNT	TGSNN.....	.NITLQCKIK
B_US_P896_	FFYCNTAQLF	NSTWNVTTG.TNG.	TEGND.....	.IITLQCRIK
B_US_RF_M1	FFYCNTTQLF	NSTWNSTEG.SNNT	GGND.....	.TITLPCRIK
B_US_SF2_K	FFYCNTTQLF	NNTWRLNHT.EG..	TKGND.....	.TIILPCRIK
B_US_WEAU1	FFYCNTSQLF	NSTWHANGT.WKNT	EGADN.....	.NITLPCRIK
B_US_WR27	FFYCNTSQLF	NSTWNSTEG.NS..	TWSDK.....	.IIRLPCRIK
B_US_YU2_M	FFYCNTSQLF	..TWNDTRK.LN..	.NTGR.....	.NITLPCRIK
BF1_BR_93B	FFYCNTSGLF	NDTVDN....		GTITLPCRIK
C_BR_92BR0	FFYCNTSSLF	NSTYT.....PNST	ENITGT..EN	SIITIPCRIK
C_BW_96BW0	FFYCNTSRLF	NESYS.....FNES	HWSND...TN	ATITLPCRIK
C_BW_96BW1	FFYCNTSKLF	NGTYI.....QPNS	.TEDTP...N	STITLPCRIK
C_BW_96BW1	FFYCNTSQLF	NSTYN.....S.TY	MPS...NNTG	TNITLQCRIK
C_BW_96BW1	FFYCNTSSKLL	NSSYN.....GTSY	RGTESN...S	SIITLPCRIK
C_ET_ETH22	FFYCNTSNLF	NSTKL.....E...	LFNSS...TN	LNITLQCRIK
C_IN_93IN1	FFYCNTSGLF	NGTYM.....PTYM	PNGTESN.SN	STITIPCRIK
C_IN_93IN9	FFYCNTSGLF	NGTYM.....TSSD	GNS.....S	STITIPCRIK
C_IN_93IN9	FFYCNTSSLF	DSLFN.....PNGT	RNDT.....N	LTITIPCRIK
C_IN_94IN1	FFYCNTSGLF	NSTYM.....SGTY	MNSSADM.NS	SYITIPCRIK
C_IN_95IN2	FFYCNTSGLF	NRTYM.....PNDT	KSNSSSN.PN	ANITIPCRIK
CRF01_AE_C	FFYCNTTKLF	NSTWT.....TNE	IMEEFKGTNS	STITLPCRIK
CRF01_AE_C	FFYCNTTALF	NSTWI.....N.G	TMQEVNGTNS	GNITLPCRIK
CRF01_AE_C	FFYCNTTRLF	N.....ISTNGTTN	GTITLPCRIK
CRF01_AE_T	FFYCNTTQLF	NNTCI.....GNE	TMK...GCNG	.TITLPCRIK
CRF01_AE_T	FFYCNTTQLF	NSTWT.....GNE	TME...GSNG	.TITLPCRIK
CRF01_AE_T	FFYCNTTRLF	NNTCI.....GNK	TMK...ECND	.TIILPCRIK
CRF01_AE_T	FFYCNTTKLF	NSTWI.....GNE	TIG...SSG	.NIILPCRIK
CRF01_AE_T	FFYCNTTKLF	NNTCL.....GNE	TMA...GCND	.TITLPCRIK

CRF01_AE_T	FFYCNTTKLF	NSTWR.....GNE	TIESREGYNK	.TIILPCKIK
CRF02_AG_F	FFYCNTSELF	NSTW.....	..NSTWDNSS	NHIESNHT.E	GNITLQCRK
CRF02_AG_F	FFYCNTSELF	N.....	...STWDNSL	NHTESNHT.E	DNITLQCRK
CRF02_AG_G	FFYCNTSGLF	NSTWYKN...	..STWYSNST	ASSNHTEL.N	STITLQCKIK
CRF02_AG_N	FFYCNTSKLF	N.....	...STWDNSN	STANHTGS.N	DTITLQCRK
CRF02_AG_S	FFYCNTSNLF	NRTWNHNGTW	NAPGPFNDTE	DKTINGTE.D	KTITLQCRK
CRF02_AG_S	FFYCNTAELF	NSTWASN...	.TNGIWASNI	NASNNKDA.N	DTITLKCKIK
CRF03_AB_R	FFYCNTTKLF	NSTWNGTEE.LN..	.NTEG.....	DIVTLPCRK
CRF03_AB_R	FFYCNTTKLF	NSTWNNTTEE.SN..	.NTKG.....	DIVTLPCRK
CRF04_cpx_	FFYCNTTPLF	NSTHMQNGT.NIT.	S.TDSTN...	STITLQCRK
CRF04_cpx_	FFYCNTSGLF	NSTYMFNST.NRTN	T.TNGTN...	STITLPCRK
CRF04_cpx_	FFYCNTSGLF	NRTYMVNKN.ETNS	T.NTTDE...	KIIRLPCRK
CRF05_DF_B	FFYCDTSKLF	NATVFNDTV.FNAT	MFNND...SD	KNILPCKIK
CRF05_DF_B	FFYCNTSGLF	NVTVP.....NNE.....	.TITLPCRK
CRF06_cpx_	FFYCNTSNLF	NTSDFNTS.R..G	NDTN.....	TTITLPCRK
CRF06_cpx_	FFYCNTSQLF	NNNITDSNE.T.....	TNFTLPCRK
CRF06_cpx_	FFYCNTSQLF	NSSIPESE.T.....	DIITLPCRK
CRF06_cpx_	FFYCNTSQLF	NSSNLNNNS.	SDNN.....	GTITLPCRIN
CRF11_cpx_	FFYCNTSGLF	NNTWLFNST.WNSS	QELNGT...E	PNITLPCRK
CRF11_cpx_	FFYCNTSGLF	NSTWYANDN.TSTQ	NDMQSN...D	.TITLPCRK
D_CD_84ZR0	FFYCNTSGLF	NSAWNISGH.STGL	N.....D..	TIITIPCRK
D_CD_ELI_K	FFYCNTSGLF	NSTWNISAW.NNIT	ESNNS.TN..	TNITLQCRK
D_CD_NDK_M	FFYCNTSRLF	NSTWNQTN.TGFNN..	GTVTLPCRK
D_UG_94UG1	FFYCNTTRLF	NSTWKRNS.EWSR	D..NT.PD..	ETITLQCRK
F1_BE_VI85	FFYCDTSGLF	NDTGSN....N	GTITLPCRK
F1_BR_93BR	FFYCNTDELF	NDTKFND...TG...FN	GTITLPCRK
F1_FI_FIN9	FFYCNTSLLF	NNTVPN....N	GTITLPCRK
F1_FR_MP41	FFYCDTSGLF	NESEKY....N	GTIILPCKIK
F2_CM_MP25	FFYCNTTILF	NHTRVNDIL.SNNH	TR.....EN	DTITLPCRK
F2KU_BE_VI	FFYCNTTRLF	NDTLNHT...ID	QNITLPCRK
G_BE_DRCBL	FFYCNTSGLF	NNSILKSNI.	SENN.....	DTITLNCKIK
G_NG_92NG0	FFYCNTSGLF	NNNISNIN..N.....	ETITLPCRK
G_SE_SE616	FFYCNTSGLF	NSSLLRSNS.	SE.N.....	GTITLPCRK
H_BE_VI991	FFYCNTTKLF	NSTWTNSSY.TNDT	YNSNSTEDIT	GNITLQCKIK
H_BE_VI997	FFYCNTSGLF	NSSWTGDNI.NMPN	DTG.....	KNITLPCRK
H_CF_90CF0	FFYCNTSGLF	NSSWEMHTN.YTSN	DTKG...N..	ENITLPCRK
J_SE_SE702	FFYCNTSTLF	NSSWDENNI.KDTN	STNDN.....	TTITIPCKIK
J_SE_SE788	FLYCNTSKLF	NSSWDKNSI.EATN	DTSX.....	ATITIPCKIK
K_CD_EQTB1	FSYCDTTDTV	DDTEEE....ED	TTITIPCRK
K_CM_MP535	FFYCNTTKLF	NETGE.....N	GTITLPCRK
N_CM_YBF30	FFYCNTSKLF	NEELLN....ETG.	EPITLPCRIR
O_CM_ANT70	FFYCNTAKMF	NYTFS.....CNGTTC	SVSNVSQ.G.	NNGTLPCRKL
O_CM_MVP51	FFYCNTSGMF	NYTFIN....CTKSGC	QEIKGSNETN	KNGTIPCKLR
O_SN_99SE_	FFYCNTSKMF	NYTFS.....CIGTNC	TSNQNSSNS.	NDTRIYCRK
O_SN_99SE_	FFYCNTSQMF	NYTFS.....CTRINC	IRQSNSS...	INGTISCRIK
U_CD___83C	FFYCNTSELF	TGIWNG....TWDK	NCTSTESNCT	GNITLPCRK

	501				550
00BW0762_1	QIINMWQGVG	KAMYAPPIAG	NIICKSNITG	LLLTRDGGEE	N.....TTE
00BW0768_2	QIINMWQEVG	RAMYAPPIEG	NITCKSNITG	LLLVRDGGKT	ED....NKSE
00BW0874_2	QIINLWQEVG	RAIYAPPIAG	NITCKSNITG	LLLTRD.GG.	NNS....TTE
00BW1471_2	QIINMWQGVG	QAMYAPPIAG	NITCRSNITG	LLLTRDGGIN	...EDDNTE
00BW1616_2	QIINLWQGVG	RAMYAPPIAG	NITCKSNITG	LLLTRDGGGE	N.....NSTE
00BW1686_8	QIINMWQEVG	RAIYAPPIAG	KITCISNITG	TLLTRDGGVS	NTTE...GNE
00BW1759_3	QIINMWQEVG	RAMYAPPIEG	NITCNSSITG	LLLTRDGGKN	S...TNNGTE
00BW1773_2	QIINMWQKVG	RAMYAPPIAG	NITCKSNITG	LLLTRDGGNT	S....STEE
00BW1783_5	QIINMWQGVG	QAIYAPPIAG	NITCKSNITG	LLLTRDGG..	NN...TENTE
00BW1795_6	QIINMWQKVG	RAMYAPPIEG	NITCISNITG	LLLTRDGG..	YE...ANHTE
00BW1811_3	QIINLWQEVG	RAMYAPPIAG	NITCKSNITG	LLLTRDGGGS	NTTN...ATE
00BW1859_5	QIINMWQEVG	RAMYAPPIAG	NITCKSKITG	LLLTRDGGKQNESK
00BW1880_2	QIINMWQGVG	RAMYAPPIEG	NITCNSNITG	LLLTRNRGRE	NGD...NTTE
00BW1921_1	QIINMWQGVG	RAIYAPPIEG	NITCKSNITG	LLLTRDGGKG	NDT....AE
00BW2036_1	QIINMWQKVG	RGIYAPPIEG	SITCNSNITG	LLLVRDGG..	IN...TSTVE
00BW2063_6	QIINMWQGVG	RAMYAPPIAG	NITCTSNITG	LILTRDGGG.	NE...TNETE
00BW2087_2	QIINMWQEVG	RAMYAPPIAG	NITCKSNITG	ILLTRDGGED	TKN....KTE
00BW2127_2	QIVNMWQGVG	RAIYAPPIAG	NITCNSSITG	LLLLRDGGTE	TENN...RTE
00BW2128_3	QIINLWQEVG	RAMYAPPIEG	NITCKSNITG	LLLTRDGGTN	..N...NTE
00BW2276_7	QIINMWQGVG	RAIYASPIEG	SITCKSNITG	LLLVHDGG..	NSNT...STE
00BW3819_3	QIINMWQEVG	RAIYAPPIAG	NITCTSNITG	LLLTRDGEPS	TE.....
00BW3842_8	QVINMWQRVG	QAIYAPPIEG	IITCNSSITG	LLLVRDGD..	NQ...TSDTE
00BW3871_3	QIINMWQEVG	RAIYAPPIRG	IITCTSNITG	LLLTRDGGNT	GGN....TTE
00BW3876_9	QIINMWQEVG	RAMYAPPIAG	NITCTSNITG	LLLTRDGG.N	GG....NTE
00BW3886_8	QFIRMWQRVG	QAMYAPPIAG	NITCRSNITG	LLLTRDG...KNDTE
00BW3891_6	QIINMWQGVG	RAMYAPPIAG	RIICKSNITG	LLLVRDGGQD	N...VMNATE
00BW3970_2	QIINMWQKVG	RAIYAPPIAG	KITCKSNITG	LLLVRDGGGG	NN....TATE
00BW5031_1	QIINMWQGVG	RAMYAPPIAG	NIICKSNITG	VLLTYDGGEE	N.....E
96BW01B21	QIINMWQGVG	RAMYAPPIKG	SITCRSNITG	LLLTRDGGLN	RS...TEEPE
96BW0407	QIINMWQGVG	RAIYAPPIAG	NITCVSNITG	LLLTWDGGHQ	SN.....E
96BW0502	QIINMWQKVG	RAMYAPPIAG	NLTCESDITG	LLLTRDGGKT	G....PNDTE
96BW06_J4	QIINMWQEVG	RAIYAPPIAG	NITCKSNITG	LLLTRDGGLN	NDS.....E
96BW11_06	QFINLWQEVG	RAMYAPPIAG	NIICKSNITG	LLLTRDG...	.D...KNDSE
96BW1210	QIINRWQEVG	RAMFAPPIAG	NITCKSNITG	ILLVRDGGNT	SEN.....IE
96BW15B03	QIINMWQKVG	RAIYAPPIEG	NITCSSSITG	LLLARDGG..	LD...NVTE
96BW16_26	QIINMWQGVG	RAMYAPPIEG	NITCKSNITG	LLLVRDGGTE	ENN...TGTE
96BW17A09	QIINMWQGXG	QAMYVPPIAG	NITCRSNITG	LLLTRDGGK.	...VTGNTTE
96BWM01_5	QIINMWQGVG	RAMYASPIAG	NITCKSNITG	LLLTRDGG..	NE...TSGIE
96BWM03_2	QIINTWQEVG	RAIYAPPIAG	NIICISNITG	LLLTRDGGKT	ND...TNDTE
98BWMC12_2	QIINMWQEVG	RAMYAPPIAG	NITCRSNITG	LLLTRD.GGN	TTE....TKE
98BWMC13_4	QIINMWQGVG	RAMYAPPIAG	NITCISNITG	LILTRDGG..	VN...RSDTE
98BWMC14_a	QIINMWQEVG	RAIYAPPIKG	NITCESNITG	LLLTRDGGSN	DTT.....E
98BWM014_1	QIINMWQGVG	QAMYAPPIAG	NITCKSNITG	ILLTRDGGIN	NTN....GTE
98BWM018_d	QIINMWQKVG	RAIYAPPIAG	NITCSSRITG	LLLTRDGGKNDTHE
98BWM036_a	QIINMWQEVG	RAMYAPPIAG	NITCKSNITG	LLLVRDGGNN	NTT.....E
98BWM037_d	QIINMWQKVG	RAMYANPIEG	NITCRSNITG	LLLENDG...	N.....M
99BW3932_1	QIINMWQKVG	RAMYAPPIAG	NITCKSNITG	LLLVRDGGTA	TD.....E
99BW4642_4	QIINMWQEVG	RAMYAPPIAG	NITCQSNITG	LLLTRDGGTE	TD....NKTE
99BW4745_8	QIINMWQEVG	RAMYAPPIEG	NITCKSNITG	LLLVRDGGGK	N...ATNDTE
99BW4754_7	QIINMWQEVG	RAMYAPPIAG	RIICNSTITG	LILTRDGGNT	N.....NTE
99BWMC16_8	QIINRWQEVG	RAMYAPPIAG	NITCTSNITG	LLLVRDGGRT	SD....STKE
A2_CD_97CD	QIINMWQRVG	RAMYAPPIAG	VIKCTSNITG	MILTRDG..G	KNS....INE
A2_CY_94CY	QIINMWQRVG	RAMYAPPIAG	IIKCTSNITG	IILTRDG..G	NNG....TNE
A2D___97KR	QIVNMWQRVG	RAMYAPPING	TIKCTSNITG	MILTRDGNSG	GNA....TNE
A2G_CD_97C	QIINMWQRVG	RAMYAPPIAG	IINCTSNITG	IILTRDGEKG	GDN....TIE
A_BY_97BL0	QIINMWQRVG	QAMYAXPIKX	SIRCESNITG	LLLTRDGXGX	TNX....SNE
A_KE_Q23_A	QIINMWQRAG	QAMYAPPPIG	VIKCESNITG	LLLTRDGGKD	NN....VNE
A_SE_SE659	QIINMWQRAG	KAMYAPPPIQG	VIRCESNITG	LILTRDG.GD	AG....ENE
A_SE_SE725	QIINMWQRAG	QAIYAPPPIG	IIRCESNITG	LLLTRDG.GV	VNS....TNE
A_SE_SE753	QIINMWQRVG	QAMYAPPPIRG	AIRCKSNITG	LLLTRDGGNS	NSS....TNE

A_SE_SE853	QIINMWQRAG	KAIYAPPIPG	IIKCVSNITG	LILTRDG.GS	NNS....TNE
A_SE_SE889	QIINMWQRAG	QAIYAPPIQG	VIRCESNITG	LILTRDG.GN	DNN....ESE
A_SE_UGSE8	QIINMWQRTG	QATYAPPIPG	VIQCRSNITG	LLLTRDGGVT	NNT....NNE
A_UG_92UG0	QIINMWQRVG	QAMYAPPIQG	VIKCESNITG	LILTRDG.GV	NSS....DSE
A_UG_U455_	QIINMWQRVG	QAMYAPPIQG	VIRCESNITG	LLLTRDG.GT	NNT....KNE
AC_IN_2130	QIINMWQRVG	QAMYAPPIQG	IIKCVSNITG	LILTRDGK.S	SNS....TDE
AC_RW_92RW	QIINMWQRTG	QAMYAPPIQG	VISCVSNITG	LLLTRDG.GN	NNT....TTE
AC_SE_SE94	QIIRMWQRTG	QAIYAPPIPG	EINCVSNITG	LLLTRDG..G	NNI....TNE
ACD_SE_SE8	QIINMWQRVG	QAMYALPIRG	VIRCESNITG	LILTRDG.GN	NTS....TNE
ACG_BE_VI1	QIINMWQEVG	RAMYANPIAG	NITCNSNITG	LLLTRDGGVN	ET....TETE
AD_SE_SE69	QIINMWQRAG	RAIYAPPIQG	VINCVSNDITG	LILTRDGGVN	.NT.N....E
AD_SE_SE71	QIINMWQRVG	QAMYAPPIQG	VIKCTSNITG	LILTRDG.GG	NNS....INA
ADHK_NO_97	QIVNMWQRVG	QAMYAPPIKG	NITCVSNITG	LILTIDXG..	.N.MSAENF
ADK_CD_MAL	QIINMWQKTG	KAMYAPPIAG	VINCLSNITG	LILTRDGGNS	.SD.NS.DNE
AG_BE_VI11	QIVRMWQRVG	QAMYAPPIAG	KITCRSNITG	LILTRDGGNP	N....NTNNE
AG_NG_92NG	QIVRMWQRVG	QAMYAPPIAG	DITCRSNITG	LLLTRDGGVN	N....TGNE
AGHU_GA_VI	QIVNMWQRVG	RAMYAPPIAG	NITCRSNITG	IILTRDGG..	.SN.NESTNE
AGU_CD_Z32	QIVNMWQRVG	QAMYAPPIKG	VIKCESNITG	ILLTRDGVG.	NNT....ANE
AJ_BW_BW21	QIVRMWQRVG	QAIYAPPIAG	NITCTSNITG	LLLTRDGGYT	.N.NTNGTE
B_AU_VH_AF	QIINMWQKVG	KAMYAPPING	QIRCSSNITG	LILTRDGGNQENKTE
B_CN_RL42	QIVNMWQEVG	KAMYAPPIEG	QIRCSSNITG	LLLTRDGGNN	.E..S.KPTE
B_DE_D31_U	QIINMWQEVG	KAMYAPPIG	QIRCSSNITG	LLLTRDGGKN	.K..D.NETE
B_DE_HAN_U	QIINMWQEVG	KAMYAPPIGG	LIRCSSNITG	LILTRDGGND	.N..S.STTE
B_FR_HXB2	QIINMWQKVG	KAMYAPPISG	QIRCSSNITG	LLLTRDGGNS	.N..N..ESE
B_GA_OYI_	QIVNMWQEVG	KAMYAPPISG	QIRCSSKITG	LLLTRDGGKNTTNGIE
B_GB_CAM1	QIINRWQEVG	KAMYAPPITG	TISCSSNITG	LLLTRDGGRG	.E..N..ETE
B_GB_GB8_C	QIVNMWQEVG	KAMYAPPITG	QIRCASHITG	LLLTRDGGRE	.N..NTNETE
B_GB_MANC_	QILNLWQEVG	KAMYAPPISG	QISCSSNITG	LLLTRDGGNT	.NT.TGNTTE
B_KR_WK_AF	QIINRWQEVG	KAMYAPPISG	LIRCSSNITG	LLLTRDGGNE	.NN.GTNGTE
B_NL_3202A	QIINMWQGVG	KAMYAPPISG	QIRCSSNITG	LLLTRDGGKD	.E..NKTGTE
B_TW_TWCYS	QIINMWQRVG	KAMYAPPIEG	LIKCSSNITG	LMLTRDGGTN	.D....SEVE
B_US_BC_L0	QIINMWQEVG	KAMYAPPIEG	QIRCTSNITG	LLLTRDGGTS	.D..T.NTTE
B_US_DH123	QIINMWQEVG	KAMYAPPISG	QIWCCSNITG	LLLTRDGGKNSSTE
B_US_JRCSF	QIINMWQEVG	KAMYAPPIKG	QIRCSSNITG	LLLTRDGGK.NESEIE
B_US_MNCG_	QIINMWQEVG	KAMYAPPIEG	QIRCSSNITG	LLLTRDGGKD	.T..DTNDTE
B_US_P896_	QIINMWQKVG	KAMYAPPITG	QIRCSSNITG	LLLTRDGGNSTETETE
B_US_RF_M1	QIVNMWQEVG	KAMYAPPISG	QIKCISNITG	LLLTRDGGED	.T..T.NTTE
B_US_SF2_K	QIINMWQEVG	KAMYAPPIGG	QISCSSNITG	LLLTRDGGTN	.V..T.NDTE
B_US_WEAU1	QIINRWQEVG	KAMYAPPIEG	QIRCLSNITG	LLLTRDGGSS	.E..E.NQTE
B_US_WR27	QIINMWQEVG	KAMYAPPIDG	QIRCSSNITG	LLLTRDGGN.SNETTE
B_US_YU2_M	QIINMWQEVG	KAMYAPPIRG	QIRCSSNITG	LLLTRDGGK.DTNGTE
BF1_BR_93B	QIVNMWQEVG	RAMYAAPPIAG	NITCSSNITG	LLLTRDGG..	Q....NNQTEE
C_BR_92BR0	QIINMWQGVG	RAMYAPPIEG	ILTCRSNITG	LLLTRDGGTGMHDTE
C_BW_96BW0	QIINMWQGVG	RAIYAPPIAG	NITCISNITG	LLLTRDGGTT	RNN....ESE
C_BW_96BW1	QFINLWQEVG	RAMYAPPIAG	NIICKSNITG	LLLTRDG...	.D...KNDSE
C_BW_96BW1	QIINRWQEVG	RAMFAPPIAG	NITCKSNITG	ILLVRDGGNT	SEN....IE
C_BW_96BW1	QIINMWQKVG	RAIYAPPIEG	NITCSSSITG	LLLARDGG..	LD...NVTTE
C_ET_ETH22	QIINMWQGVG	RAMYAPPIEG	IIMCRSNITG	LLLTRDGAKE	PH....STKE
C_IN_93IN1	QIINMWQEVG	RAMYAPPIAG	NITCTSNITG	LLLVHDGGIK	EN.DTENKTE
C_IN_93IN9	QIINMWQEVG	RAMYAPPIEG	NITCKSNITG	LLLVRDGGAE	AK...TNNTE
C_IN_93IN9	QIINMWQEVG	RAMYAPPIAG	NITCKSNITG	LLLVRDGGRG	ND...TENNTE
C_IN_94IN1	QIINMWQEVG	RAMYAPPIAG	NITCKSNITG	ILLERDG..G	SG...SNGTE
C_IN_95IN2	QIINMWQEVG	RAMYAPPIEG	KITCRSNITG	LLLVRDGGED	KNNTETNKTE
CRF01_AE_C	QVVNMWQEVG	KAMYAPPISE	AVNCVSNITG	IILTRDGGNA	TNET.....
CRF01_AE_C	QIVNMWQEVG	RAMYAPPISE	VINCVSNITG	ILLTRDGGIN	QNQTNK..NE
CRF01_AE_C	QVIKMWQEVG	QAMYAPPIDE	AINCVSNITG	ILLVRDGGKI	ENET....IE
CRF01_AE_T	QIINMWQGTG	QAMYAPPIDG	KINCVSNITG	ILLTRDGG..	ANNTS...NE
CRF01_AE_T	QIIRMWQGAG	QAMYAPPISG	IINCVSNITG	ILLTRDGGG.	ANNTN...NE
CRF01_AE_T	QIINMWQGVG	QAMYNPPISG	NINCVSNITG	ILLTRDGGGG	NGTNN...EE
CRF01_AE_T	QIINMWQEVG	QAMYAPPITG	KINCVSNITG	ILLTRDGG..	ANNKS...SE
CRF01_AE_T	QIINMWQGAG	QAMYAPPISG	RINCVSNITG	ILLTRDGG..	VNNTD...NE

CRF01_AE_T	QIINMWQGAG	QAMYAPPING	TINCISNITG	ILLTRDGGD.	NNNTI...NE
CRF02_AG_F	QIVNMWQKVG	LAMYAPPISG	EIRCKSNITG	LLLTRDG.GS	NNS....TNE
CRF02_AG_F	QIVNMWQKVG	RAMYAPPPIG	EIRCESNITG	LLLTRDG.GS	NNS....TNE
CRF02_AG_G	QIINMWQKVG	QAMYAPPIQG	VIRCDNITG	LLLTRDG.GS	NNN....TPE
CRF02_AG_N	QIVNMWQKVG	QAMYAPPIQG	IIRCDNITG	LLLTRDG.G.	NNS....TNE
CRF02_AG_S	QIVRMWQKVG	QAMYAPPPIG	EIRCESNITG	LLLTRDG.GN	DNN....NTE
CRF02_AG_S	QIINMWQKVG	QAIYAPPIEG	VIRCDNITG	ILLTRDG.GD	NTN....GDE
CRF03_AB_R	QIINMWQEVG	KARYAPPIAG	QIRCSSNITG	LLLTRDGGNQ	.S....NVTE
CRF03_AB_R	QIINMWQEVG	KAMYAPPIAG	QIRCSSNITG	LLLTRDGGNQ	.N....NVTE
CRF04_cpx_	QFVRMWQEVG	QAMYASPIAG	SINCSSDITG	IILTRDG...GTNNT
CRF04_cpx_	QIVRMWQGVG	QAMYAPPIAG	SINCSSDITG	IILTRDGGIS	NNN.ETNDNE
CRF04_cpx_	QIVNRWQEVG	QAIYAPPLQG	SLTATQVITG	IILTRDGG..	.NR.SDTGNE
CRF05_DF_B	QIVRMWQGVG	QAMYAAPPIAG	NIACNSTITG	ILLARDGGNG	.ND.SSNDTE
CRF05_DF_B	QIINMWQGVG	QAMYAAPPIAG	NITCNSNITG	ILLTRDG..G	.VN.ITNDTE
CRF06_cpx_	QIVRMWQRVG	QAMYAPPIAG	NITCVSNITG	IILTRDGN.N	EN....VSE
CRF06_cpx_	QIVRMWQRVG	QAMYAPPIAG	NIICTSNITG	LLLTRDGGRN	DS....NSE
CRF06_cpx_	QIVRMWQRVG	QAIYAPPIAG	NITCISNITG	LLLTRDGN.T	NT....TSE
CRF06_cpx_	QIIRMWQRVG	QAMYAPPIAG	NITCTSNITG	LLLTRDGH.N	D.....TE
CRF11_cpx_	QIVRMWQRVG	QAMYAPPIQG	EIRCDNITG	LLLTRDGG..LNSTNE
CRF11_cpx_	QIINMWQRVG	QAVYAPPIQG	ELRCDNITG	LLLTRDGGEG	.N.DTIGKE
D_CD_84ZR0	QIINMWQEVG	KAMYAPPIEG	QINCSSNITG	LLLTRDGGAN	.NT.Q...ND
D_CD_ELI_K	QIIKMWQAG.	.AIYAPPIER	NILCSSNITG	LLLTRDGGIN	.NS.T...NE
D_CD_NDK_M	QIVNLWQRVG	KAMYAPPIEG	LIKCSSNITG	LLLTRDGGAN	.NS.S...HE
D_UG_94UG1	QIINMWQEVG	KAMYAPPIEG	FINCSSNITG	LLLTRDGGAI	.NS.SQ..NE
F1_BE_VI85	QIVNMWQGVG	RAMYTSPIAG	NITCNSNITG	LLLTRDGG..NESNIE
F1_BR_93BR	QIVNMWQEVG	RAMYANPIAG	NITCNSNITG	LLLTRDGG..LNSTNE
F1_FI_FIN9	QFVNMWQEVG	RAMYAAPPIAG	NITCNSNITG	LLLTRDGG..	QS..NNSDSE
F1_FR_MP41	QIINMWQGVG	QAMYSAPIAG	RINCNSTITG	LLLTRDGG..	QSN.DTNRTE
F2_CM_MP25	QIVNMWQRVG	QAMYAPPIAG	KIQCNSNITG	LLLTRDGG..EGNESE
F2KU_BE_VI	QIINRWQGVG	QAMYAPPIAG	NITCRSNITG	MILTRDGGNS	N...DTIDNE
G_BE_DRCBL	QIVRMWQRVG	QAMYAPPIAG	NITCRSNITG	LILTRDGGDN	N....STSE
G_NG_92NG0	QIVRMWQKVG	QAMYALPIAG	NLVCKSNITG	LILTRDGGNN	N....DSTEE
G_SE_SE616	QIVRMWQRVG	QAMYAPPIAG	NIECNSSITG	LILTRDGGNN	NNT.NTSESE
H_BE_VI991	QIVNMWQRVG	QAMYAPPIRG	NITCISNITG	LILTFD....	..R.NNTNNV
H_BE_VI997	QIVNMWQRVG	QAMYAPPIKG	SITCVSNITG	LILTYDED..	..K.GNNDNV
H_CF_90CF0	QIVNMWQRVG	RAMYAPPIQG	NIMCVSNITG	LILTIDEG..	..N.ASAENY
J_SE_SE702	QIVRMWQRTG	QAIYAPPIAG	NITCKSNITG	LLLTRDGGNR	.NG.SENGTE
J_SE_SE788	QIVRMWQRTG	QAIYAPPIAG	NITCTSNITG	LLLTRDGGNR	GNG.SENGTE
K_CD_EQTB1	QIINMWQKVG	QAIYAPPTAG	NITCRSNITG	MILTRDGGND	N...NTRTEE
K_CM_MP535	QIINMWQKVG	KAIYAPPIAG	SINCSSNITG	MILTRDGGNNTHNE
N_CM_YBF30	QIVNLWTRVG	KGIYAPPIRG	VLNCTSNITG	LVLEYSGGPDTKET
O_CM_ANT70	QVVRSWIRGQ	SGLYAPPIKG	NLTCHSNITG	MILQMDNTWN	SSNN....NV
O_CM_MVP51	QLVRSWMKGE	SRIYAPPIPG	NLTCHSNITG	MILQLDQPWN	STGE....N
O_SN_99SE_	QVVRSWIQGG	SGLYAPPRKG	NLTCHSLITG	MILQLDMPWN	STNNS...NA
O_SN_99SE_	QVVRSWIQGG	SGLYAPPRPG	YLTCNSSITG	MILQLDKTWN	RTNNS...ES
U_CD___83C	QVVRTWQGVG	QAMYAPPIEG	TIRCSSNITG	LLLTRDGGNG	N....ATQNE

00BW0762_1	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGI	APTSAKRRVV	EREKR.....
00BW0768_2	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
00BW0874_2	IFRPQGGNMK	DNWRSELYKY	KVVEVKPLGV	APTKAKRRVV	EREKR.....
00BW1471_2	IFRPGGGNMR	DNWRSKLYKY	KVVEIKPLGV	APNKAKRRVV	EREK.R....
00BW1616_2	TFRPAGGEMR	DNWRSELYKY	KVVEVKPLGI	APTEAKRRVV	QREKR.....
00BW1686_8	TFRPGGGDMR	NNWRSELYKY	KVVEIRPLGV	APTEARRRVV	EREK.R....
00BW1759_3	IFRPGGGDMR	DNWRSELYKY	KVVKIKPLGI	APTKAQRRVV	KREKR.....
00BW1773_2	IFRPEGGDMR	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
00BW1783_5	TFRPGGGDMR	DNWRNELYKY	KVVEIKPLGI	APTSAKRRVV	EREK.R....
00BW1795_6	IFRPIGGDMR	DNWRSELYKY	KVVEIKPLGL	APTESKRRVV	EREK.R....
00BW1811_3	TFRPGGGDMR	DNWRSELYKY	KVVEVKPLGL	APTEAKRRVV	EREK.R....
00BW1859_5	IFRPGGGDMR	NNWRSELYKY	KVVEIKPLGL	APTGAARRVV	EREK.R....
00BW1880_2	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREKR.....
00BW1921_1	IFRPEGGDMK	NNWRSELYKY	KVVEIRPLGV	APTKAKRRVV	EREK.....
00BW2036_1	TFRPEGGNMR	DNWRSELYKY	KVVEIKPLGV	APTEAARRVV	EKQK.R....
00BW2063_6	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKAKRRVV	EREK.R....
00BW2087_2	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
00BW2127_2	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
00BW2128_3	TFRPVGGDMR	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	KREK.R....
00BW2276_7	IFRPGGGDMR	DNWRSELYKY	KVVEVKPLGI	APTEAKRRVV	EREK.R....
00BW3819_3	TFRPGGGDMR	DNWRSELYKY	KVVEVKPLGI	APTGAARRVV	EREK.R....
00BW3842_8	TFRPQGGEMR	DNWRSELYKY	KVVEIKPLGV	APTTAKRRVV	EREK.R....
00BW3871_3	IFRPEGGDMR	NNWRNELYKY	KVVEIKPLGI	APTGAARRVV	EREK.R....
00BW3876_9	TFRPGGGNMK	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
00BW3886_8	TFRPGGGNMR	DNWRNELYKY	KVVEIKPLGI	APTEAKRRVV	EREK.R....
00BW3891_6	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTSAKRRVV	EREK.....
00BW3970_2	IFRPGGGNMK	DNWRSELYKY	KVVEIKPLGI	APTGAARRVV	GREK.R....
00BW5031_1	TFRPAGGNMK	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREK.....
96BW01B21	IFRPGGGDMR	NNWRSELYKY	KVVEIKPLGV	APTGAARRVV	EREK.R....
96BW0407	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTEARRRVV	EREKR.....
96BW0502	IFRPGGGDMR	DNWRNELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
96BW06_J4	TFRPIGGEMR	NNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREK.R....
96BW11_06	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKAKRRVV	EREK.R....
96BW1210	TFRPGGGNMK	DNWRSELYKY	KVVEVKPLGI	APTRAKRRVV	EREK.R....
96BW15B03	IFRPQGGDMK	DNWRNELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
96BW16_26	IFRPEGGDMR	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREK.R....
96BW17A09	TFRPGGGNMR	DNWRSELYKY	KVVEVKPLGV	APTAARRRVV	EREK.R....
96BWM01_5	IFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKSKRRVV	GREK.R....
96BWM03_2	IFRPGGGNMK	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
98BWMC12_2	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	ERGK.....
98BWMC13_4	IFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKAKRRVV	EREK.R....
98BWMC14_a	TFRPEGGDMR	NNWRSELYKY	KVVEIRPLGI	APTGAARRVV	NREK.R....
98BWM014_1	TFRPGGGDMR	DNWRSELYKY	KVVEVKPLGI	APTKAQRRVV	EREK.R....
98BWM018_d	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGV	APSEAKRRVV	EREK.....
98BWM036_a	TFRPGGGNMK	DNWRSELYKY	RVVEIKPLGI	APTGAARRVV	EREK.R....
98BWM037_d	TFRPGGGDMK	DNWRSELYKY	KVVEIKPLGI	APTEAKRRVV	EREK.R....
99BW3932_1	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTEAKRRVV	EREK.R....
99BW4642_4	TFRPGGGDMR	DSWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
99BW4745_8	IFRPEGGDMR	NNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	DKEK.....
99BW4754_7	IFRPIGGNMR	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREKR.....
99BWMC16_8	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTEAKRRVV	EREKR.....
A2_CD_97CD	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGI	APTEARRRVV	QREK.R....
A2_CY_94CY	TFRPGGGDMR	DNWRSELYKY	KVVKLEPLGV	APTRAKRRVV	EREK.R....
A2D_97KR	TFRPGGGDMR	DNWRSELYKY	KVVKLEPLGV	APTRARRRVV	EREK.....
A2G_CD_97C	VFRPVGGDMR	DNWRSELYKY	KVVKIKPLGI	APTRARRRVV	EKEK.R....
A_BY_97BL0	TFRPIXGDXR	NNWRSELYKY	KVVKIEPIXV	APTRAKRRXX	EREK.R....
A_KE_Q23_A	TFRPGGGDMR	DNWRSELYKY	KVVEIEPLGV	APTRAKRRVV	EREK.R....
A_SE_SE659	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTQARRRVV	KREK.R....
A_SE_SE725	TFRPGGGNMK	DNWRSELYKY	KVVKIEPLGV	APTRARRRVV	QREK.R....
A_SE_SE753	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	EREK.R....

A_SE_SE853	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	EREK.R....
A_SE_SE889	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	EREK.R....
A_SE_UGSE8	TFRPGGGDMR	DNWRSELYKY	KVVKLEPLGV	APTKAQRRVV	KREK.R....
A_UG_92UG0	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKARRRVV	EREK.R....
A_UG_U455_	TFRPGGGDMR	DNWKSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....
AC_IN_2130	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRARRRAV	GREK.R....
AC_RW_92RW	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....
AC_SE_SE94	TFRPGGGDMQ	DNWRSELYKY	KVVQIEPLGV	APTKARRRVV	EREK.R....
ACD_SE_SE8	TIRPAGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKARRRVV	EREK.R....
ACG_BE_VI1	IFRPGGGNMK	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
AD_SE_SE69	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R...V
AD_SE_SE71	TFRPGGGDMR	DNWRSELYKY	KVVKIEPVG1	APNRAKRRVV	EREK.R....
ADHK_NO_97	TFRPGGGDMR	DNWRSELYKY	KVVXXXPLGV	APTXARRRVV	QREK.R....
ADK_CD_MAL	TLRPGGGDMR	DNWISELYKY	KVVRIEPLGV	APTKAKRRVV	EREK.R...A
AG_BE_VI11	TFRPGGGDMR	DNWRSELYQY	KVVKIKSLGV	APTKARRRVV	EREK.R...A
AG_NG_92NG	TFRPGGGDMR	DNWRSELYKY	KIVKIKPLGI	APTKARRRVV	ER GK.R...A
AGHU_GA_VI	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRARRRVV	EREK.R...A
AGU_CD_Z32	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	AREK.R....
AJ_BW_BW21	IFTPTGRNMR	DNWRSELYKY	KVVKIEPIGV	APTRAKRRVV	GREK.R...A
B_AU_VH_AF	IFRPGGGDMR	DNWRSELYKY	KVVRIEPLGV	APTKAKRRVV	QREK.R...A
B_CN_RL42_	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKARRRVV	QREK.R...A
B_DE_D31_U	TFRPGGGNMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_DE_HAN_U	IFRPGGGNMR	DNWRNELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_FR_HXB2_	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_GA_OYI_	IFRPAGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKARRRVV	QREK.R...A
B_GB_CAM1_	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_GB_GB8_C	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_GB_MANC_	TFRPGGGNMR	DNWRSELYKY	KVVKVEPLGI	APTKAKRRVV	QREK.R...A
B_KR_WK_AF	TFRPEGGNMK	DNWRSKLYKY	KVVRIEPLGI	APTRARRRVV	QREK.R...A
B_NL_3202A	IFRPGGGDMK	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	QREK.R...A
B_TW_TWCYS	VFRPGGGDMK	DIWRNELYKY	KVVKVEPLGL	APTRARRRVV	QREK.R...A
B_US_BC_L0	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTTAKRRVV	QREK.R...A
B_US_DH123	IFRPGGGDMR	DNWRSELYKY	KVVRVEPLGI	APTKAKRRVV	QREK.R...A
B_US_JRCSE	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R....
B_US_MNCG_	IFRPGGGDMR	DNWRSELYKY	KVVTIEPLGV	APTKAKRRVV	QREK.....
B_US_P896_	IFRPGGGDMR	DNWRSELYKY	KVVRIEPIGV	APTRAKRRTV	QREK.R....
B_US_RF_M1	IFRLGGGNMR	DNWRSELYKY	KVVRIEPLGV	APTRAKRRVV	QREK.R...A
B_US_SF2_K	VFRPGGGDMR	DNWRSELYKY	KVIKIEPLGI	APTKAKRRVV	QREK.R...A
B_US_WEAU1	IFRPGGGNMK	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_US_WR27_	IFRPGGGDMR	DNWRSXLYKY	KVXXIEPLGV	APTKXKRRVX	XREK.R...X
B_US_YU2_M	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
BF1_BR_93B	TFRPGGGNMK	DNWRSELYKY	KVVEIEPLGV	APTKAKRQVV	KREK.R...A
C_BR_92BR0	IFRPEGGDMR	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREK.R....
C_BW_96BW0	IFGPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTEARRRVV	EREKR.....
C_BW_96BW1	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKAKRRVV	EREK.R....
C_BW_96BW1	TFRPGGGNMK	DNWRSELYKY	KVVEVKPLGI	APTRAKRRVV	EREK.R....
C_BW_96BW1	IFRPQGGDMK	DNWRNELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
C_ET_ETH22	IFRPEGGDMR	DNWRSELYKY	KVVEIKPLGV	APTKPKRRVV	EREK.....
C_IN_93IN1	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTAAKRRVV	EREK.R....
C_IN_93IN9	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTTAKRRVV	EREK.R....
C_IN_93IN9	IFRPGGGDMR	NNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREKRA....
C_IN_94IN1	TFRPGGGDMR	DNWRSELYKY	KVVEIQPLGV	APTEAKRRVV	ER GK.R....
C_IN_95IN2	TFRPGGGDMR	DNWRSELYKY	KVVEVKPLGV	APTTAKRRVV	EREK.R....
CRF01_AE_C	.FRPGGGNMK	DNWRSELYKY	KVVQIEPLGI	APTRARRRVV	EREK.R....
CRF01_AE_C	TFRPGGGNIK	DNWRSELYKY	KVVQIEPLGI	APTKARRRVV	EREK.R....
CRF01_AE_C	TFRPGGGNMK	DNWRSELYKY	KVVQIEPLGV	APTGAKRRVV	EREK.R....
CRF01_AE_T	TFRPGGGNIK	DNWRSELYKY	KVVQIEPLGI	APTRAKRRVV	EREK.R....
CRF01_AE_T	TFRPEGGNIK	DNWRSELYKY	KVVQIEPLGI	APTRAKRRVV	EREK.R....
CRF01_AE_T	TFRPGGGNMK	DNWRNELYKY	KVVEIEPLGI	APTKAKRRVV	EREK.R....
CRF01_AE_T	TFRPGGGNIK	DNWRSELYKY	KVVEIEPLGI	APTRAKRRVV	EREK.R....
CRF01_AE_T	TFRPGGGNIK	DNWRSELYKY	KVVQIEPLGI	APTRAKRRVV	EREK.R....

CRF01_AE_T	TFRPGGGNIK	DNWRSELYKY	KVVQIEPLGI	APSKAKRRVV	EREK.R....
CRF02_AG_F	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRPKRRVV	EREK.R....
CRF02_AG_F	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGI	APTHAKRRVV	EREK.R....
CRF02_AG_G	IFRPGGGNMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....
CRF02_AG_N	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....
CRF02_AG_S	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APSHAKRRVV	EREKRA....
CRF02_AG_S	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APSHAKRRVV	EREK.R....
CRF03_AB_R	IFRTGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	QREK.R...A
CRF03_AB_R	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
CRF04_cpx_	IFRPGGGDMR	DNWRSELYKY	KVVKIEPIGV	APNKARRRVV	QREK.....
CRF04_cpx_	TLRPGGGDMR	DNWRSELYKY	KVVKIEPVGI	APTGARRRVV	QKEK.R....
CRF04_cpx_	TFRPGGGDMR	DNWRSELYKY	KVVQIEPVGV	APTRARRRVV	QREK.R....
CRF05_DF_B	IFRPGGGDMR	DNWRSELYKY	KVVEIQPLGI	APTRAKRQVV	KREK.R...A
CRF05_DF_B	TFRPGGGDMR	DNWRSELYKY	KVVEIEPLGV	APTRAKRQVV	QREK.R...A
CRF06_cpx_	TFRPGGGDMR	DNWRSELYKY	KVVKIKPLGI	APTWARRRVV	GREK.R...A
CRF06_cpx_	TFRPGGGDMR	DNWRSELYKY	KVVKIKPLGI	APTRARRRVV	GKEKRA...V
CRF06_cpx_	IIRPGGGDMR	DNWRSELYKY	KVVKIKPLGI	APTEARRRVV	GREK.R...A
CRF06_cpx_	IFRPGGGNMK	DNWRSELYKY	KVVKIKPLGI	APTKARRRVV	GREKRA...V
CRF11_cpx_	TFRPTGGDMR	DNWRSELYKY	KVVEIKPLGV	APTRAKRRVV	EREK.R...A
CRF11_cpx_	TFRPTGGDMR	NNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R...A
D_CD_84ZR0	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	EREK.R...A
D_CD_ELI_K	TFRPGGGDMR	DNWRSELYKY	KVVQIEPLGV	APTRAKRRVV	EREK.R...A
D_CD_NDK_M	TIRPGGGDMR	DNWRSELYKY	KVVKIEPIGV	APTKARRRVV	EREK.R...A
D_UG_94UG1	TFRPGGGDMR	NNWRSELYKY	KVVKLEPIGL	APTAARRRVV	EREK.R...A
F1_BE_VI85	TFRPEGGNMK	DNWRSELYKY	KVVEIEPLGV	APTKAKRQVV	QREK.R...A
F1_BR_93BR	TFRPGGGDMR	DNWRSELYKY	KVVEIEPLGV	APTKAKRQVV	KREK.R...A
F1_FI_FIN9	TFRPGGGDMR	DNWRSELYKY	KVVEIEPLGV	APTRPKRPVV	RRER.R...A
F1_FR_MP41	TFRPEGGNMK	DNWRSELYKY	KVVEIEPLGV	APTKARRRVV	QREK.R...A
F2_CM_MP25	TLRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRQVV	QREK.R...A
F2KU_BE_VI	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGI	APTKARRRVV	QREK.R...G
G_BE_DRCBL	IFRPGGGDMR	NNWRSELYKY	KTVKIKSLGI	APTRARRRVV	EREK.R...A
G_NG_92NG0	TFRPGGGDMR	DNWRSELYKY	KTVKIKSLGV	APTRARRRVV	EREK.R...A
G_SE_SE616	IFRPGGGDMR	DNWRSELYKY	KTVKIKSLGV	APTRARRRVV	EREK.R...A
H_BE_VI991	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTEARRRVV	EREK.R....
H_BE_VI997	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTEARRRVV	EREK.R....
H_CF_90CF0	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGI	APTKTRRRVV	EREK.R....
J_SE_SE702	TFRPTGGDMR	DNWRSELYKY	KVVEIEPLGV	APTKAKRRVV	EREK.R...A
J_SE_SE788	TFRPTGGDMR	DNWRSELYKY	KVVEIEPLGV	APTKAKRRVV	EREK.R...A
K_CD_EQTB1	TFRPGGGDMR	DNWRSELYKY	KVVQIEPLGI	APTRARRRVV	QREK.R...A
K_CM_MP535	TFRPGGGDMR	DNWRSELYKY	KVVQIEPLGI	APTRARRRVV	QREK.R...A
N_CM_YBF30	IVYPSGGDMR	DNWRSELYKY	KVVSIEPIGV	APGKAKRRTV	SREK.R...A
O_CM_ANT70	TFRPIGGDMR	DIWRTELFNY	KVVRVKPFSV	APTARIAPVI	STRTHR.EKR
O_CM_MVP51	TLRPVGGDMR	DIWRTELFNY	KVVQIKPFSV	APTKMSRPVI	NIHTPHREKR
O_SN_99SE_	TFRPTGGDMR	DIWRTELFKY	KVVVKVPFSV	APTKIAPVI	GTGTQR.EKR
O_SN_99SE_	TFRPIGGDMR	DIWRTELFKY	KVVKIKPFSV	APTKIAPVI	GTGTRR.EKR
U_CD___83C	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....

	601				650
00BW0762_1	AVGIGAVFLG	.FLGAAGSTM	GAASITLMVQ	ARQLLSGIVQ	QQNNLLRAIE
00BW0768_2	AVGIGAVLLG	.FLGAAGSTM	GAASITLTVQ	ARQVLSGIVQ	QQSNLLRAIE
00BW0874_2	AVGIGAVFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW1471_2	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLMRAIE
00BW1616_2	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
00BW1686_8	AVGIGAVLLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW1759_3	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW1773_2	AVGIGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW1783_5	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQNNLLRAIE
00BW1795_6	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW1811_3	AVGIGAVFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQSNLLKAIE
00BW1859_5	AVGIGAVFLG	.FLGAAGSTM	GAASTTLTAQ	ARQVLSGIVQ	QQSNLLRAIE
00BW1880_2	AVGIGAVFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW1921_1	RAALGAVLLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
00BW2036_1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW2063_6	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW2087_2	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	TKQLLSGIVQ	QQSNLLKAIE
00BW2127_2	AVGIGAVILG	.FLGAAGSTM	GAASITLTVQ	ARQLLFGIVQ	QQNNLLRAIK
00BW2128_3	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW2276_7	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLFGIVQ	QQSNLLRAIE
00BW3819_3	AVGIGAVFLG	.FLGAAGSTM	GAASITLTIQ	ARQLLSGIVQ	QQSNLLRAIE
00BW3842_8	AVGIGAVILG	.FLSAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW3871_3	AVGIGAVFLG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ	QQSNLLRAIE
00BW3876_9	AVEIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW3886_8	AVGIGAVILG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ	QQSNLLRAIE
00BW3891_6	RAAIGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARKLLSGIVQ	QQSNLLRAIE
00BW3970_2	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
00BW5031_1	RAALGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BW01B21	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BW0407	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BW0502	AVGIGAVCLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
96BW06_J4	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	AKQLLSGIVQ	QQSNLLKAIE
96BW11_06	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BW1210	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BW15B03	AVGIGAVIFG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ	QQSNLLRAIE
96BW16_26	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLQAIE
96BW17A09	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BWM01_5	AVTFGAMFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BWM03_2	AVGIGAVLLG	.FLGTAGSTM	GAASITLTVQ	ARQVLSGIVQ	QQSNLLRAIE
98BWMC12_2	AAGLGAVLFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
98BWMC13_4	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLRAIE
98BWMC14_a	AVGVAAVFLG	.FLSAAGSTM	GAASITLTVQ	ARQSLSGIVQ	QQSNLLRAIE
98BWM014_1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
98BWM018_d	RAALGAVFLG	.FLGAAGSTM	GAASITLTVQ	TRKLLSGIVQ	QQSNLLKAIE
98BWM036_a	AVTLGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
98BWM037_d	AVGIGAVFLG	.FLGAAGSTM	GAASITLMVQ	ARQLLSGIVQ	QQSNLLRAIE
99BW3932_1	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
99BW4642_4	AVGIGAVLLG	.FLGAAGSTM	GAASIALTAQ	ARQVLSGIVQ	QQSNLLRAIE
99BW4745_8	RAIAGAVFLG	.FLGVAGSTM	GAASVALTVQ	ARQLLSGIVQ	QQSNLLRAIE
99BW4754_7	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
99BWMC16_8	AVTIGAMFLG	.FLSAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
A2_CD_97CD	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLTGIVQ	QQSNLLKAIE
A2_CY_94CY	AVGLGAVFLG	.FLGAAGSTM	GAASLTLTVQ	ARQLLSGIVQ	QQSNLLQAIE
A2D_97KR	RAAVGLFFLG	.FLGAAGSTM	GAASVTLTVQ	ARQLLSGIVQ	QQSNLLKAIE
A2G_CD_97C	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLKAIE
A_BY_97BL0	AIGLXAAFLX	.FLGAAXSTX	GAASMTLTVQ	ARQLLSGIVQ	QQSNLLXAIX
A_KE_Q23_A	AVGIGAVFLG	.FLGAAGSTM	GATSITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
A_SE_SE659	AVGLGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVR	QQSNLLKAIE
A_SE_SE725	AVGLGALFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
A_SE_SE753	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE

A_SE_SE853	AIGIGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSXIVQ	QQSNLLRAIE
A_SE_SE889	AIGIGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLMAIE
A_SE_UGSE8	AVGLAAVFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
A_UG_92UG0	AVTLGAVFIG	.FLGTAGSTM	GAASITLTVQ	ARKLLSGIVQ	QQSNLLRAIE
A_UG_U455_	AVGLGAIFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
AC_IN_2130	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
AC_RW_92RW	AVGLGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
AC_SE_SE94	AVGMGAVFIG	.FLGAAGSTM	GAASVTLTVQ	ARQLLSGIVR	QQSNLLRAIE
ACD_SE_SE8	AVGIGAVFLG	.FLGAAGSAM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
ACG_BE_VI1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
AD_SE_SE69	AG.LGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLKAIE
AD_SE_SE71	AVGIGVFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
ADHK_NO_97	AVGMGAFFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
ADK_CD_MAL	IG.LGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
AG_BE_VI11	VGLG.AVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLRAIE
AG_NG_92NG	VGLG.AVFLG	.FLGAAGSTM	GAGSITLTVQ	VRQLLSGIVQ	QQSNLLRAIE
AGHU_GA_VI	IVGVGAVFLG	.FLGVAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
AGU_CD_Z32	AIGMGAFFLG	.FLGAAGSTM	GAASITLTVH	VRQLLSGIVQ	QQSNLLRAIE
AJ_BW_BW21	VGIMGAMFLG	.FLGTAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
B_AU_VH_AF	VGMIGAMILG	.FLGAAGSTM	GAASLALTVQ	TRQLLSGIVQ	QQNNLLRAIE
B_CN_RL42	VTIGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_DE_D31_U	VGLLGAVFLG	.FLGAAGSTM	GARSMLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_DE_HAN_U	VGMLGAMFLG	.FLGAAGSTM	GARSITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_FR_HXB2_	VG.IGALFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_GA_OYI_	VGMLGAMFLG	.FLGAAGSTM	GARSMTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_GB_CAM1_	VGAIGALFLG	.FLGAAGSTM	GAVALTLTVQ	TRQLLSGIVQ	QQNNLLRAIE
B_GB_GB8_C	VGMIGAMFLG	.FLGAAGSTM	GAASLTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_GB_MANC_	VGMLGAMFLG	.FLGAAGSTM	GARSITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_KR_WK_AF	VT.FGALFLG	.FLGAAGSTM	GCTSMTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_NL_3202A	VG.IGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_TW_TWCYS	VG.IGALFLG	.FLGAAGSTM	GAASLTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_BC_L0	VG.IGALFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_DH123	VG.IGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_JRCSF	AVGIGALFLG	.FLGAAGSTM	GARSMTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_MNCG_	RAAIGALFLG	.FLGAAGSTM	GAASVTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_P896_	AVGIGAVFLG	.FLGAAGSTM	GAASVTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_RF_M1	VTIGAMFLG	.FLGAAGSTM	GAGSITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_SF2_K	VGIVGAMFLG	.FLGAAGSTM	GAVSLTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_WEAU1	VGMLGAMFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_WR27_	VGVIGVMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_YU2_M	VG.LGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
BF1_BR_93B	VG.MGALFLG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ	QQNNLLRAIE
C_BR_92BR0	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLRAIE
C_BW_96BW0	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
C_BW_96BW1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARRLLSGIVQ	QQSNLLRAIE
C_BW_96BW1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
C_BW_96BW1	AVGIGAVIFG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ	QQSNLLRAIE
C_ET_ETH22	RAALGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
C_IN_93IN1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ	QQSNLLRAIE
C_IN_93IN9	AVGIGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
C_IN_93IN9	VVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
C_IN_94IN1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
C_IN_95IN2	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF01_AE_C	AVGIGAMIFG	.FLGAAGSTM	GAASLTLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF01_AE_C	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF01_AE_C	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRTIE
CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF01_AE_T	AVGIGALIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE

CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF02_AG_F	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF02_AG_F	AVGLGAVFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF02_AG_G	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF02_AG_N	AVGLGAVFLG	.FLGAAGSTM	GARSITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
CRF02_AG_S	LVGLGAFFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
CRF02_AG_S	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLKAIE
CRF03_AB_R	VG.IGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
CRF03_AB_R	VG.IGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
CRF04_cpx_	AVGIGAMFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF04_cpx_	AVGLGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF04_cpx_	AVGIGAVFFG	LFLGAAGSTM	GAASITLTVQ	ARQLLFGIVQ	QQSNLLRAIE
CRF05_DF_B	MG.IGAMFLG	.FLAAAGSTM	GAASIALTVQ	ARQLLSGIVQ	QQNNLLQAIE
CRF05_DF_B	VG.VGALLIG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQNNLLQAIE
CRF06_cpx_	VGLG.AMFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLRAIE
CRF06_cpx_	VGLG.AVFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLRAIE
CRF06_cpx_	VGIG.AFFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLRAIE
CRF06_cpx_	VGLG.AVFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVH	QQSNLLRAIE
CRF11_cpx_	VGIG.AVLFG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLKAIE
CRF11_cpx_	VGIG.AVLLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLKAIE
D_CD_84ZR0	IG.LGAMFLG	.FLGAAGSTM	GAASMTLTVQ	ARQVLSGIVQ	QQNNLLRAIE
D_CD_ELI_K	IG.LGAMFLG	.FLGAAGSTM	GARSVTLTVQ	ARQLMSGIVQ	QQNNLLRAIE
D_CD_NDK_M	IG.LGAVFLG	.FLGAAGSTM	GAASVTLTVQ	ARQLMSGIVH	QQNNLLRAIE
D_UG_94UG1	IG.LGALFLG	.FLGTAGSTM	GAVSLTLTVQ	ARQVLSGIVQ	QQNNLLRAIE
F1_BE_VI85	AG.LGALFLG	.FLGDSREHM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
F1_BR_93BR	VG.LGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
F1_FI_FIN9	VA.IGAVFLG	.FLSAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLQAIE
F1_FR_MP41	VG.IGALFLR	.FLGAAGSNI	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
F2_CM_MP25	VG.MGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARNLLSGIVQ	QQSNLLKAIE
F2KU_BE_VI	AG.LGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSDLLRAIE
G_BE_DRCBL	VGVG.AIFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLRAIE
G_UG_92NG0	VGLG.AVFLG	.FLGAAGSTM	GAASITLTAQ	VRQLLSGIVQ	QQSNLLRAIE
G_SE_SE616	VGLG.AVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQGNLLRAIE
H_BE_VI991	AVGMGAFFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIQ
H_BE_VI997	AVGMGAFFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIQ
H_CF_90CF0	AVGMGASFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIQ
J_SE_SE702	VGIG.AVFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLKAIX
J_SE_SE788	VGIG.AVFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLKAIE
K_CD_EQTB1	VG.IGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
K_CM_MP535	VG.LGAVFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
N_CM_YBF30	AFGLGALFLG	.FLGAAGSTM	GAASITLTVQ	ARTLLSGIVQ	QQNILLRAIE
O_CM_ANT70	AVGLGMLFLG	.VLSAAGSTM	GAAATTLAVQ	THTLLKGIVQ	QQDNLLRAIQ
O_CM_MVP51	AVGLGMLFLG	.VLSAAGSTM	GAAATALTVR	THSVLKGIVQ	QQDNLLRAIQ
O_SN_99SE_	AVGLGMLFLG	.VLSAAGSTM	GAAATALAVQ	TQSLMKGIVQ	QQDNLLRAIQ
O_SN_99SE_	AVGLGMLFLG	.VLSAAGSTM	GAAATTLAVQ	THTLMKGIVQ	QQDNLLRAIQ
U_CD_83C	AVGMGALFLG	.FLGAAGSTM	GAASMALTAQ	ARQLLSGIVQ	QQNNLLRAIE

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00BW0768_2	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGLWGCSG	KLICTTSVHW
00BW0874_2	AQQHMLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPR
00BW1471_2	AQQHMLQLTV	WGIKQLQARV	LALERYLQDQ	QLLGIWGCSG	KLICTPVPW
00BW1616_2	AQQHMLQLTV	WGIKQLQARV	LAIERYLRDQ	QLLGIWGCSG	KLICTTNVPW
00BW1686_8	AQQHMLQLTV	WGIKQLQTRV	LAMERYLKDQ	QLLGLWGCSG	KIICTTNVPW
00BW1759_3	AQQHMLQLTV	WGINQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
00BW1773_2	AQQHLLQLTV	WGIKQLQTRV	LSIERYLQDQ	QLLGIWGCSG	KLICTTAVPW
00BW1783_5	AQQHMLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
00BW1795_6	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
00BW1811_3	AQQHLLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
00BW1859_5	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
00BW1880_2	AQQHMLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGMWGCSG	KIICTTVPW
00BW1921_1	AQQHLLQLTV	WGIKQLQTRV	LAIERYLKDQ	QILGIWGCSG	KLICTTSPW
00BW2036_1	AQQHMLQLTV	WGIKQLQARV	LAIERYLRDQ	QLLGLWGCSG	KLICTTVPW
00BW2063_6	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICPTAVPW
00BW2087_2	AQQHLLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
00BW2127_2	AQQHLLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
00BW2128_3	ARRHLLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
00BW2276_7	AQQHMLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
00BW3819_3	AQQHLLQLTV	WGIKQLQTRV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
00BW3842_8	AQQHMLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTNVPW
00BW3871_3	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGLWGCSG	KLICTTNVPW
00BW3876_9	AQQHLLQLTV	WGIKQLQTRV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
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00BW3891_6	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTNVPW
00BW3970_2	AQHLLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
00BW5031_1	AQQHMLQLTV	WGIKQLQARV	LAIERYLRDQ	QLLGIWGCSG	KIICTTAVPW
96BW01B21	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTNVPW
96BW0407	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTNVPW
96BW0502	AQQHLLQLTV	WGIKQLQTRI	LAVERYLKDQ	QLLGIWGCSG	KLICTTAVPW
96BW06_J4	AQQHMLQLTV	WGIKQLQTKV	LAIERYLKDQ	QLLGFWGCSG	KLVCTTAVPW
96BW11_06	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
96BW1210	AQQHMLQLTV	WGIKQLQARV	LALERYLRDQ	QLLGIWGCSG	KLICTTNVPW
96BW15B03	AQQHMLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTVPW
96BW16_26	AQQHLLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
96BW17A09	AQQHMLQLTV	WGIKQLQARV	LALERYLKGQ	QLLGIWGCSG	KLICTTSPW
96BWM01_5	AQQHMLQLTI	WGIKQLQTRV	LAVERYLRDQ	QLLGIWGCSG	KLICTTAVPW
96BWM03_2	AQQHMLQLTV	WGIKQLRARV	LAIERYLKDQ	QLLGVWGCSG	RLICTTAVPW
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98BWM013_4	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
98BWM014_a	AQQHLLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLSLWGCSG	RLICTTNVPW
98BWM014_1	AQQHMLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
98BWM018_d	AQQHMLQLTV	WGIKQLQARV	LALERYLRDQ	QLLGIWGCSG	KLICTTNVPW
98BWM036_a	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
98BWM037_d	AQQHLLQLTV	WGIKQLQARV	LAMERYLKDQ	QLLGIWGCSG	KLICTTAVPW
99BW3932_1	AQQHLLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
99BW4642_4	AQQHMLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGLWGCSG	KLICTTAVPW
99BW4745_8	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KIICTTAVPW
99BW4754_7	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
99BWM016_8	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGYSG	KLICTTVPW
A2_CD_97CD	AQQQMLRLTV	WGIKQLQARV	LALERYLQDQ	QLLGIWGCSG	KLICATDVRW
A2_CY_94CY	AQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICATTVPW
A2D_97KR	AQQHMLRLTV	WGIKQLQARV	LAVERYLQDQ	QLLGIWGCSG	KLICTTFVPW
A2G_CD_97C	AQQHLLKLTV	WGIKQLQARV	LALERYLQDQ	QLLGLWGCSG	KLICTTIVPW
A_BY_97BL0	AQQXLLKLTV	XGIKQLQARX	LAVEXYLKQD	QXLRIXGCSX	KLICTTNVPX
A_KE_Q23_A	AQQHLLKLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTNVPW
A_SE_SE659	AQQHLLKLTV	WGIKQLQARI	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
A_SE_SE725	AQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
A_SE_SE753	VQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTVPW

A_SE_SE853	AQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
A_SE_SE889	AQQHLLKLTV	WGIKQLQAQV	LAVERYLRDQ	QLLGIWGCSG	KLICTTTVPW
A_SE_UGSE8	AQQHMLRLTV	WGIKQLQARV	MAVERYLKDQ	QLLGIWGCSG	KIICTTAVPW
A_UG_92UG0	AQQHLLKLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICPTNVPW
A_UG_U455_	AQQHLLKLTV	WGIKQLQARV	LAVERYLQDQ	QLLGIWGCSG	KLICTTTVPW
AC_IN_2130	AQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
AC_RW_92RW	AQQHLLKLTV	WGIKQLQARV	LALERYLRDQ	QLLGIWGCSG	KLICTTNVPW
AC_SE_SE94	AQQHLLKLTV	WGIKQLQARI	LAVERYLKDQ	QLLGIWGCSG	KIICTTNVPW
ACD_SE_SE8	AQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICATNVPW
ACG_BE_VI1	AQQHMLQLTV	WGIKQLQTRV	LAIERYLQVQ	QLLGIWGCSG	KLICTTSVPW
AD_SE_SE69	AQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
AD_SE_SE71	AQQHLLKLTV	WGIKQLQARV	LALERYLKDQ	QLLGIWGCSG	KLICPTTVPW
ADHK_NO_97	AQQHMLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
ADK_CD_MAL	AQQHLLQLTV	WGIKQLQARV	LAVERYLQDQ	RLLGMWGCSG	KHICTTFVPW
AG_BE_VI11	AQQHMLQLTV	WGIKQLQARV	LAVERFLKDQ	QLLGIWGCSG	KLICTTNVPW
AG_NG_92NG	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
AGHU_GA_VI	AQQHLLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTNVPW
AGU_CD_Z32	AQQHLLKLTV	WGIKQLQARI	LAVERYLKDQ	QLLGIWGCSG	KIICPTNVPW
AJ_BW_BW21	AQQHLLRLTV	WGIKQLQAKI	LAVERYLQDQ	QLLGIWGCSG	KFICTTTVP.
B_AU_VH_AF	AQQHLLQLTV	WGIKQLQARI	LAVERYLEDQ	QLLGIWGCSG	KLICTTSVPW
B_CN_RL42_	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTAVPW
B_DE_D31_U	AQQHLLQLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTAVPW
B_DE_HAN_U	AQQHLLQLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTTVPW
B_FR_HXB2_	AQQHLLQLTV	WGIKQLQARI	LAVERYLKDQ	QLLGIWGCSG	KLICTTAVPW
B_GA_OYI_	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTTVPW
B_GB_CAM1_	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTAVPW
B_GB_GB8_C	AQQHLLRLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTTVPW
B_GB_MANC_	AQQHLLQLTV	WGIKQLQARV	LAVERYLQDQ	QLLGIWGCSG	KLICTTAVPW
B_KR_WK_AF	AQQHLLQLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTNVPW
B_NL_3202A	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTAVPW
B_TW_TWCYS	AQQHMLQLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICNTNVPW
B_US_BC_L0	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTAVPW
B_US_DH123	AQQHMLQLTV	WGIKQLQARV	LAVERYLQDQ	QLLGIWGCSG	KLICTTTVPW
B_US_JRCSF	AQQHMLQLTV	WGIKQLQARV	LAVERYLKDQ	QLMGIWGCSG	KLICTTAVPW
B_US_MNCG_	AQQHMLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGFWGCSG	KLICTTTVPW
B_US_P896_	AQQHMLQLTV	WGIKQLQARV	LALERYLRDQ	QLMGIWGCSG	KLICTTSVPW
B_US_RF_M1	AQQHLLQLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTTVPW
B_US_SF2_K	AQQHLLQLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTAVPW
B_US_WEAU1	AQQHLFELTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTTVPW
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B_US_YU2_M	AQQHLLQLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTTVPW
BF1_BR_93B	AQQHLLQLTV	WGIKQLQARI	LAVERYLKDQ	QLLGLWGCSG	KLICTTDVPW
C_BR_92BR0	AQQHMLQLTV	WGIKQLQTRV	LAIERYLRDQ	QLLGIWGCSG	KLICTTAVPW
C_BW_96BW0	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTNVPW
C_BW_96BW1	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
C_BW_96BW1	AQQHMLQLTV	WGIKQLQARV	LALERYLRDQ	QLLGIWGCSG	KLICTTNVPW
C_BW_96BW1	AQQHMLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTTVPW
C_ET_ETH22	AQQHMLQLTV	WGIKQLQTRV	LAIERHLRDQ	QLLGIWGCSG	KLICTTAVPW
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C_IN_95IN2	AQQHLLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
CRF01_AE_C	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	KFLGLWGCSG	KIICTTNVPW
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CRF01_AE_T	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	KFLGLWGCSG	KIICTTAVPW
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CRF01_AE_T	AQQHMLQLTV	WGIKQLQARV	LAVERYLKDQ	KFLGLWGCSG	KIICTTAVPW
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CRF01_AE_T	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	KFLGLWGCSG	KIVCTTAVPW
CRF02_AG_F	AQQHLLKLTV	WGIKQLQARV	LALESYLRDQ	QLLGIWGCSG	KLICTTNVPW
CRF02_AG_F	AQQHLLKLTV	WGIKQLQARV	LALERYLRDQ	QLLGIWGCSG	KLICTTTVPW
CRF02_AG_G	AQQHLLKLTV	WGIKQLQARV	LALERYLSDQ	QLLGIWGCSG	KLICTTNVPW
CRF02_AG_N	AQQHLLKLTV	WGIKQLQARV	LALERYLRDQ	QLLGIWGCSG	KLICTTTVPW
CRF02_AG_S	AQQHLLRLTV	WGIKQLQARV	LALAYLKDQ	QLLGIWGCSG	KLICTTTVPW
CRF02_AG_S	AQQHLLKLTV	WGIKQLQARV	LALERYLKDQ	QLLGIWGCSG	KLICTTTVPW
CRF03_AB_R	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTAVPW
CRF03_AB_R	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTAVPW
CRF04_cpx_	AQQHLLRLTV	WGIKQLQARV	LALESYLRDQ	QLLGIWGCSG	KLICTTNVPW
CRF04_cpx_	AQQHLLKLTV	WGIKQLQARV	LALESYLRDQ	QLLGIWGCSG	KLICTTNVPW
CRF04_cpx_	AQQQLRLTV	WGVKQLQARV	LALESYLRDQ	QLLGIWGCSG	RLICTTNVPW
CRF05_DF_B	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGLWGSSG	KHICSTSVPW
CRF05_DF_B	AQQHLLQLTV	WGIKQLQARV	LAVERYLRDQ	QLLGLWGCSG	KLICTTSVPW
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CRF06_cpx_	AQQHLLQLTV	WGIKQLQARI	LAVERYLKDQ	QLLGIWGCSG	KLICPTNVPW
CRF06_cpx_	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICPTNVPW
CRF06_cpx_	AQQHLLQLTV	WGIKQLQARV	LALERYLKDQ	QLLGIWGCSG	KLICPTNVPW
CRF11_cpx_	AQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
CRF11_cpx_	VQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
D_CD_84ZR0	AQQHLLQLTV	WGIKQLQARI	LAVERYLKDQ	QLLGIWGCSG	KHICTTTVPW
D_CD_ELI_K	AQQHLLQLTV	WGIKQLQARI	LAVERYLKDQ	QLLGIWGCSG	KHICTTNVPW
D_CD_NDK_M	AQQHLLQLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	RHICTTNVPW
D_UG_94UG1	AQQHLLQLTV	WGIKQLQARI	LAVESYLRDQ	QLLGIWGCSG	KHICTTNVPW
F1_BE_VI85	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
F1_BR_93BR	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGLWGCSG	KLICTTNVPW
F1_FI_FIN9	AQQHMLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGLWGCSG	KLICTTNVPW
F1_FR_MP41	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
F2_CM_MP25	AQQHLLQLTV	WGIKQLQARI	LAVERYLKDQ	QLLGIWGCSG	KLICPTTVPW
F2KU_BE_VI	AQQHLLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTNVPW
G_BE_DRCBL	AQQHLLQLTV	WGIKQLRARV	LALERYLKDQ	QLLGIWGCSG	KLICTTNVPW
G_NG_92NG0	AQQHLLQLTV	WGIKQLQSRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTNVPW
G_SE_SE616	AQQHLLQLTV	WGIKQLQARL	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
H_BE_VI991	AQQHMLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
H_BE_VI997	AQQHMLQLTV	WGVKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
H_CF_90CF0	ARQHMLQLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTNVPW
J_SE_SE702	AQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
J_SE_SE788	AQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
K_CD_EQTB1	AQQQMLQLTV	WGIKQLRARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTNVPW
K_CM_MP535	AQQHLLQLTV	WGIKQLRARI	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
N_CM_YBF30	AQQHLLQLSI	WGIKQLQAKV	LAIERYLRDQ	QILSLWGCSG	KTICYTTVPW
O_CM_ANT70	AQQQLRLSV	WGIRQLRRL	LALETLLQNQ	QLLSLWGCKG	KLVCYTSVKW
O_CM_MVP51	AQQHLLRLSV	WGIRQLRRL	QALETLLQNQ	QLLNWLWGCKG	KLICYTSVKW
O_SN_99SE_	AQQQLRLSV	WGIRQLRRL	LALETLLQNQ	QLLNWLWGCKG	KLICYTSVKW
O_SN_99SE_	AQQQLRLSV	WGIRQLRRL	LALETLLQNQ	QLLNWLWGCKG	RLVCYTSVKW
U_CD___83C	AQQHLLQLTV	WGIKQLQARV	LAVERYLESQ	QLLGLWGCSG	KLICTTTVPW

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00BW1471_2	NSSWSN....	KSVDDIWKN.	.MTWMEWDKE	INNYTKIYIN	LLEKSQKQQE
00BW1616_2	NSSWST....	RNYSDIWNN.	.MTWMQWDRE	IDNYTDIYR	LLEESQNQQE
00BW1686_8	NASWSN....	KSQEDIWNN.	.MTWMPWDRE	INNYTRTIYE	LLEESQSQQE
00BW1759_3	NHSWSN....	KSEEDIWNH.	.TTWMQWDRE	ISNYTDTIYR	LLEDSQNQQE
00BW1773_2	NSSWSN....	RSQDDIWEN.	.MTWMQWDKE	ISNYTNTIYN	LLEKSQNQQE
00BW1783_5	NTSWSN....	KSQNDIWDN.	.MTWMQWDRE	ISNYTGIIYN	LLEESQIQQE
00BW1795_6	NVSWSN....	KSYKAIWDN.	.MTWMQWDRE	ISNYTDTIYS	LLEDSQNQQE
00BW1811_3	NNSWSN....	KSFTEDIWDN.	.MTWMEWDRE	ISNYTNTIYR	LLEKSQNQQE
00BW1859_5	NSSWSN....	KSQADIWDN.	.MTWMQWDRE	ISNYTDTIYR	LLEDSQIQQE
00BW1880_2	NDSWSN....	KSQEYIWGN.	.MTWMQWDRE	INNYTNTIYR	LLENSQNQRE
00BW1921_1	NSSWSN....	KSLTEIWDN.	.MTWMQWDRE	ISNYTETIYR	LLEDSQNQQE
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00BW2063_6	NASWSN....	KSHDEIWEN.	.MTWMQWDRE	ISNYTDIYR	MLEDSQNQQE
00BW2087_2	NSSWSN....	KSQAEIWDN.	.MTWMQWDRE	ISNYTNTIYK	LLEDSQLQQE
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00BW2128_3	NSSWSN....	RSKTEIWDN.	.MTWMQWDRE	ISNYTETIYR	LLEESQNQQE
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00BW3842_8	NSSWSN....	KSLEDIWDN.	.MTWMQWDRE	ISNYTREIYK	LLEESQNQQE
00BW3871_3	NLSWSN....	KSQKDIWES.	.MTWMQWDNE	ISNYTGIIYE	LLEDSQNRQE
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96BW0407	NNSWSN....	KSLNYIWEN.	.MTWMEWDRE	ISNYSDTIYR	LLEDSQNQQE
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96BW06_J4	NSSWSN....	KSLGDIWDN.	.MTWMQWDRE	ISNYTGTIYR	LLEDSQNQQE
96BW11_06	NASWSN....	KSQEEIWGN.	.MTWMQWDRE	ISNYTDTIYR	LLEVSQNQQE
96BW1210	NSSWSN....	KTENEIWEN.	.MTWMQWERE	IDNYTDTIYR	LLEVSQNQQE
96BW15B03	NSSWSN....	KTQGEIWEN.	.MTWMQWDKE	ISNYTGIIYR	LLGESQNQQE
96BW16_26	NVSWSN....	RSEDDIWNN.	.MTWMQWDRE	INNYTNTIYR	LLEESQNQQE
96BW17A09	NSTWSN....	KSLDDIWQN.	.MTWMEWDRE	INNYTNTIYR	LLEESQNQQE
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98BWMC13_4	NASWSN....	KSQGEIWEN.	.MTWMQWDRE	INNYTDTIYR	LLEESQNQQE
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CRF03_AB_R	NTSWSN....	KPLDEINN..	.MTWMEWERE	INNYTGIIYN	LIEESQNQQE
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G_BE_DRCBL	NTSWSN....	KSYPEIWN.	.MTWIEWERE	IDNYTYHIYS	LIEESQIQQE
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H_BE_VI991	NSSWSN....	KSLDEIWDN.	.MTWMEWDKQ	INNYTDEIYR	LLEVSQNQQE
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O_CM_MVP51	NTSWSGRYN.	DDS..IWDN.	.LTWQQWDQH	INNVSSIIYD	EIQAAQDQQE
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00BW1616_2	KNEKDLLALD	SWNSLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW1686_8	QNEKDLLALD	SWKNLWNWFD	ISNWLWYIKI	FIIIVGGLIG	LRIIFAVLSI
00BW1759_3	INEKDLLALD	SWKNLWNWFD	ITKWLWYIKI	FIMIVGGIIG	LRIIFAVLSI
00BW1773_2	KNEKDLLALD	SWKNLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW1783_5	KNEKDLLALD	SWNNLWNWFT	ITNWLSYIKI	FIMIVGGLIG	LRIIFAVLSL
00BW1795_6	KNEKDLLALD	SWKNLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW1811_3	INEKDLLALD	SWKNLWSWFD	ISNWLWYIRI	FIMIVGGLIG	LRIIFAVLSI
00BW1859_5	KNEKDLLALD	SWKNLWSWFD	ITNWLWYIRI	FIIIVGGLIG	LRIIFAVLSI
00BW1880_2	QNEKDLLALD	SWKNLN.WFS	IT.HLWYIKI	FIMIVGGLIG	LRIVLVLSV
00BW1921_1	KNEKDLLALD	SWNNLWNWFS	ITKWLWYIKI	FIIIIGGLIG	LRIIFAVLSI
00BW2036_1	QNEKDLLALD	SWKNLWTWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW2063_6	KNERDLLALD	SWKNLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSM
00BW2087_2	NNEKDLLALD	SWNNLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW2127_2	QNEKDLLALD	RWDSLWNWFG	ISKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW2128_3	KNEEDLLALD	SWDSLWNWFS	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW2276_7	QNEKDLLALD	SWKNLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW3819_3	QNEKDLLALD	SWKNLWTWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFTVFSI
00BW3842_8	INEKDLLALD	SWNSLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW3871_3	KNEKDLLALD	SWKNLWNWFD	ITNWLWYIKI	FIIIIGGLIG	LRIIFAVLSI
00BW3876_9	QNEKDLLALD	SWNSLWSWFD	ITRWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW3886_8	KNEQELLALD	SWKSLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSL
00BW3891_6	RNEKDLLAMD	SWKNLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
00BW3970_2	QNEQDLLALN	KWQHLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW5031_1	QNEKDLLALD	SWKNLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW01B21	KNEKDLLALD	SWQNLWNWFS	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
96BW0407	KNEKDLLALD	SWNNLWNWFS	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW0502	KNEKDLLALD	SWQNLWNWFS	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW06_J4	KNEKDLLALD	SWKNLWNWFG	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW11_06	KDEKDLLALD	SWQNLWNWFD	IPKWLWYIKI	FIMIVGGLIG	LRIIFAVISM
96BW1210	QNEKDLLALD	SWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW15B03	QNEKDLLALD	SWNNLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW16_26	KNEKDLLALD	SWNSLWNWFS	IVNWLRYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW17A09	KNEQELLALD	SWANLWNWFA	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSV
96BWM01_5	RNEKDLLALD	SWKTLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BWM03_2	KNEQDLLALD	SWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
98BWMC12_2	ENEKDLLALD	SWKNLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
98BWMC13_4	KNEKDLLALD	SWKNLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSM
98BWMC14_a	KNEKDLLALD	KWKDLRNWFD	ISNWLWYIRI	FIMIVGGLIG	LRIIFAVLSI
98BWM014_1	KNEKDLLALD	SWNNLWTWFG	ISSWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
98BWM018_d	RNEKDLLALD	SWNNLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
98BWM036_a	QNEKDLLALD	SWQSLWNWFS	ITKRLWYIKI	FIMIVGGLIG	LRIIFAVLSI
98BWM037_d	QNEKDLLALD	SWQNLWSWFS	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSL
99BW3932_1	KNEKDLLALD	SWQNLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
99BW4642_4	KNEKDLLALD	SWKNLWTWFD	ISNWLWYIRI	FIMIVGGLIG	LRIIFAVLSI
99BW4745_8	QNEKELLALD	RWDTLWSWFD	ITNWLWYIRL	FIMIVGGLIG	LRIIFAVLSI
99BW4754_7	KSEKDLLALD	SWKNLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSV
99BWMC16_8	RNEKDLLALD	SWKNLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
A2_CD_97CD	KNEQDLLALD	KWANLWNWFD	ITRWLWYIKI	FIMIVGGLIG	LRIVIAIISV
A2_CY_94CY	KNEQDLLALD	KWADLWSWFD	ISHWLWYIRI	FIMIVGGLIG	LRIVFAIITV
A2D_97KR	KNEKDLLALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVMAIISV
A2G_CD_97C	KNKQDLLALD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
A_BY_97BL0	KNXQDLLALD	KAG.LXSXXD	ISNWLXYIXI	FIIIVGGLIX	LRIIFAVLSI
A_KE_Q23_A	KNEKELLELD	KWANLWSWFD	ISNWLWYIKI	FIIIVGGLIG	LRIVFAVLSV
A_SE_SE659	MNEQDLLALD	KWANLWNWFD	ITNWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
A_SE_SE725	KNEQDLLALD	KWANLWNWFE	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVFSV
A_SE_SE753	KNEQDLMALD	KWTNLWTWFS	ISNWLWYIRI	FIMIVGGLIG	LRIVFAVLAI

A_SE_SE853	KNEQDLLALD	KWASLWNWFD	ISRWLWYIRI	FIMIVGGLIG	LRIVFAVLSV
A_SE_SE889	KNEQDLLALD	KWANLWNWFD	ISKWLWYIKI	FIMIVGGLIG	LRIVIAVISI
A_SE_UGSE8	KNEKELLELD	KWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLTV
A_UG_92UG0	RNEKDILLELD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGLIG	LRIVFAVLSV
A_UG_U455	KNELDLLALD	KWANLN.WFN	ISNWLWYIRL	FVIIVGGLIG	LRIVFTVLSI
AC_IN_2130	KNEQDLLALD	KWADLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSV
AC_RW_92RW	KNEQDLLALD	KWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
AC_SE_SE94	KNEQDLLALD	KWASLWNWFD	ISKWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
ACD_SE_SE8	KNEQDLLALD	KWGSLWNWFE	ISKWLWYIRI	FIMIVGGLIG	LRIVFAVLSV
ACG_BE_VI1	QNEKDLLALD	KWQNLWSWFN	ISNWLWYIKI	FIMIVGGLIG	LRIIFAILS
AD_SE_SE69	KNEQDLLALD	KWANLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSL
AD_SE_SE71	MNEQDLLQLD	KWASLWNWFD	ITNWLWYIRI	FIIIVGGLIG	LRIVFAVLSL
ADHK_NO_97	XNEQDLLALD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGVIG	LRIVFAVLSI
ADK_CD_MAL	KNEKELLELD	KWASLWNWFS	ISKWLWYIRI	FIIIVGGLIG	LRIIFAVLSL
AG_BE_VI11	KNEQDLLSLD	KWASLWTWFD	IANWLWYIRI	FIMIVGGLIG	LRVVFVAVLN
AG_NG_92NG	KNEQDLLALD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
AGHU_GA_VI	KNEQELLALD	KWASLWSWFD	ISKWLWYIRI	FIMIVGGLIG	LRIFFAVLSM
AGU_CD_Z32	INERDLLALD	KWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
AJ_BW_BW21	KNEQDLLSLD	KWASLWNWFS	ISNWLWYIRI	FIMIVGGLIG	LRIIFAVLAI
B_AU_VH_AF	KNEQELLALD	KWASLWNWFS	ITKWLWYIKI	FIMIVGGLVG	LRIVFAVLSL
B_CN_RL42	KNELELLELD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLVG	LRIVFAVLSI
B_DE_D31_U	KNEQELLELN	KWENLWSWFD	ISNWLWYIKI	FIMIVGGLVG	LRIVFAVLSI
B_DE_HAN_U	KNEQELLELD	KWASLWSWYD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
B_FR_HXB2	KNEQELLELD	KWASLWNWFN	ITNWLWYIKL	FIMIVGGLVG	LRIVFAVLSI
B_GA_OYI	KNEQELLELD	KWAGLWSWFS	ITNWLWYIRI	FIIIVGGLVG	LRIVFAVLSI
B_GB_CAM1	KNEKDILLELD	TWASLWNWFD	ITNWLWYIKI	FIMIIGGLIG	LRIVFTILSL
B_GB_GB8_C	KNEQELLELD	KWANLWNWFD	ITNWLWYIKI	FIMIIGGLIG	LRIIFAVIST
B_GB_MANC	KNEQELLELD	KWGSLWSWFS	ITNWLWYIKI	FIMIVGGLVG	LRIVFAVLSL
B_KR_WK_AF	KNEQELLELD	KWASLN.WFN	ITKWLWYIKI	FIMIVGGLVG	LRIIFFVLSI
B_NL_3202A	KNEQELLELD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLVG	LRIIFAVLSI
B_TW_TWCYS	KNEQDILLELD	KWASLWNWFD	ITNWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
B_US_BC_L0	KNEQELLELD	KWASLWNWFT	ITNWLWYIKI	FIMIVGGLIG	LRIVFTVLSI
B_US_DH123	KNEQELLALD	KWASLWNWFN	ISNWLWYIKI	FIMIVGGLIG	LRIVFSVLSI
B_US_JRCSF	KNEQELLELD	KWASLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIVFSVLSI
B_US_MNCG	KNEQELLELD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLVG	LRIVFAVLSI
B_US_P896	KNEKELLELD	KWASLWNWFD	ITNWLWYIRL	FIMIVGGLIG	LRIVFAVLSI
B_US_RF_M1	KNEQELLELD	KWANLWNWFD	ITQWLWYIRI	FIMIVGGLVG	LKIVFAVLSI
B_US_SF2_K	KNEQELLELD	KWASLWNWFS	ITNWLWYIKI	FIMIVGGLVG	LRIVFAVLSI
B_US_WEAU1	KNEQELLELD	KWASLWTWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFTVLSI
B_US_WR27	KNEQELLELD	KWASLWNWFN	ITQWLWYIKI	FXMIVGGLIG	LRIVFAVLSI
B_US_YU2_M	KNEQELLALD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFVLSI
BF1_BR_93B	KNEQELLALD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
C_BR_92BR0	KNEQDLLALD	KWQNLWTWFG	ITNWLWYIKI	FIKIVGGLIG	LRIIFAVLSI
C_BW_96BW0	KNEKDLLALD	SWNNLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIIFAALSI
C_BW_96BW1	KNEKDLLALD	SWKNLWNWFD	ISKWLWYIKI	FIMIVGGLIG	LRIIFAVISM
C_BW_96BW1	QNEKDLLALD	SWANLWNWFN	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
C_BW_96BW1	QNEKDLLALD	SWNNLWSWFN	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
C_ET_ETH22	KNEKDLLALD	KWENLWNWFN	ITNWLWYIKI	FIMIVGGVIG	LRIIFAVLSI
C_IN_93IN1	KNEKDLLALD	SWKNLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
C_IN_93IN9	KNEKDLLALD	SWKNLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
C_IN_93IN9	RNEKDLLALD	SWESLWNWFS	ISKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
C_IN_94IN1	KNEKDLLALD	SWKNLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
C_IN_95IN2	ENEKDLLALD	SWKNLWNWFD	ITKWLWYIKI	FIIIVGGLIG	LRIIFAVISI
CRF01_AE_C	KNEQDLLALD	KWANLWNWFS	ITNWLWYIKI	FIMVVGGLIG	LRIVFAVLSI
CRF01_AE_C	RNEKDLLALD	KWASLWNWFD	ITRWLWYIKI	FIIIVGGLIG	LRIVFAVLSI
CRF01_AE_C	RNEKDILLELD	KWTSLWNWFD	ITRWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
CRF01_AE_T	RNEKDILLELD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF01_AE_T	RNEKDILLELD	KWANLWNWFS	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF01_AE_T	RNEKDILLELD	KWASLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF01_AE_T	KNEKDILLELD	KWASLWNWFD	ITSWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF01_AE_T	RNEKDILLELD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI

CRF01_AE_T	RNEKDLLKLD	KWASLWNWFD	ISRWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
CRF02_AG_F	KNEQDLLALD	QWANLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLTI
CRF02_AG_F	KNEKDLLALD	KWESLWNWFN	ITKWLWYIKI	FIMIVGGLIG	LRIVLAVLTV
CRF02_AG_G	KNEQDLLALD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFVVLAI
CRF02_AG_N	KNEQDLLALD	KWASLWNWFD	ITNWLWYIRI	FIMIVGGLIG	LRIVFAVLTI
CRF02_AG_S	KNEQDLLALD	KWASLWDWFS	ISSWLWYIRI	FIIIVGGLIG	LRIVFAVLAI
CRF02_AG_S	KNEQDLLALD	KWASLWNWFD	ITNWLWYILI	FLMVVGGLIG	LRIVFAVLAI
CRF03_AB_R	KNEQEILALD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGLVG	LRIIFAVLSI
CRF03_AB_R	KNEQEELLALD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGLVG	LRIIFAVLSI
CRF04_cpx_	KNEQDLLALD	KWASLWNWFS	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF04_cpx_	KNEQDLLAFD	KWANLWNWFN	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF04_cpx_	KNEQDLLALD	KWANLWSWFD	ISHWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF05_DF_B	KNEQEELSLD	QWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFTVLSI
CRF05_DF_B	KNEKDLLALD	KWASLWNWFS	ISNWLWYIRI	FIMIVGGLIG	LRIVFTVLSV
CRF06_cpx_	KNEQDLLALD	KWANLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVISI
CRF06_cpx_	KNEQDLLALD	KWASLWSWFD	ISNWLWYIRI	FVIIVGGLLG	LRIVFAVFSI
CRF06_cpx_	KNEQDLLALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF06_cpx_	KNEQEELLALD	KWASLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LKIVFAVLSL
CRF11_cpx_	KNEQDILLSL	KWASLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSV
CRF11_cpx_	KNEQDLLALD	KWASLWNWFD	ISNWLWYIRI	FIMIVGGLIG	LRIIFAVLSI
D_CD_84ZR0	KNEKELLELD	KWASLWNWFS	ITQWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
D_CD_ELI_K	KNEKELLELD	KWASLWNWFS	ITQWLWYIKI	FIMIIGGLIG	LRIVFAVLSL
D_CD_NDK_M	KNEKELLELD	KWASLWNWFS	ITKWLWYIKL	FIMIVGGLIG	LRIVFAVLSV
D_UG_94UG1	KNEQEELKLD	TWASLWNWFS	ITQWLWYIKI	FIMIVGGLIG	LRIVFAVLSV
F1_BE_VI85	KNEQEELLALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
F1_BR_93BR	KNEQEELLALD	KWASLWNWFD	ITQWLWYIKI	FIMIVGGLIG	LRIVFTVLSI
F1_FI_FIN9	RNEQEELLELD	KWDSLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
F1_FR_MP41	KNEQEELLALD	KWASLWSWFD	ISNWLWYIKI	FIMIVGGMIG	LRIVFAVLSI
F2_CM_MP25	KNEQDLLALD	KWDNLWNWFS	ITRWLWYIEI	FIMIIGSLIG	LRIVFTVLSI
F2KU_BE_VI	KNEQDLLALD	QWASLWSWFN	ITQWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
G_BE_DRCBL	KNEQDLLALD	QWASLWSWFS	ISNWLWYIRI	FVMIVGGLIG	LRIVFAVLSI
G_NG_92NG0	KNEQDLLALD	KWASLWNWFD	ISNWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
G_SE_SE616	KNEQDLLALD	QWASLWNWFG	ITRWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
H_BE_VI991	KNEQDLLALD	KWANLWNWFS	ITNWLWYIRI	FIMIVGGIIG	LRIVFAVLSI
H_BE_VI997	QNEQDLLALD	KWDSLWNWFS	ITNWLWYIKI	FIIIVGALIG	LRIIFAVLSI
H_CF_90CF0	KNEQDLLALD	KWASLWTWFD	ISHWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
J_SE_SE702	TNEKDLLALD	KWTNLWNWFN	ISNWLWYIKI	FIMIIGGLIG	LRIIFAVLAI
J_SE_SE788	NNEKDLLALD	KWTNLWNWFN	ISNWLWYIKI	FIMIIGGLIG	LRIIFAVLAI
K_CD_EQTB1	KNEQDLLALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFTVLSV
K_CM_MP535	KNEQDLLALD	KWASLWNWFD	ITKWLWYIKI	FIMIIGGLIG	LRIAFAVLSV
N_CM_YBF30	TNEKSLEELD	QWDSLWSWFG	ITKWLWYIKI	AIMIVAGIVG	IRIISIVITI
O_CM_ANT70	QNEKKLEELD	EWASIWNWLD	ITKWLWYIKI	AIIIVGALVG	VRVIMIVLNI
O_CM_MVP51	KNVKALLELD	EWASLWNWFD	ITKWLWYIKI	AIIIVGALIG	IRVIMIILNL
O_SN_99SE_	QNEKKLEELD	EWASIWNWLD	ITKWLWYIKI	AIIIVGALIG	VRIVMIVLNL
O_SN_99SE_	HNEKKLEELD	EWASIWNWLD	ITKWLWYIKI	AIIIVGALIG	VRIVMIVLNL
U_CD_83C	KSEKDLEELD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIVFTVFSI

00BW0762_1	VNRVRQGYSP	LSFQTLTP..	NQR.GPDRLG	GIEEEGGEQD	RDRSIRLVSG
00BW0768_2	VNRVRQGYSP	LSFQTLIP..	NPR.GPDRLG	RIEEEGGEQD	KDRSIRLVSG
00BW0874_2	VNRVRQGYSP	LSFQTLTP..	SPR.EPDRLG	RIEEEGGEQD	KDRSIRLVGG
00BW1471_2	VNRVRQGYSP	LSFQTLIP..	NPR.GPDRLE	RIEEEGGEQD	RGRSVRLVSG
00BW1616_2	VNRVRQGYSP	LSFQTLTP..	NPR.ELDRLG	RIEEEGGEQD	RDRSIRLVSG
00BW1686_8	VNRVRQGYSP	LSLQTLTP..	NPR.GPDRPR	GIEEEGGEQD	KDRSIRLVNG
00BW1759_3	VNRVRQGYSP	SSFQTLIP..	NPE.GPDRLR	RIEEEGGEQD	RDRSIRLVNG
00BW1773_2	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	RIEEEGGEQD	RDRSVRLVSG
00BW1783_5	VNRVRQGYSP	LSFQTLIP..	NPR.GPDRLE	RIEEEGGEQD	RDRSIRLVSG
00BW1795_6	VNRVRQGYSP	LSFQTLIP..	NPR.GPDRLG	RIEEEGGEQD	RDRSIRLVSG
00BW1811_3	VNRVRQGYSP	LSFQTLIP..	NPG.GPDRLG	RIEEEGGEQD	RDRSVRLVNG
00BW1859_5	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	GIEEEGGEQD	RDRSIRLVNG
00BW1880_2	VNRVRQGYSP	LSLQTLSP..	NQR.GLDRLG	RIEEEGGEQD	RDKSIRLVSG
00BW1921_1	VNRVRQGYSP	LSLQTLTP..	NPR.ELDRLG	RIEEEGGEQD	RGRSIRLVNG
00BW2036_1	VNRVRQGYSP	LSFQTLTP..	NPR.GLDRLG	RIEEEGGEQD	RGRSIRLVQG
00BW2063_6	VNRVRQGYSP	LSFQTLTP..	NPR.GPDKLE	RIEEEGGEQD	RNRSIRLVSG
00BW2087_2	VNRVRQGYSP	LSFQTLTP..	NPR.EPDRLG	RIEEEGGEQD	RERSIRLVSG
00BW2127_2	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	RTEEEGGEQD	NDRSIRLASG
00BW2128_3	VKRVRQGYSP	LSFQTLTP..	NPG.GPDRLG	RIEEEGGEQD	REKSVRLVNG
00BW2276_7	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	GIEEEGGEQD	RDRSIRLVSG
00BW3819_3	VNRVRQGYSP	LSLQTLTP..	SPR.GPDGLR	GIEEEGGEQD	KDRSIRLVNG
00BW3842_8	VNRVRQGYSP	LSLQTLTP..	NPR.ELDRLG	RIEEEGGEQD	RDRSIRLVNG
00BW3871_3	VNRVRQGYSP	LSLQTLTP..	NPR.ELDRLG	RIEEEGGEQD	KDRSIRLVNG
00BW3876_9	VNRVRQGYSP	LSFQTLTP..	NPR.EPDRPG	RIEKEGGEQD	KRSRIRLVSG
00BW3886_8	VNRVRQGYSP	LSFQTLTP..	NTR.ELDRLG	RIEEEGGEQD	RDRSIRLLNG
00BW3891_6	VNRVRQGYSP	LSFQTLIP..	NPR.GLDRLG	RIEEEGGEQD	RDRSIRLVNG
00BW3970_2	VNRVRQGYSP	LSLQTLTP..	NQR.EPDRLG	RIEEEGGEQD	RKRSIRLVSG
00BW5031_1	VNRVRQGYSP	LSFQTLTP..	SQR.ELDRLG	RIEEEGGEQD	RDRSIRLANG
96BW01B21	VNRVRQGYSP	LSFQTLTQ..	NPG.GPDGLG	RIEEEGGEQD	KDRSIRLVNG
96BW0407	VNRVRQGYSP	LSFQTLIP..	NPR.RSDRLG	RIEEEGGEQD	RGRSIRLVSG
96BW0502	VNRVRQGYSP	LPFQTLTP..	NPR.EPDRLG	RIEEEGGEQD	RGRSIRLVSG
96BW06_J4	VNRVRQGYSP	LSFQTLPP..	NPR.GIDRLG	RIEEEGGEQD	RDRSIRLVNG
96BW11_06	VKRVRQGYSP	LSFQTLTP..	NPR.GPDRLE	RIEEEGGEQD	RNRSIRLVSG
96BW1210	VNRVRQGYSP	LSFQTLIP..	SPR.EPDKLE	RIEEEGGEQD	RDRSIRLVSG
96BW15B03	VNRVRQGYSP	LSFQTLTP..	NPR.GLDRLG	RIEEEGGEQD	RDRSIRLVQG
96BW16_26	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	RIEEEGGEQD	RDRSVRLVHG
96BW17A09	VNRVRQGYSP	LSLQTLTP..	NPR.GPDGLE	RIEEEGGEQD	RGRSIRLVSG
96BWM01_5	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLE	GIEEEGGEQD	KDRSIRLVSG
96BWM03_2	VNRVRQGYSP	LPFQTLTP..	NPR.ELDRLG	RIEEEGGEQD	RDRSIRLVSG
98BWMC12_2	VNRVRQGYSP	LSFQTLNP..	NPR.GLDRLG	RIEEEGGEQD	KSTSIRLVNG
98BWMC13_4	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLE	RIEEEGGEQD	RDRSIRLVNG
98BWMC14_a	VNRVRQGYSL	TSLQTHLP..	NAG.GLDRLD	RIGEEGGEQD	RHRSIRLVSG
98BWM014_1	VNRVRQGYSP	LSFQTLTP..	VPR.EPDRLG	GIEEEGGEQD	RDRSVRLVNG
98BWM018_d	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	RIEEEGGEQD	RDRSIRLVSG
98BWM036_a	INRVRQGYSP	LSFQTLTP..	TPR.DPDRLR	GIEEEGGEQD	RDRSIRLVSG
98BWM037_d	VNRVRQGYSL	TSFQTVIP..	NPR.GPDRPR	GIEEEGGEQD	RDRSIRLVSG
99BW3932_1	VNRVRQGYSL	LSFQTLTP..	NPR.GPDRLG	GIEEEGGEQD	RDRSIRLVNG
99BW4642_4	VNRVRQGYSP	LSFQTLTP..	NPR.ELDRLG	RIEEEGGEQD	RDRSVRLVNG
99BW4745_8	VNRVRQGYSP	LSLQTLTP..	SPR.RPDRLG	GIEEEGGEQD	RTRSIRLVNG
99BW4754_7	VNRVRQGYSP	LSFQTLTP..	NQR.GPDRLG	EIEEEGGEQD	RDRSIRLVNG
99BWMC16_8	VNRVRQGYSP	LSFQTLAP..	NPG.GLDRLG	RIEEEGGEQD	RGRSIRLVNG
A2_CD_97CD	VKRVRQGYSP	LSFQIPTP..	NPE.GLDRPG	RIEEEGGEQD	RDRSIRLVSG
A2_CY_94CY	VNRVRQGYSP	VSFQIPTP..	SPE.GPDRPR	GTEEEGGEQD	RDRSIRLVNG
A2D_97KR	VNRVRQGYSP	VSFQIPPP..	TPE.DPDRHG	RIEDGGGEQD	RDRSVRLVSG
A2G_CD_97C	VNRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	RIEEGGGEQD	RDRSVRLVSG
A_BY_97BL0	INRARXXYSP	LSLQTLTP..	HPE.RPDRPX	RIKEEGXEQD	RDRSIRLVSG
A_KE_Q23_A	INRVRQGYSP	LSFQTHTP..	NPR.GLDRPE	RIEEEDGEQD	RGRSIRLVSG
A_SE_SE659	INRVRQGYSP	LSFQTHTP..	NPG.GLDRPG	RIEEEGGEQD	RDRSIRLVSG
A_SE_SE725	INRVRQGYSP	LSFQTHTP..	DPR.GLDRPR	RIEEEGGEQD	RGRSIRLVSG
A_SE_SE753	INRVRQGYSP	LSFQIHTP..	NPR.DPDRPG	RIEEEGGEQD	RDRSIRLASG

A_SE_SE853	INRVRQGYSP	LSFQIHTP..	NPG.DLDRPG	RIEEEGGEQD	RGRSIRLVSG
A_SE_SE889	INRVRQGYSP	LSFQIHTP..	SPG.GLDRPG	RIEEEGGEQD	RNRSIRLVNG
A_SE_UGSE8	IKRVRQGYSP	LSFQIHTP..	SPR.DPDRPG	RIEEEGGEQG	RDRSIRLVSG
A_UG_92UG0	INRVRQGYSP	LSFQTHTP..	NPR.GLDRPG	RIEEEGGEQD	RGRSIRLVSG
A_UG_U455	INRVRQGYSP	LSFQTLAP..	IPE.GLGRPG	RIEEEGGEQG	KDRSIRLVSG
AC_IN_2130	INRVRQGYSP	LSFRTHTP..	NPG.GLDRPG	RIEEEDGEQG	KDRSIRLVSG
AC_RW_92RW	VNRVRQGYSP	LSFQTLIP..	NPR.GPDRLG	GIEEEGGEQD	RGRSIRLVSG
AC_SE_SE94	INRVRQGYSP	LSFQIHTP..	NPG.GPDRPG	RTEEEGGEQD	RDRSIRLVSG
ACD_SE_SE8	INRVRQGYSP	LSFQTHTP..	NPE.GVDRPG	RIEEEGGEQG	RDRSIRLVSG
ACG_BE_VI1	VNRVRQGYSP	LSFQTLIP..	NPR.GPDRPG	EIEEGGGEQD	RDTSTRLVSG
AD_SE_SE69	VNRVRQGYSP	LSFQTLIP..	APRGP.DRPE	GIEEEGGEQG	RGRSIRLVNG
AD_SE_SE71	INRVRQGYSP	LSFQTHTP..	NPR.DLDRPE	RIEEEGGEQD	RTRSIRLVSG
ADHK_NO_97	VNRVRQGYSP	LSFQTLIP..	NPRGA.DRPE	GIEEEGGEQD	XNRSIRLVNG
ADK_CD_MAL	VNRVRQGYSP	LSLQTLIP..	TFRGPPDRPE	GIEEEGGEQG	RGRSIRLVNG
AG_BE_VI11	INRVRQGYSP	LSFQILTP..	HQRDP.DRPG	RIEEEGGEQD	RDTSRRLVGG
AG_NG_92NG	VNRVRQGYSP	LSFQTLTH..	HQREP.DRPE	RIEEEGGEQD	RDRSVRLVSG
AGHU_GA_VI	VNRVRQGYSP	LSFQTLFP..	NQREP.DRPE	GIEEEGGEQG	RSRSIRLVNG
AGU_CD_Z32	INRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	GIEEGGGEQD	RDRSIRLVSG
AJ_BW_BW21	VNRVRQGYSP	LSLQTLIP..	NPTEV.DRPG	GIEEGGGEQG	KTRSIRLVNG
B_AU_VH_AF	VKKVREGYSP	LSLQIRPP..	APRGP.DRPE	GIEEEGGEQD	RDKSVRLVDG
B_CN_RL42	VNRVRQGYSP	LSLQTRFP..	AQRGP.GRPE	GIEEEGGERD	RDRSERLVTG
B_DE_D31_U	VNSVRQGYSP	LSFQTRLP..	APRGP.DRPE	GIEEEGGDRD	RDRSNRLVKG
B_DE_HAN_U	VNRVRQGYSP	LSFQTLIP..	ATRGP.RQPE	EIEEEGGERD	RGRSVRLVSG
B_FR_HXB2	VNRVRQGYSP	LSFQTHLP..	TPRGP.DRPE	GIEEEGGERD	RDRSIRLVNG
B_GA_OYI	VNRVRQGYSP	LSFQTRLP..	TQRGP.DRPE	GIEEEGGERD	RDRSGRLVDG
B_GB_CAM1	VNRVRQGYSP	LSFQTRFP..	VPRGP.DRPE	GIEEEGGGRD	RDTSGRLVTG
B_GB_GB8_C	VNRVRQGYSP	LSLQTHLP..	TPRGP.DRPE	GIEEEGGEQD	RDRSIRLVNG
B_GB_MANC	VNRVRQGYPP	LSFQTHLP..	APRGP.DRPG	GIEEEGGEGD	RDRSSRLVHG
B_KR_WK_AF	VNRVRQGYSP	LSFQTHFP..	SPRGP.DRPG	GIEEGEGGED	SGGSSHLVDG
B_NL_3202A	VNRVRQGYSP	LSFQTRLP..	APRGP.DRPE	GIEEEGGERD	RDRSGRLVNG
B_TW_TWCYS	VNRVRQGYSP	LSFQTHLP..	TPRGP.DRPE	GIDEEGGERD	RDRSERSVDG
B_US_BC_LO	VNRVRQGYSP	LSFQTHLP..	TPRGP.DRPE	GIEEEGGERD	RDRSGRLVNG
B_US_DH123	VNRVRQGYSP	LSFQTRFP..	ASRGP.DRPE	GIEEEGGDRD	RDRSSPLVDG
B_US_JRCSE	VNRVRQGYSP	LSFQTLIP..	ATRGP.DRPE	GIEEEGGERD	RDRSGQLVNG
B_US_MNCG	VNRVRQGYSP	LSLQTRPP..	VPRGP.DRPE	GIEEEGGERD	RDTSGRLVHG
B_US_P896	VNRVRQGYSP	LSFQTLIP..	ASRGP.DRPE	GTEEEGGERD	RDRSGPLVNG
B_US_RF_M1	VNRVRQGYSP	LSFQTHLP..	APRGP.DRPE	GIEEGEGGERD	RDRSGGAVNG
B_US_SF2_K	VNRVRQGYSP	LSFQTRLP..	VPRGP.DRPD	GIEEEGGERD	RDRSVRLVDG
B_US_WEAU1	VNRVRQGYSP	LSFQTHLP..	APRGP.DRPE	GIEEEGGERD	RDRSGRLVDG
B_US_WR27	XNRVRQGXSP	LSFQTLIP..	VPRGP.DRPE	GIEEEGGERD	RDRSNRLVHG
B_US_YU2_M	VNRVRQGYSP	LSFQTHLP..	AQRGP.DRPD	GIEEEGGERD	RDRSGPLVDG
BF1_BR_93B	VNRVRKGYS	LSLQTRFP..	SPREP.DRPE	GIEEGGGEPG	KDRSVRLVNG
C_BR_92BR0	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	GIEEEGGEQD	RDRSIRLVSG
C_BW_96BW0	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	GIEEEGGEQD	RDRSIRLVSG
C_BW_96BW1	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLE	RIEEEGGEQD	RNRSIRLVSG
C_BW_96BW1	VNRVRQGYSP	LSFQTLIP..	SPR.EPDKLE	RIEEEGGEQD	RDRSIRLVSG
C_BW_96BW1	VNRVRQGYSP	LSFQTLTP..	NPR.GLDRLG	RIEEEGGEQD	RDRSIRLVQG
C_ET_ETH22	VNRVRQGYSP	LSFQTLIP..	HPR.GPDRLG	GIEEEGGEQG	RDRSIRLVNG
C_IN_93IN1	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	RIEEEGGEQD	KDRSIRLVNG
C_IN_93IN9	VNRVRQGYSP	LSFQTPTP..	NPG.GPDRLG	RIEEEGGEQG	KDRSIRLVNG
C_IN_93IN9	VNRVRQGYSP	LSFQTLTP..	NPG.GPDRLG	RIEEEGGEQD	NRSIRLVNG
C_IN_94IN1	VNRVRQGYSP	LSFQTPTP..	NPG.GPDRLG	RIEEEGGGQD	NRSIRLVNG
C_IN_95IN2	VNRVRQGYSP	LSFQTLTP..	NPG.GPDRLG	RIEEEGGEQD	KDRSIRLVSG
CRF01_AE_C	VNRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	RIEEGGGEEG	KDRSIRLVSG
CRF01_AE_C	VNRVRQGYSP	LSFQTLTH..	QQR.EPDRPE	RIEEESGEQG	RDRSIRLVSG
CRF01_AE_C	VNRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	RIEEGGGEQD	KDRSVRLVSG
CRF01_AE_T	VNRVRQGYSP	LSFQTPIH..	HQR.EPDRPE	RIEEGGGEQG	RDRSVRLVSG
CRF01_AE_T	VNRVRQGYSP	LSLQTPTH..	HQR.EPDRPE	RIEEGGGEQG	RDRSVRLVSG
CRF01_AE_T	VNRVRQGYSP	LSFQTPTH..	HQRGEPRPE	RIEEGGGEQG	RDRSVRLVSG
CRF01_AE_T	VNRVRQGYSP	LSFQTPH..	HQR.EPDRPE	RIEEEGGEQG	RDRSVRLVSG
CRF01_AE_T	VNRVRQGYSP	LSFQTPSH..	HQK.EPDRPE	GIEEGGGEQG	RDRSVRLVSG

CRF01_AE_T	VNRVRQGYSP	LSFQTLTH..	HQR.DPDRPE	RIEEGGGEQ	RDRSVRLVSG
CRF02_AG_F	INRVRQGYSP	LSFQTLTH..	HQR.GPDRPE	RIEEGGGEQD	RDRSGRLVSG
CRF02_AG_F	IKRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	RIEEGGGEQD	KDRSVRLVSG
CRF02_AG_G	INRVRQGYSP	LSFQILTP..	NPR.GPDRPE	GIEEGGGEQD	RDRSIRLVSG
CRF02_AG_N	INRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	RIEEGGGEQD	KDRSVRLVSG
CRF02_AG_S	INRVRQGYSP	LSFQTLTH..	HQR.EPGRPE	RIEEGGGGQD	RDRSVRLVSG
CRF02_AG_S	INRVRQGYSP	LSFQTLTH..	HQR.GADRPE	GIEEGGGEQD	RDRSVRLVSG
CRF03_AB_R	VNRGRQGYSP	LSFQTRLP..	AQRGP.DRPE	GIEEEDGERD	RDTSIRLVNR
CRF03_AB_R	VNRVRQGYSP	LSFQTRLP..	TQRGP.DRPE	GIEEEGGERD	RDTSIRLVNG
CRF04_cpx_	VNRVRQGYSP	LSLQTLIPT.	TQRGL.DRPG	GTEEEGGEQD	RSRSIRLVNG
CRF04_cpx_	VNRVRQGYSP	LSFQTLIP..	TQREP.GRPE	GTEEEGGEQD	RSRSIRLVNG
CRF04_cpx_	VKRVRQGYSP	LSSQTLIPT.	TQRGP.DRPE	GTEGGGGEQD	RIESIRLVNG
CRF05_DF_B	VNRVRKGYSP	LSFQTPFP..	APRGP.DRPE	ETEEGGGEQD	RGRSIRLVNG
CRF05_DF_B	VNRVRKGYSP	LSFQTLIP..	GPRGP.DRPE	GTEEEGGEQ	RDRSVRLTGT
CRF06_cpx_	VNRVRQGYSP	LSLQTLIP..	NPTGA.DRPG	EIEEGGGEQ	RTRSIRLVNG
CRF06_cpx_	VNRVRQGYSP	LSLQTLIP..	NPTGA.DRPG	EIEEGGGEQ	RTRSIRLVNG
CRF06_cpx_	VNRVRQGYSP	LSLQTLIP..	NPAEV.DRPG	GIEEGGGEQ	RNRSIRLVNG
CRF06_cpx_	VKRVRQGYSP	LSLQTLIP..	NSAGV.DRPG	EIEGGGGEQD	RTRSIRLVNG
CRF11_cpx_	VNRCRQGYSP	LSFQTLNP..	TQGEA.DRPG	GIEEGGGEQ	RTRSIRLVSG
CRF11_cpx_	VNRCRQGYSP	LSFQALTP..	SQGEA.DRPG	GTKEGGGEQ	RTSSIRLVSG
D_CD_84ZR0	VNRVRQGYSP	LSFQTLIP..	APRGP.DRPE	GIEEGGGEQD	RGTSIRLVNG
D_CD_ELI_K	VNRVRQGYSP	LSFQTLIP..	APRGP.DRPE	GTEEEGGERG	RDRSVRLVNG
D_CD_NDK_M	VNRVRQGYSP	LSFQTLIP..	VPRGP.DRPE	EIEEGGGERG	RDRSVRLVNG
D_UG_94UG1	VNRVRQGYSP	LSFQTLIP..	APREP.DRPE	GIEEGGGERD	RGRSIRLVNG
F1_BE_VI85	VNRVRKGYSP	LSLQTLIP..	SPRGP.DRPE	GIEEGGGEQ	KDRSVRLVTG
F1_BR_93BR	VNRVRKGYSP	LSFQTHIP..	SPREP.DRPE	GIEEGGGEQ	KDRSVRLVTG
F1_FI_FIN9	VNRVRKGYSP	LSLQTLIP..	APTEP.DRPE	GIEEGGGEQ	KDRSVRLVNG
F1_FR_MP41	VNRVRKGYSP	LSLQTLIP..	SPRGP.DRPE	GIEEGGGEQD	RNRSVRLVNG
F2_CM_MP25	INRVRQGYSP	LSLQTLIP..	NSRGP.ERPG	GIEEGGGEQD	KDRSIRLVSG
F2KU_BE_VI	VNRVRQGYSP	LSFQTLIP..	SPRGP.DRPE	GTEEGGGEQD	RDRSTRLVSG
G_BE_DRCBL	VNRVRQGYSP	LSFQTLIP..	HQREP.DRPA	GIEEGGGEQD	RDRSIRLVSG
G_NG_92NG0	VNRVRQGYSP	LSFQTLTH..	HQREP.DRLG	KTEEGGGEQD	RDRSTRLVSG
G_SE_SE616	VNRVRQGYSP	LSFQTLTH..	HQREP.DRPE	GIEEGGGEQ	RGRSVRLVSG
H_BE_VI991	VNRVRQGYSP	LSLQTLIP..	NQRGP.DRPR	EIEEGGGEQD	RDRSIRLVNG
H_BE_VI997	VGRVRQGYSP	LSFQTLIP..	NPRGP.DRPE	GIEEGGGEQD	RGRSVRLVNG
H_CF_90CF0	VNRVRQGYSP	LSFQTLVP..	NPRGP.DRPE	GTEEGGGEQD	RDRSVRLVNG
J_SE_SE702	VNRVRQGYSP	LSFQTLIP..	NPTEA.DRPG	GIEEGGGEQ	RTRSIRLVNG
J_SE_SE788	VNRVRQGYSP	LSFQTLIP..	NPTEA.DRPG	GIEEGGGEQ	RTRSIRLVNG
K_CD_EQTB1	VNRVRQGYSP	LSFQTLTP..	SPRGP.DRPE	GIEEGGGEQD	KDRSVRLVSG
K_CM_MP535	VNRVRQGYSP	LSFQTLIP..	TSRGA.DRPE	GIEEGGGEQD	KNRSVRLVSG
N_CM_YBF30	IARVRQGYSP	LSLQTLIPT.	ARG..PDRPE	ETEGGVGEQD	RGRSVRLVSG
O_CM_ANT70	VKNIRQGYQP	LSLQIPNHH.	QEE..AGTPG	RTGGGGGEEG	RPRWIPSPQG
O_CM_MVP51	VKNIRQGYQP	LSLQIPVPH.	RQE..AETPG	RTGEEGGEGD	RPKWTALPPG
O_SN_99SE_	VKNIRQGYQP	LSFKTHIHH.	QPE..AEAPG	GTGEGGGGERG	MPTLIPWPQG
O_SN_99SE_	VRNIRHGYP	LSFQTPTHHQ	QPE..AQAPG	GTGEGGGGERD	RLRSIPSPQG
U_CD_83C	INRVRQGYSP	LSFQTLIP..	TPR.GPDRPG	RTEEGGGEED	NNRSVRLVNG

	851				900
00BW0762_1	FLALFWDDLR	SLCLFSYHRL	RDFILVAARA	VELLGRSSLK	GLQRGWEILK
00BW0768_2	FLALVWDDLR	RLCLFSYHRL	RDFILVATRA	VELLGHSSLR	GLQRGWEALK
00BW0874_2	FLALAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGRSSLR	GLQRGWEILK
00BW1471_2	FLTLAWDDLR	SLCIFLYRLL	SDFISIAART	VNLLGQNSLR	GLQRGWEALK
00BW1616_2	FLALAWDDLR	SLCLFSYHRL	RDFTLIAARA	VETLGR....	...RGWEALK
00BW1686_8	FLALAWDDLR	SLCLFSYHQL	RDFILIVARA	VELLGRNSLR	GLQRGWEILK
00BW1759_3	FLALFWDDLR	SLCLFSYHRL	RDLILVTARA	VELLG.....	...QRGWEALK
00BW1773_2	FLALTWDDLR	SLCLFCYHRL	RDFILIAARV	VELLGRSSLR	GLQKGWEALK
00BW1783_5	FLALAWDDLR	SLCLFSYHRL	RDFILVTARA	VELLGRSSLR	GLQRGWEILK
00BW1795_6	FLALAWDDLR	SLCLFCYRRL	RDFILVTARA	VELLGRSSLK	GLQRGWEILK
00BW1811_3	FFALAWDDLR	SLCLFCYHRL	RDFILVTARA	VELLGHSSLK	GLQRGWEILK
00BW1859_5	FLALAWDDLR	SLCLFSYHRL	RDCILIAARA	VELLGHSSLR	GLQRGWEVLK
00BW1880_2	FLALAWDDLR	SLCLFSYHRL	RDFILVTARA	VELLGRSGLK	GLQRGWEILK
00BW1921_1	FLPLVWEDLR	SLCLFSYHRL	RDLILVVARA	VELLGRSSLR	GLQKGWETLK
00BW2036_1	FLALAWDDLR	NLCLFSYHQL	RDLILVTTRV	VELLGRSSLR	GLQRGWEALK
00BW2063_6	FLALAWDDLR	SLCLFCYHRL	KDFVLVTARV	VELLGLSSLK	GLQRGWEILK
00BW2087_2	FLPLFWDDLR	SLCLFSYHRL	RDLILIAARA	VELLGRSSLR	GLQRGWEILK
00BW2127_2	FLAPAWDDLR	SLCLFSYHRL	RDLILVTARV	VELLGRS...	...GWEALK
00BW2128_3	FLALFWDDLR	SLCLFSYHRL	RDFILIAARV	VELLGRSSLR	GLQRGWETLK
00BW2276_7	FLALAWDDLR	SLCLFSYHRL	RDFILVTARA	VELLGRSSLR	GLQRGWEVLK
00BW3819_3	FLALAWDDLR	SLCLFSYHRL	RDLTLVTARG	IELMGRSSLR	GLQKGWEALK
00BW3842_8	FLALAWEDLR	SLCLFSYHRL	RDLILVTARA	VELLGRSSLR	GLQRGWEALK
00BW3871_3	FLALAWDDLR	SLCLFSYHRL	RDFILIVARV	VELLGRSSLR	GLQKGWETLK
00BW3876_9	FLALAWDDPR	SLCLFSYHRL	RDFILVVVRA	VELLGRSSLK	GLKRGWEALE
00BW3886_8	FLAIAWDDLR	SLCLFSYHRL	RDFILLIARA	VELLGRSSLK	GLQRGWEALK
00BW3891_6	FLALAWEDLR	SLCLFSYHRL	RDFILVTARA	VELLGRSSLR	GLQRGWEALK
00BW3970_2	FLALAWDDLR	SLCLFSYHHL	RDFILIAARV	VELLGR....	...RGWDILK
00BW5031_1	FLALAWEDLR	SLCLFSYRHL	RDFILIVVRA	VELLGRSSLR	GIQKGWDALK
96BW01B21	FLPLVWDDLR	NLCLFSYHRL	RDFILVIARA	VELLGRSSLR	GLQRGWETLK
96BW0407	FLALAWDDLR	SLCLFSYHRL	RDFILIAARA	AELLGRSGLR	GLQKGWETLK
96BW0502	FLALAWDDLR	SLCLFSYHRL	RDFILIAARV	LELLG.....	...QRGWEALK
96BW06_J4	FLALAWDDLR	SLCLFSYHQL	RDFILVVARA	VELLGRSSLR	GLQRGWEALK
96BW11_06	FLALAWDDLR	SLCLFCYHRL	RDFTLVTARA	VELLGRSSLK	GLQRGWEILK
96BW1210	FLALAWDDLR	SLCLFSYHRL	RDSILVAART	VELLGRSSLR	GLQRGWEALK
96BW15B03	FLALAWDDLR	SLCLFSYHRL	RDLILVTARV	VELLGRSSLR	GLQRGWEALK
96BW16_26	FLALAWDDLR	SLCLFSYHRL	RDFILVAVRV	VELLGR....	...RGWEALK
96BW17A09	FLALAWDDLR	SLCIFLYHHL	RDFILIAART	VNLLGQSSLR	GLQRGWEALK
96BWM01_5	FLALAWDDLR	SLCLFCYHRL	RDFILVTARA	VELLGRSSLK	GLQRGWEILK
96BWM03_2	FLALAWDDLR	SLCLFSYHRL	RDFLLVTVRA	AELLGRSSLR	GLQRGWEALK
98BWMC12_2	FLAIAWDDLR	SLCLFSYHRL	RDFILIAARA	VELLGRSSLR	GLQRGWEALK
98BWMC13_4	FLALAWDDLR	NLCLFCYHRL	RDFILVTARA	VELLGRSSLT	GLQRGWEILK
98BWMC14_a	LLALAWDDLR	SVRLFSYHQL	RNFILIVARA	VELLGR....	...RGWETLK
98BWM014_1	FLALFWDDLR	SLCLFSYHRL	RDLILIAVRA	VELLGRSSLW	GLQKGWEALK
98BWM018_d	FLALAWDDLR	SLCLFSYHRL	RDFILIAARA	VELLGHSLR	GLQRGWEILK
98BWM036_a	FLALAWDDLR	SLCLFSYHRL	RDFILVTARV	VELMGRSSLK	GLQRVWEILK
98BWM037_d	FLALAWDDLR	SLCLFSYHQL	RDFILLIARV	VERLGYSRLR	GLQRGWEALK
99BW3932_1	FFSLAWDDLR	SLCLFSYHRL	RDLILVTVRV	VELMGRCSLR	GLQRGWEALK
99BW4642_4	FLALAWDDLR	SLCLFSCHRL	RDCILIAVRA	VELLGRSSLK	GLQRGWEALK
99BW4745_8	FLALAWDDLR	SLCLFSYHHL	RDFILVTARA	VELLGRSSLR	GLQRVWEALK
99BW4754_7	FLAIVWDDLR	SLCLFSYHRL	RDFILIAARA	VELLGRSSLK	GLQRGWEILK
99BWMC16_8	FLAIAWEDLR	SLCLFSYHRL	RDLTLIVTRA	VELLGRSSLK	GLQRGWEALK
A2_CD_97CD	FLALAWDDLR	SLCLFSYHRL	RDCILIAARI	VELVGHSSLK	GLRLGWEGLK
A2_CY_94CY	FFALAWDDLR	SLCLFSYHRL	RDCILIAART	VELLGHCSLK	GLRLGWEGLK
A2D___97KR	FLALVWEDLR	SLCLFSYHRL	RDCISIAART	VELLGHSSLK	GLRLGWEGLK
A2G_CD_97C	FLALAWDDLR	SLCLFCYHRL	RDSILIAART	VELLRHSSLK	GLRLGWEGLK
A_BY_97BL0	FLALAXDDLX	SLCLFSYHRL	RDFISIAART	XELLKRSSLX	GLRLXXXGLK
A_KE_Q23_A	FLALAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGHSSLK	GLRLGWEGLK
A_SE_SE659	FLALAWDDLR	SLCLFSYHHL	RDLILIAART	VELLGHSSLK	GLRLGWEGLK
A_SE_SE725	FLALAWDDLR	SLCLFSYHRL	RHFILIATTT	VELLGHSSLK	GLRLGWEGLK
A_SE_SE753	FLTLAWEDLR	SLCLFSYHRL	RDLILIAART	VELLGHSSLK	GLRLGWEGLK

A_SE_SE853	FLALAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGQR...GWEGLK
A_SE_SE889	FLALAWDDLR	SLCLFCYRRL	RDFILIVART	VELLGHSSLR	GLRLGWEGLK
A_SE_UGSE8	FLALAWDDLR	SLCRFSYHRL	RDFISIATRI	VELLG.....QGLK
A_UG_92UG0	FLALAWDDLR	NLCLFSYHRL	RDFILIAART	VELPGHSSLK	GLRLGWEGLK
A_UG_U455_	FLAIAWDDLR	NLCLFSYHRL	RDFALIVARA	VELLGRSSLK	GLRLGWEGLK
AC_IN_2130	FLALFWDDLR	SLCLFSYHRL	RDFILIAKRT	VELLGHSSLK	GLRLGWEGLK
AC_RW_92RW	FLALAWDDLR	SLCLFSYHRL	RDLLLIAART	VELLGRSSLR	GLQRGWETLK
AC_SE_SE94	FLALAWDDLR	SLCLFSYHRL	RDFILI....	..LG.HSSLK	GLRLGWEGLK
ACD_SE_SE8	FLALAWDDLR	SLCLFSYHRL	RDLILIAARI	VELLGRR...GWEAIK
ACG_BE_VI1	FFALAWDDLR	SLCIFLYHHL	RDLLLIATRA	VELLG.....	..QRGWEALK
AD_SE_SE69	FSALIWDLLR	NLCLFSYHRL	RDLLLIALRI	VELLGRR...GWEALK
AD_SE_SE71	FLAIAWDDLR	SLCLFSYHRL	RDLILIAARI	VELLGRR...GWEALK
ADHK_NO_97	FLPLVWEDLR	NLCLFSYRRL	RDLLLILART	VTLLGSR...GWETLK
ADK_CD_MAL	FSALIWDLLR	NLCLFSYHRL	RDLLLIAATRI	VELLGRR...GWEALK
AG_BE_VI11	FLTLVWDDLR	SLCLFSYHRL	RDLVLIAART	LELLGRSGLR	GLRLGWEGLK
AG_NG_92NG	FLALAWDDLR	NLCLFSYHRL	RDLVLIAART	AELLRRSSLQ	GLRLGWEGLK
AGHU_GA_VI	FLPLIWEDLR	NLCLFSYRHL	RDLLLIVART	VELLGKR...GWGALK
AGU_CD_Z32	FLPLAWDDLR	SLCLFCYHRL	RDCALIAARI	VETLIRR...GWETLK
AJ_BW_BW21	FLALAWEDLR	NLCLFSCHRL	RDFALIAART	VDTLGRR...GWEILK
B_AU_VH_AF	FLALIWDLLR	SLCLFSYHRL	RDLLLIAARI	VELLGRR...GWEALK
B_CN_RL42_	FLSLIWEDLR	SLCLFSYHRL	RDLLLIVARI	VELLGRR...GWEVLR
B_DE_D31_U	FLALIWDLLS	SLCLFLYHRL	RDLLLIAARI	VELLGRR...GWEVLK
B_DE_HAN_U	FLALFWDDLR	SLCLFSYRRL	RDLLLIVAKI	VETLGRR...GWEVLK
B_FR_HXB2_	SLALIWDLLR	SLCLFSYHRL	RDLLLIVTRI	VELLGRR...GWEALK
B_GA_OYI_	FLALIWDLLR	SLCLFSYHRL	RDLILIVARI	VELLGRR...GWEVLK
B_GB_CAM1_	FLALIWDLLR	SLCLFSYHRL	RDLLLIVARI	VELLGRR...GWEALK
B_GB_GB8_C	FLALFWDDLR	SLCLFSYHRL	RDLLLIVTRI	VGLLGRR...GWEALK
B_GB_MANC_	FLALVWDDLR	SLCLFSYHRL	RDLLSIAARI	VELLGRR...GWEILK
B_KR_WK_AF	FLTLIWVDLR	SLCLFSYHLL	RDLLLIVTRS	VELLGLR...GWEILK
B_NL_3202A	FLALIWDLLR	SLCLFSYHRL	RDLLLIVTRI	VELLGRR...GWEVLK
B_TW_TWCYS	FLAIIWVDLR	SLCLFSYHRL	RDLLLIVTRI	VELLGRR...GWEALK
B_US_BC_L0	FLALFWDDLR	SLCLFSYHRL	RDLILVTRI	VELLGRR...GWEALK
B_US_DH123	FLAIIWVDLR	TLFLFSYHRL	RDLLLIVTRI	VELLGRR...GWELLK
B_US_JRCSF	FLALIWVDLR	SLFLFSYHRL	RDLLLTVTRI	VELLGRR...GWEILK
B_US_MNCG_	FLAIIWVDLR	SLFLFSYH.H	RDLLLIAARI	VELLGRR...GWEVLK
B_US_P896_	FLALFWVDLR	NLCLFLYHLL	RNLLLIVTRI	VELLGRR...GWEALK
B_US_RF_M1	FLTLIWDDLR	TLCSFSYHRL	RDLLLIVVRI	VELLGRR...GWEALK
B_US_SF2_K	FLALIWEDLR	SLCLFSYRRL	RDLLLIAART	VEILGHR...GWEALK
B_US_WEAU1	FLTLIWVDLR	SLCLFLYHRL	IDLLLIAKRI	VELLGRR...
B_US_WR27_	LLALIWDLLR	SLCLFSYHRL	RDLISIVARI	VELLGRR...GWEILK
B_US_YU2_M	FLAIIWVDLR	SLCLFSYHRL	RDLLLIVTRI	VELLGRR...GWGVLK
BF1_BR_93B	FLALVWDDLR	NLCLFSYRHL	RDFILIAARI	VDRGLKR...GWEALK
C_BR_92BR0	FLALAWDDLR	SLCLFSYHRL	RDLILIAARA	VELLGRSSLR	GIQRGWEILK
C_BW_96BW0	FLALVWDDLR	SLCLFSYHRL	RDFILIAARA	AELLGRSSLR	GLQKGWETLK
C_BW_96BW1	FLALAWDDLR	SLCLFCYHRL	RDFTLVAARA	VELLGRSSLK	GLQRGWEILK
C_BW_96BW1	FLALAWDDLR	SLCLFSYHRL	RDSILVAART	VELLGRSSLR	GLQRGWEALK
C_BW_96BW1	FLALAWDDLR	SLCLFSYHRL	RDLILVTARV	VELLGRSSLR	GLQRGWEALK
C_ET_ETH22	FLAIFWDDLR	SLCLFSYHRL	RDLILIAART	VELLGRSSLK	GLQRGWETLK
C_IN_93IN1	FLALAWDDLR	NLCLFSYHRL	RDFISVAARV	VELLGRS...SWEALK
C_IN_93IN9	FLALAWDDLR	NLCLFSYHRL	RDFILVAARV	VELLGRNSLR	GLQRGWEALK
C_IN_93IN9	FLALAWDDLR	SLCLFSYHRL	RDFILVAVRA	VELLGRSSLR	GLQRGWEALK
C_IN_94IN1	FLALAWDDLR	SLCLFSYHRL	RDFILVAARV	VELLGHNSLR	GLQRGWEALK
C_IN_95IN2	FLALFWDDLR	NLCLFSYHRL	RDFILVAARV	LELLGRSRLR	GLQRGWEALK
CRF01_AE_C	FLSLAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGHSSLK	GLRRGWEGLK
CRF01_AE_C	FLALAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGHSSLQ	GLRRRWEGLK
CRF01_AE_C	FLALVWDDLR	SLCLFSYHRL	RDFILIAART	VELLGHSSLE	GLRRGWEGLK
CRF01_AE_T	FLSLAWDDLR	SLCLFSYHRL	RDFILIATRT	VELLGHSSLK	GLRRGWEGLK
CRF01_AE_T	FLTLAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGRSSLK	GLRRGWEGLK
CRF01_AE_T	FLALAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGHSSLK	GLRRGWEGLK
CRF01_AE_T	FLALAWDDLR	SLCLFLYHRL	RDFILIAART	VELLGHSSLK	GLRRGWEGLK
CRF01_AE_T	FLALAWDDLR	SLCLFSYHRL	RDLTLIAART	VELLGHSSLK	GLRRGWEGLK

CRF01_AE_T	FLALAWDDLR	SLCLFLYHRL	RDFILIAART	VELLGHSSLK	GLRRGWEGLK
CRF02_AG_F	FLALAWDDLR	SLCLFSYHRL	RDFVLIABRA	VELLGHSSLK	GLRLGWEALQ
CRF02_AG_F	FLALAWDDLR	SLCLFSYHRL	RDFVLIABRA	VELLGHSSLK	GLRLGWEALK
CRF02_AG_G	FLALAWDDLR	NLCLFSYHRL	RDLILIAART	VEILGHR...VWQILK
CRF02_AG_N	FLALAWDDLR	SLCLFSYHRL	RDLILIAART	VELLGHNCLK	GLRLGWGALK
CRF02_AG_S	FLALAWDDLR	SLCLFSYHRL	RDFVSIVART	VELLGHRR...GWEALK
CRF02_AG_S	FLALAWDDLR	SLCLFLYHRL	RDFVLIART	VELLGHSSLK	GLRLGWEALK
CRF03_AB_R	FLALIWDLLR	SLCFFIYHHL	RDLILIAARI	VELLGRR...GWEALK
CRF03_AB_R	FLALIWDLLR	SLCLFIYHHL	RDLILIAART	VELLGRR...GWEALK
CRF04_cpx_	FLPLIWDLLR	NLCLFSYRHL	RNLLLVART	VELLGIR...GWEALK
CRF04_cpx_	FLPLIWDLLR	NLCLFSYHHL	RNLLLVART	VELLGRR...GWEALK
CRF04_cpx_	FLPLVWDLLR	NLCLFSYRQL	RNLLLVAKT	VELLGIR...GWGTLK
CRF05_DF_B	FSALIWDLLR	NLCLFSYHHL	RDLTLIVRI	VELLGRR...GWEALK
CRF05_DF_B	LSTLIWDLLR	NLCLFSYHRL	RDLILIAARI	VELLGRR...GWEALK
CRF06_cpx_	FLALAWDDLR	SLCLFSYHRL	RDFGLIAART	VEILGRR...GWEILK
CRF06_cpx_	FLALAWDDLR	SLCLFSYHRL	RDFVLIART	VGTLGHR...GWEILK
CRF06_cpx_	FLALAWDDLR	SLCLFSYHRL	RDFVLIART	VETLGRR...GWEILK
CRF06_cpx_	FLALAWEDLR	SLCRFSYHLL	RDFVLIVLRT	VETLGHR...GWEILK
CRF11_cpx_	FLAIAWDLLR	NLCLFSYHRL	RDFILIVARI	VETLGHR...GWEILK
CRF11_cpx_	FLALAWDDLR	NLCLFLYHQL	RDFILIVARI	VETLGRR...GWESLK
D_CD_84ZR0	FSALIWDLLR	NLCLFSYHRL	RELILIAARI	VELLGRR...GWEALK
D_CD_ELI_K	FSALIWDLLR	SLCLFSYHRL	RDLILIAARI	VELLGRR...GWDILK
D_CD_NDK_M	LFALFWDDLR	NLCLFSYHRL	RDSILIAARI	VELLGRR...GWEALK
D_UG_94UG1	LSALIWDLLR	NLCLFSYHRL	RDLILIAARI	VELLGRR...GWEAIK
F1_BE_VI85	FLALAWDDLR	NLCLFSYRHL	RDFILIAARI	VDRGLRR...GWEALK
F1_BR_93BR	FLALAWDDLR	NLCLFSYRHL	RDFILIAARI	VDRGLKR...GWEALK
F1_FI_FIN9	FLALVWDLLR	NLCLFSYRHL	RDFILIAARI	VDRGLRR...GWEALK
F1_FR_MP41	FLSLVWDLLR	NLCLFSYRHL	RDFILIAART	VDRGLTR...GWETLK
F2_CM_MP25	FLALAWDDFR	SLCVFSYHCL	RNFILIAART	VDKGLKR...GWEVLK
F2KU_BE_VI	FLALAWDDLR	NLCLFSYRHL	RDLILIVARI	LERGLRG...SWEILK
G_BE_DRCBL	FLALAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGRNSLK	GLRLGWEALK
G_NG_92NG0	FLALAWDDLR	SLCLFSYHRL	RDLVLIAART	VELLGRSSLK	GLRLGWEGLK
G_SE_SE616	FLPLIWDLLR	SLCLFSYHRL	RDSILIVART	VELLGRSSLK	GLRLGWEGLK
H_BE_VI991	FLPLVWEDLR	NLCLFSYRRL	RDLISIVART	VELLGRR...GWEALK
H_BE_VI997	FLPIVWDLLR	SLCLFSYRLL	RDSLLIVIRT	VELLGRR...GREALK
H_CF_90CF0	FLPVVWDLLR	SLSLFSYRLL	RDLILIVVRT	VELLGRR...GREALK
J_SE_SE702	FLALAWDDLR	SLCLFSYHRL	RDFVLIART	VGTLGLR...GWEILK
J_SE_SE788	FLALAWDDLR	NLCLFSYHRL	RDFVLIART	VGTLGLR...GWEILK
K_CD_EQTB1	FLALAWDDLR	NLCLFSYRHL	RDLVLIAARI	LDRGLKG...SWEALK
K_CM_MP535	FLALAWDDLR	NLCLFSYRQL	RNLILIVTRI	LERGLRG...GWEALK
N_CM_YBF30	FSALVWEDLR	NLLIFLYHRL	TDSLILIRRT	LELLGQSLSR	GLQLLNELR
O_CM_ANT70	FLPLLYTDLR	TIILWYHLL	SNLASGIQKV	ISYLRGLWI	LGQKIINVC
O_CM_MVP51	FLQQLYTDLR	TIILWYHLL	SNLISGIRRL	IDYLGGLWI	LGQKTIEAC
O_SN_99SE_	FLPLLYTDLR	TIILWSYHLL	SNLASGIQTV	ISHLGLGLWT	LGQKIISAC
O_SN_99SE_	FLPLLYTDLR	TIILWSYHLL	SNLASGIQTV	ISHLGLGLWI	LGQKIISAC
U_CD_83C	FLALAWEDLR	SLCIFSYHRL	RDLILIVVKG	...LRR....GWEALK

	901				950
00BW0762_1	YLGILVQYWG	LELKKS AISL	FDTIAIAVAE	GTDR IIEAIQ	RICRAICNIP
00BW0768_2	YLG NLVLYWG	LELKKS AISL	LDSIAIAVAE	GTDR ILEAVQ	RIWGAI RNIP
00BW0874_2	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIELIQ	RICRAIYNIP
00BW1471_2	YLGSLGQYWG	QELKKSAINL	FDTIAIAVAE	GTDR IIEAVQ	RAVRAILHIP
00BW1616_2	YLGSLVQYWG	LELKKS AVSL	LDTIAIAVAE	GTDR ILEVTV	RICRVIRNIP
00BW1686_8	YLGSLIQYWG	LELKKS AISL	LDTIAIAVAG	GTDR FIELIQ	RIYRAIRNVP
00BW1759_3	YLGSLGQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIELIQ	TICRAIRNIP
00BW1773_2	YLG NLVQDWG	LELKKS AISL	FDAIAIAVAE	GTDR IIELIQ	RTGRAICNIP
00BW1783_5	YLGTLVQYVW	LELKKS AISL	LDATAITVAG	GTDR IIELIQ	RIGRAILSIP
00BW1795_6	YLGSLVQYWG	LELKKS AISL	LDTVAIAVAE	GTDR IIELIQ	RGYRAICNIP
00BW1811_3	YLGSLVQYWG	LELKKS AISL	LDTIAIAVGE	GTDR IIEIIQ	RICRAIRNTP
00BW1859_5	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIDLIQ	RICRAILRIP
00BW1880_2	YLGSLIQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIEGIIQ	RICRIIRNIP
00BW1921_1	YLGSLIQYWG	LELKKS AISL	LDTIAIATAE	GTDR IIEVIQ	RICRVIRNIP
00BW2036_1	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIELVQ	RIGRGIYNIP
00BW2063_6	YLGSLVQYWG	LELKKS AISL	LNTTAIAVAE	GTDR VIELLQ	RIGRAICNIP
00BW2087_2	YLGSLVQYWG	LELRKSASSL	LDTIAIAVAE	GTDR IIEVIQ	IICRAILHIP
00BW2127_2	YLG NLVLYWG	LELKKS AISL	FDTIAVAVAE	GTDR ILEVVIQ	RICRAIRNIP
00BW2128_3	YLGSLVQYWG	LELKKS AVSL	LNTIAIVVAE	GTDR IELIQ	RLRR AFLNIP
00BW2276_7	YLG NLAQYWG	LELKKS AISL	INTIAIAVGE	RTDR IIELIQ	TLCRAIHNIP
00BW3819_3	YLG NLVQYWG	LELKRS AISL	LDTIAIAVAE	GTDR IIEFLQ	RIFRAIRNIP
00BW3842_8	YLG NLVQYWG	LELKKS AISL	LDAIAIAVGE	GTDR ILELLQ	RIGRGICNIP
00BW3871_3	YLGSLIQYWG	LELKKSAINL	LDTTAIAVAE	GTDR FIELIQ	RICRAVRNIP
00BW3876_9	YLG NGLGYWG	LELKKS AISL	LNTIAIAVAE	GTDR VIEFVL	RICRAIRHIP
00BW3886_8	YLGSLVQYWG	LELKKSATS L	LDTIAIAVAE	GTDR IIE TVL	RICRAILHIP
00BW3891_6	YLGSLVQYWG	LELKKS AISL	LDTIAIVVAE	GTDR IIELVL	GICRAIRNVP
00BW3970_2	YLASLVQYWG	LELKKG AISL	LDSIAIAVAE	GTDR IIAFIQ	RLFRAICNLP
00BW5031_1	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIEVVQ	RLYRAILNIP
96BW01B21	YLG NLLLYWG	LEPKKSAINL	LDTTAIAVAE	GTDR IELVLQ	GICRAIRNIP
96BW0407	FLGSLVQYWG	LELKKS AISL	LDTTAIAVAE	GTDR IIEIAQ	RICRAICNVP
96BW0502	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIEFIQ	RICRAIRNIP
96BW06_J4	YLGSLIQYWG	LELKRS TISL	LDTVPIAVPE	GTDR IIELIQ	RIWRAICNIP
96BW11_06	YLGSLVQYWG	LELKKS AISL	LDTTAIAVAE	GTDR IIEVLQ	RIGRAIRNTP
96BW1210	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIELTQ	RVFRAIRNIP
96BW15B03	YLGSLVQYWG	LELKKSATS L	LDSIAIAVAE	GTDR IIEVIQ	RIYRAF CNIP
96BW16_26	YLGSLVQYWG	LELKKSAINL	LDTIAIAVAE	GTDR IIDFIL	RICRAIRNIP
96BW17A09	YLGSLGQYWG	QELKKSAINL	LDTIAIAVAE	GTDR IIEVLQ	GAIRAILNIP
96BWMO1_5	YLGSLVQYWG	LELKKS AISL	LDTTAIAVAE	GTDR IIEVLQ	RVGRAIRNTP
96BWMO3_2	YLGSLVRYWG	LELKKS AISL	LDTIAVAVAE	GTDR IIEVIQ	GICRGIRNIP
98BWMC12_2	YLGSLVQYWG	LELKKS AISL	LDTTAIAVAE	GTDR IIEIVL	RICRAICNVR
98BWMC13_4	YLGSLVQYWG	LELKKS AISL	LDTTAIAVAE	GTDR IIELLQ	RIGRAIRNTP
98BWMC14_a	YLG NLIQYWG	LELKKSAINL	LDTLAI AVAE	GTDR IIELIQ	RVCRAILNIP
98BWMO14_1	YLG NLVQYWG	LKLKKS AISL	FDTIAIAVAE	GTDR IIELIQ	IICRAIRNIP
98BWMO18_d	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIELVQ	RICRGVLNIP
98BWMO36_a	YLGSLVQYWG	LELKKS AISL	LDTIAIATAE	GTDR IIELIQ	RICRAIYNIP
98BWMO37_d	YLG NLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIEFIQ	RICRAIRNLP
99BW3932_1	YLGSLVQYWG	LELKKS AISL	LDATAVAVAE	GTDR IELIIQ	RIFRAICNIP
99BW4642_4	YLGSLVQYWG	LELKKSATS L	IDAIAIAVAE	GTDR IIDLIQ	RICRAIRNIP
99BW4745_8	YLGSLVQYWG	LELKKS AISL	FDTIAIAVAE	GTDR IIELVL	RICGAIRNIP
99BW4754_7	YLG SIVQYWG	LKLKKS AISL	LDTTAIAVAE	GTDR IIELLR	RFCRAIYSIP
99BWMC16_8	YLGSLGQYWG	LELKKS AIGL	LDTIAIAVAE	GTDR IIELIQ	RTFRAICNIP
A2_CD_97CD	HLWNLLVYWG	QELKTS AIRT	LDTIAVAVAE	WTD RVIEIGQ	RACRAIRNIP
A2_CY_94CY	NLWNLLLYWG	RELKNS AISL	FDTIAVAVAE	WTD RVIEIGQ	RAFRAILNIP
A2D_97KR	YLWNLLLYWG	RELKNS AISL	FNATAIAVAE	WTD RVIEIVQ	RACRAIINIP
A2G_CD_97C	YLWNLLLYWG	QELKNSASNL	LDTVAIAVAN	WTD RVIEAAQ	GACRAIRNVP
A_BY_97BL0	YXXNLXGYXG	QELKSSAINL	IDTIAIAVAX	XTDXVIEIGQ	RFCRAIRNIP
A_KE_Q23_A	YLWNLLSYWG	RELKISAINL	VDTIAIAVAG	WTD RVIEIAQ	RIGRAILHIP
A_SE_SE659	YLG NLLLYWG	RELKISAINL	LDTTAIAVAG	WTD RVIEIVQ	GIGRAFLHIP
A_SE_SE725	YLG NLLLYWG	QELKLS AISL	FDTPAIAVAG	WTD RGIELIQ	RIGRAILNIP
A_SE_SE753	YLWNLLLYWG	RELKSSAINL	VDTIAIAVAG	WTD RIEIGL	RIGRAFLHIP

A_SE_SE853	YLWNLLVYWI	RELKISAIISL	LDTIAIAVAG	WTDRVIELGQ	RLCRAILHIP
A_SE_SE889	YLKNLLSYWG	RELKLSAINL	LDTIAIIVAG	WTDRVIEIGQ	GFCRAIFHP.
A_SE_UGSE8	YLGNNLLYWI	RELKISAIISL	FDTIAIAVAG	WTDRVIEIGQ	RIGRAILHIP
A_UG_92UG0	YLGNNLLYWG	RELKISAINL	LDTIAIAVAG	WTDRVIVTVQ	RLGRAILNIP
A_UG_U455_	YLWNLLLYWG	RELKISAITL	LDAVAVAVAG	WIDRVIEIGQ	TIGRAILNIP
AC_IN_2130	YLWNLLVYWG	RELKISAIKL	VDTIAIVVAG	WTDRIIEIGQ	GIGRAILHIP
AC_RW_92RW	YLGNNLVQYWG	LELKRSAINL	LDTTAIVVAE	GTDRIIELIQ	RISRAIYNIP
AC_SE_SE94	YLWNLLLYWG	RELKRISAINL	LDTIAIATAS	WTDRVIELGQ	RICRAILNIP
ACD_SE_SE8	YLWNLLQYWI	QELKNSAINL	FNTIAIAVAE	GTDRVIEIGQ	RIGRAILNTP
ACG_BE_VI1	LLGNILLYWS	QELKNSAINL	LDTIAIAVAN	WTDRVIEIGQ	RAGRAFLNIP
AD_SE_SE69	YLWNLLQYWI	QELKNSAIISL	VDTTAIAVAE	GTDRVIVTVQ	RAFRAVLRIIP
AD_SE_SE71	YLWNLLQYWI	QELKISAIISL	VDSIAIVVAG	WTDRVIEIGQ	GIGRAILHIP
ADHK_NO_97	YLGNNLLYWG	QELKNSAINL	LNTTAIAVAE	GTDRIIIEIVQ	RTGRAILHIP
ADK_CD_MAL	YLWNLLQYWG	QELKNSAIISL	LNTTAIAVAE	CTDRVIEIGQ	RFGRAILHIP
AG_BE_VI11	YLWNLLVYWG	QELKNSAINL	LDTVAIAVAN	WTDRVIEIGQ	RAGRAILNIP
AG_NG_92NG	YLWNLLLYWG	RELKNSAINL	IDTIAIAVAN	WTDRVIEVAQ	GACRAILNIP
AGHU_GA_VI	YLWNLLLYWG	QELKSSAIISL	LDAVAIAVAN	WTDRVIEVVQ	RVGRAILNIP
AGU_CD_Z32	YLGNNLVYWG	QELKNSAINL	LDTVAIAVAD	WTDRVIEVVQ	RAGRAFLNIP
AJ_BW_BW21	YLGNNLALYWG	RELKNSAIISL	LDTIAITVAE	ATDRIIIEIAQ	RAFRAILHIP
B_AU_VH_AF	YWWNLLQYWS	QELQNSAIISL	LNATAIAVAE	GTDRVIEVVQ	RACRAILHIP
B_CN_RL42_	YWWNLLQYWI	QELKNSAIGL	LNATAIAVAE	GTDRVIEVVQ	RAYRAILHIP
B_DE_D31_U	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRVIEVVQ	RAWRAILHIP
B_DE_HAN_U	YWWNLLQYWS	QELKNSAVSL	FNTIAIAVAE	GTDRVIEVVQ	RACRAILHIP
B_FR_HXB2_	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRVIEVVQ	GACRAIRHIP
B_GA_OYI_	YWWNLLQYWS	QELKNSVISL	LNATAIAVAE	GTDRVIEIVQ	RAYRAFLNIP
B_GB_CAM1_	YWWNLLQYWS	QELRNSAVSL	FDTIAIAVAE	GTDRVIEVVQ	RACRAILHIP
B_GB_GB8_C	YWWNLLQYWI	QELKNSAIISL	LNTTAIAVAE	GTDRVIEVVQ	RAYRAILHIP
B_GB_MANC_	YWWNLLQYWS	QVLKNSAVSL	LNVTIAIAVAE	GTDRIIIEVVQ	RVGRAILHIP
B_KR_WK_AF	YLWNLLQYWS	QELKNSAVSL	LNATAVAVAE	GTDRIIIEILQ	RAYRAILNIP
B_NL_3202A	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRVIEVVQ	RACRAVLHIP
B_TW_TWCYS	YLWNLLQYWI	QELKNSAVSL	FNAIAIAVAE	GTDRVIEVVQ	RVFRAILHIP
B_US_BC_L0	YWWNLLQYWS	QELKNSAVNL	LNVTIAIAVAE	GTDRVIEVVQ	RTYRAILHIP
B_US_DH123	YLWNLLQYWS	QELKNSAVSL	LNATAIAGVE	GTDRIIIEILQ	RATRAILNIP
B_US_JRCSF	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRIIIEVVQ	RVYRAILHIP
B_US_MNCG_	YWWNLLQYWS	QELKSSAVSL	LNATAIAVAE	GTDRVIEVLQ	RAGRAILHIP
B_US_P896_	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRVIKIVQ	RACRAIRNIP
B_US_RF_M1	YWWNLLQYWS	QELKNSAVSL	LNTTAIAVAE	GTDRIIIEVAQ	RILRAFLHIP
B_US_SF2_K	YWWNLLQYWI	QELKNSAVSW	LNATAIAVTE	GTDRVIEVAQ	RAYRAILHIH
B_US_WEAU1
B_US_WR27_	YWGNNLLQYWG	QELRNSAIISL	LNATAIAVAE	GTDRVIEVGQ	RIFRAILHIP
B_US_YU2_M	YWWNLLQYWI	QELKNSAVSL	LNATAIAVAE	GTDRVIEILQ	RAFRAVLHIP
BF1_BR_93B	YLGNNLALYWS	QELKNSAIISL	LNTTAIVVAE	GTDRVIEALQ	RAGRAVLNVP
C_BR_92BR0	YLGGLVQYWS	LELKKSAIISL	FDTIAIAVAE	GTDRIIIEVIQ	GIWRAICNIP
C_BW_96BW0	FLGSLVQYWG	LELKKSAIISL	LDTTAIAVAE	GTDRIIIEIAQ	RICRAICNIP
C_BW_96BW1	YLGSLVQYWG	LELKMSAISL	LDTTAIAIAE	GTDRIIELIQ	RIGRAIRNTP
C_BW_96BW1	YLGSLVQYWG	LELKKSAIISL	LDTIAIAVAE	GTDRIIELTQ	RVFRAIRNIP
C_BW_96BW1	YLGSLVQYWG	LELKKSATSIL	LDSIAIAVAE	GTDRIIIEVIQ	RIYRAFCNIP
C_ET_ETH22	YLGSLVQYWG	LELKKSAINL	LNTTAIVVGE	GTDRFIELIQ	RIWRAFCNIP
C_IN_93IN1	YLGSLVQYWG	LELKKSAIISL	FDSIAIVVAE	GTDRIIELVQ	GFCRAIRNIP
C_IN_93IN9	YLGSLVQYWG	LELKKSAIISL	LDIIAIAVAE	GTDRIIELIQ	RTCRAIRNIP
C_IN_93IN9	YLGSLVQYWG	IELKRSAIISL	LDFTAIAVAE	GTDRIIELVL	RICRAIRNIP
C_IN_94IN1	YLGSLVQYWG	LELKKSAILL	LDIIAIAVAE	GTDRIIIEIIQ	GTCRAIRNIP
C_IN_95IN2	YLGSLVQYWG	LELKKSAINL	LDRIAIAVAE	GTDRILELVQ	RICRAIRNIP
CRF01_AE_C	YLGNNLLSYWG	QELKTSAITL	FDAIAVAVAG	WTDRVIEVVQ	RAWRALIHIP
CRF01_AE_C	YLGNNLLSYWV	QELKRISAITL	LDATAITVAG	WTDRVIEIVQ	RAWRAILHIP
CRF01_AE_C	YLGSLLSYWG	QELKTSAITL	LDATAITVAG	WTDRAIEIAQ	RACRAILHIP
CRF01_AE_T	YLGNNLLYWG	QELKISAIISL	LNTTAIAVAG	WTDRVIEVAQ	GAWRAILHIP
CRF01_AE_T	YLGNNLLYWG	QELKISAIISL	LDATAIAVAG	WTDRVIEVAQ	GAWRAILHIP
CRF01_AE_T	YLGNNLLYWG	QELKISAIISL	FDALAVVAG	WTDRVIEVAQ	GAWRAILHIP
CRF01_AE_T	YLGNNLLYWG	QELKISAIISL	LDAIAIAVAG	WTDRVIKVAQ	RAWRAILHIP
CRF01_AE_T	YLGNNLLYWG	QELKISAIISL	LDATAIAAAG	WTDRVIEVAQ	GAWRAILHIP

CRF01_AE_T	YLWNLLVYWG	QELKISVISL	LNATAIVVAG	WTDRVIEVAQ	GAWRAILHIP
CRF02_AG_F	YLGNNLLYWG	QELKNSAINL	LDTTALAVAN	WTDRVIEIGQ	RVGRAILNIP
CRF02_AG_F	YLGNNLLTYWG	QELKNSAINL	LDTTAIAVAN	WTDRVIEIGQ	RVGRAIRNIP
CRF02_AG_G	YLGNNLAQYWG	LELKNSAISL	LNTTAIVVAE	QTDRLLEFLQ	RAGRAILHIP
CRF02_AG_N	YLWNLLISYWV	QELKNSAINL	LNTTAIVVAN	WTDRAIEIGQ	RVGRAIRNIP
CRF02_AG_S	YLWNLLSYWG	QELKNSAISL	LDTTAIVVAN	WTDRVIELVQ	RAGRAILNIP
CRF02_AG_S	HLWNLLSYWG	QELKNSAINL	LDTTAVAVAN	WTDRVIEIVQ	RTGRAICNIP
CRF03_AB_R	YWWNLLQYWI	QELKSSAINL	IGTTAIAVAG	WTDRVIEIGQ	RFCRAMRNIP
CRF03_AB_R	YWWNLLQYWI	QELKSSAINL	INTTIAVAG	WTDRVIEIGQ	RFCRAIRNIP
CRF04_cpx_	YLWNFLLYWG	QELKNSAINL	FNTTAIAVAE	GTDRIEEEVQ	RACRAICNIP
CRF04_cpx_	YLWNLLLYWG	QELRNSAINL	LDTTAIAVAE	GTDRILEAVQ	RACRAIRNIP
CRF04_cpx_	YLWNLLLYWG	QEIRSSAISL	LDTTAVAVAE	GTDRIEEEVQ	RICRAILNIP
CRF05_DF_B	YLWSLPQYWS	RELKNSAISL	LNTTAVVVAE	GTDRVIEALQ	RAGRAILNIP
CRF05_DF_B	YLWSLLQYWS	QELKNSAISL	LNTTAVVVAE	GTDRILEALQ	RAGRAVLNIP
CRF06_cpx_	YLGNNLCYWG	QELQNSAISL	FDAAAIAVAN	WTDRAEVVQ	RIFRAFLNVP
CRF06_cpx_	YLGSLVWYWG	QELKNSAINL	LDTTAIAVAN	GTDRVIEIVQ	RAFRAVLNIP
CRF06_cpx_	YLWNLVQYWG	QELKNSAISL	IDTTAIAVAN	WTDRVIEVVQ	RAFRAVLNIP
CRF06_cpx_	YLGNNLVQYWG	QELKNSAISL	LDTTAIAVAN	WTDRVIEIVQ	RVFRAFLNVP
CRF11_cpx_	YLGNNLTQYWG	QELKNSAINL	LNTTAIAVAE	GTDRIEEEIVQ	RVLRGILHIP
CRF11_cpx_	YLGNNLAQYWG	QELKSSAISL	LNATAIAVAE	GTDRIEEEVAH	RALRAILNIP
D_CD_84ZR0	YLWNLLQYWS	RELKNSAISL	VDATAIAVAE	GTDRIIDIVR	RACKAVLHIP
D_CD_ELI_K	YLWNLLQYWS	QELRNSASSL	FDAIAIAVAE	GTDRVIEIIQ	RACRAVLNIP
D_CD_NDK_M	YLWNLLQYWS	QELRNSASSL	LDTTAIAVAE	RTDRVIEVVQ	RACRAILNIP
D_UG_94UG1	YLWNLLQYWI	QELKNSAVSL	FNTTAIAVAE	GTDRVIELVQ	RAVRAILNIP
F1_BE_VI85	YLGNNLTRYWS	QELKNSAISL	FNTTAIVVAE	GTDRIEEEVLQ	RAGRAVLNIP
F1_BR_93BR	YLGNNLTQYWG	QELKNSAISL	LNATAIAVAE	WTDRVIEALQ	RAGRAILNIP
F1_FI_FIN9	YLGNNIIQYWS	QELKNSAISL	FNTTAIVVAE	GTDRVIEALQ	RAVRAVLNIP
F1_FR_MP41	YLWNLAQYWS	QELKNSAISL	LNTTAIVVAE	GTDRVIEVLQ	RAGRAVLNIP
F2_CM_MP25	YLWNLAQYWG	QELKNSAISL	LDRTAIAVAE	GTDRIEEEILQ	RAGRAVLNIP
F2KU_BE_VI	YLWSLVQYWG	QELKNSAINL	LNTTAIAVAE	GTDRIEEEVFQ	RAGRAVLNIP
G_BE_DRCBL	YLWNLLLYWA	RELKNSAINL	LDTTAIAVAN	WTDRVIEVAQ	RAGRAVLNIP
G_NG_92NG0	YLWNLLLYWG	RELKNSAINL	LDTTAIAVAN	WTDRVIEVAQ	RAYRAILNIP
G_SE_SE616	YLWNLLLYWG	RELKNSAISL	LDTTAIAVAN	WTDRVIEVAQ	RACRAILNIP
H_BE_VI991	LLGNNLLLYWG	QELKNSAISL	LNTTAIAVAE	GTDRIEEEVLQ	RAWRAILHIP
H_BE_VI997	YLWNLLQYWG	QELKNSAINL	LNTTAIVVAE	GTDRIEEEIVQ	RAWRAVLHIP
H_CF_90CF0	YLWNLLQYWG	QELKNSAIDL	LNTTAIAVAE	GTDRIEEEIVQ	RAWRAILHIP
J_SE_SE702	YLVNVLVWYWG	QELKNSAISL	LNTTAIAVAE	GTDRIEEEIAQ	RAFRAILHIP
J_SE_SE788	YLVNVLVWYWG	QELKNSAISL	LNTTAIAVAE	GTDRIEEEIAQ	RAFRAILHIP
K_CD_EQTB1	YLWNLLIYWG	QELKNSAINL	LNTTAIAVAE	GTDRIEEEIVQ	RAFRALLHIP
K_CM_MP535	YLVNVLVQYWS	QELKNSAISL	LNTTAIAVAG	GTDRIEEEIGQ	RAFRALLHIP
N_CM_YBF30	HLWGILAYWG	KELRDSAISL	LNTTAIVVAE	GTDRIEEELAQ	RIGRGILHIP
O_CM_ANT70	ICAAVTQYWL	QELQNSATSL	LDTLAVAVAN	WTDGIIAGIQ	RIGTGIRNIP
O_CM_MVP51	LCGAVMQYWL	QELKNSATNL	LDTTAVSVAN	WTDGIIILGLQ	RIGQGFLHIP
O_SN_99SE_	LCIAVIQYWL	QELQNSATSL	LDTTAVAVAN	WTVTIILGIQ	RIGRGILNIP
O_SN_99SE_	ICIAVIQYWL	QELQNSATSL	LDTLAVAVAN	WTDGIIILGLQ	RIGRGILNIP
U_CD_83C	YLGNNLVLYWG	QELKNSAISL	LNATAIVVAE	GTDRIEEEVGQ	RICRAILNIP

	951	962
00BW0762_1	RRIRQGFEEA	LQ
00BW0768_2	RRIRQGFEEA	LQ
00BW0874_2	RRIRQGFEEA	LQ
00BW1471_2	RRIEQTFEPP	LL
00BW1616_2	RRIRQGVEEA	LQ
00BW1686_8	RRIRQGFETA	LL
00BW1759_3	RRIRQGFEEA	LQ
00BW1773_2	RRIRQGFEEA	LQ
00BW1783_5	RRIRQGFEEA	LQ
00BW1795_6	TRIRQGFEEA	LQ
00BW1811_3	RRIRQGFEEA	LL
00BW1859_5	RRIRQGFEEA	LL
00BW1880_2	TRIRQGFEEA	LQ
00BW1921_1	TRIRQGFEEA	LQ
00BW2036_1	RRIRQGFEEA	LQ
00BW2063_6	RRVRQGFETA	LL
00BW2087_2	RRIRQGFEEA	LL
00BW2127_2	TRIRQGFEEA	LL
00BW2128_3	SSIRQGFEEA	LQ
00BW2276_7	RRIRQGFEEA	LL
00BW3819_3	TRIRQGFEEA	LL
00BW3842_8	RRIRQGFEEA	LQ
00BW3871_3	RRLRQGFEEA	LL
00BW3876_9	RRIRQGFEEA	LL
00BW3886_8	RRIRQGFEEA	LL
00BW3891_6	TRIRQGFEEA	LQ
00BW3970_2	RRIRQGFEEA	LL
00BW5031_1	RRIRQGFEEA	LQ
96BW01B21	RRIRQGFEEA	LQ
96BW0407	TRIRQGFEEA	LQ
96BW0502	RRIRQGFEEA	LQ
96BW06_J4	RRIRQGFEEA	LL
96BW11_06	RRIRQGFETA	LL
96BW1210	RRIRQGFEEA	LQ
96BW15B03	RRVRQGFEEA	LQ
96BW16_26	RRLRQGFEEA	LQ
96BW17A09	TRIRQGLEAA	LQ
96BWM01_5	RRIRQGFEEA	LL
96BWM03_2	RRIRQGFEEA	LL
98BWMC12_2GFEEA	LQ
98BWMC13_4	RRIRQGFETA	LL
98BWMC14_a	RRVRQGFEEA	LQ
98BWM014_1	TRIRQGLEAA	LL
98BWM018_d	RRIRQGFEEA	LQ
98BWM036_a	TRIRQGFEEA	LL
98BWM037_d	RRIRQGFEEA	LL
99BW3932_1	RRIRQGFETA	LL
99BW4642_4	RRIRQGFEEA	LQ
99BW4745_8	TRIRQGFEEA	LQ
99BW4754_7	RRIRQGFEEA	LQ
99BWMC16_8	RRIRQGFETA	LL
A2_CD_97CD	RRIRQGLERA	LL
A2_CY_94CY	RRIRQGLERA	LL
A2D___97KR	RRIRQGLERA	LL
A2G_CD_97C	RRIRQGLERA	LL
A_BY_97BL0	RRIRXGAEKA	LQ
A_KE_Q23_A	VRIRQGLERA	LL
A_SE_SE659	RRIRQGFEEA	LL
A_SE_SE725	RRIRQGFEEA	LL
A_SE_SE753	RRIRQGFEEA	LL

A_SE_SE853	VRIRQGFERA	LL
A_SE_SE889	RRSKQGLKRA	LQ
A_SE_UGSE8	RRIRQGFER.	..
A_UG_92UG0	RRIRQGFERA	LL
A_UG_U455_	RRIRQGLERA	LL
AC_IN_2130	RRIRQGLERA	LL
AC_RW_92RW	SRIRQGFEEA	LQ
AC_SE_SE94	RRIRQGFERA	LL
ACD_SE_SE8	RRIRQGLERA	LL
ACG_BE_VI1	RRIRQGFERA	LL
AD_SE_SE69	ARIRQGLERV	LL
AD_SE_SE71	RRIRQGLERA	LL
ADHK_NO_97	RRIRQGFERX	LL
ADK_CD_MAL	RRIRQGFERA	LL
AG_BE_VI11	RRIRQGLERA	LL
AG_NG_92NG	RRIRQGLERA	LL
AGHU_GA_VI	RRIRQGLERA	LI
AGU_CD_Z32	RRIRQGLERA	LL
AJ_BW_BW21	VRIRQGFERA	LL
B_AU_VH_AF	RRIRQGLERL	LL
B_CN_RL42_	TRIRQGLERA	LL
B_DE_D31_U	VRIRQGLERA	LL
B_DE_HAN_U	RRVRQGLERA	LL
B_FR_HXB2_	RRIRQGLERI	LL
B_GA_OYI_	RRIRQGLERA	LL
B_GB_CAM1_	RRIRQGLERL	LL
B_GB_GB8_C	TRIRQGLERA	LQ
B_GB_MANC_	VRIRQGLERA	LL
B_KR_WK_AF	RRIRQGLERA	LL
B_NL_3202A	VRIRQGLERA	LL
B_TW_TWCYS	TRIRQGLERA	LL
B_US_BC_L0	RRIRQGLERL	LL
B_US_DH123	TRIRQGLERA	LL
B_US_JRCSF	TRIRQGLERA	LL
B_US_MNCG_	TRIRQGLERA	LL
B_US_P896_	TRIRQGLERA	LL
B_US_RF_M1	RRIRQGLERA	LL
B_US_SF2_K	RRIRQGLERL	LL
B_US_WEAU1
B_US_WR27_	RRIRQGLERV	LL
B_US_YU2_M	VRIRQGLERA	LL
BF1_BR_93B	RRIRQGLERA	LL
C_BR_92BR0	RRIRQGFEEA	LQ
C_BW_96BW0	TRIRQGFEEA	LQ
C_BW_96BW1	RRIRQGFETA	LL
C_BW_96BW1	RRIRQGFEEA	LQ
C_BW_96BW1	RRVRQGFEEA	LQ
C_ET_ETH22	RRIRQGLEAA	LQ
C_IN_93IN1	TRIRQGFEEA	LQ
C_IN_93IN9	RRIRQGFEEA	LQ
C_IN_93IN9	TRIRQGFEEA	LQ
C_IN_94IN1	RRIRQGLEAA	LQ
C_IN_95IN2	RRIRQGFEEA	LQ
CRF01_AE_C	RRIRQGLERA	LL
CRF01_AE_C	RRIRQGLERA	LL
CRF01_AE_C	RRIRQGLERA	LL
CRF01_AE_T	RRIRQGLERT	LL
CRF01_AE_T	RRIRQGLERA	LL
CRF01_AE_T	RRIRQGLERA	LL
CRF01_AE_T	RRIRQGLERA	LL
CRF01_AE_T	RRIRQGLERT	LL

CRF01_AE_T	RRIRQGLERA	LL
CRF02_AG_F	RRIRQGLERA	LL
CRF02_AG_F	VRIRQGLERA	LL
CRF02_AG_G	RRIRQGFERA	LL
CRF02_AG_N	RRIRQGFERA	LL
CRF02_AG_S	RRIRQGFERA	LL
CRF02_AG_S	RRIRQGLERA	LQ
CRF03_AB_R	RRIRQGAEKA	LQ
CRF03_AB_R	RRIRQGAEKA	LQ
CRF04_cpx_	RRIRQGLERA	LL
CRF04_cpx_	RRIRQGFeka	LL
CRF04_cpx_	RRIRQGLERA	LL
CRF05_DF_B	RRIRQGLERA	LL
CRF05_DF_B	RRIRQGLERA	LL
CRF06_cpx_	RRIRQGFERA	LL
CRF06_cpx_	TRIRQGFERA	LL
CRF06_cpx_	RRIRQGAERA	LI
CRF06_cpx_	RRIRQGFERA	LL
CRF11_cpx_	RRIRQGLERA	LL
CRF11_cpx_	RRIRQGFERA	LL
D_CD_84ZR0	TRIRQGLERA	LL
D_CD_ELI_K	RRIRQGLERS	LL
D_CD_NDK_M	RRIRQGLERL	LL
D_UG_94UG1	VRIRQGLERA	LL
F1_BE_VI85	RRIRQGAERA	LL
F1_BR_93BR	RRIRQGLERA	LL
F1_FI_FIN9	RRIRQVERA	LI
F1_FR_MP41	RRIRQGLERS	LL
F2_CM_MP25	RRIRQGLERA	LL
F2KU_BE_VI	RRIRQGFERA	LL
G_BE_DRCBL	RRIRQGLERA	LL
G_NG_92NG0	TRIRQGLERA	LL
G_SE_SE616	TRIRQGLERA	LL
H_BE_VI991	RRIRQGFERA	LL
H_BE_VI997	RRIRQGLERI	LL
H_CF_90CF0	RRIRQGFERS	LL
J_SE_SE702	RRIRQGLERA	LL
J_SE_SE788	RRIRQGLERA	LL
K_CD_EQTB1	RRIRQGFERL	LL
K_CM_MP535	RRIRQGLERA	LL
N_CM_YBF30	RRIRQGLERA	LI
O_CM_ANT70	RRIRQGLERS	LL
O_CM_MVP51	RRIRQGAERI	LV
O_SN_99SE_	RRIRQGLERS	LL
O_SN_99SE_	RRIRQGLERA	LL
U_CD___83C	RRIRQGFERA	LL

Table 13. HIV Nef Sequence Alignment
 GCG Multiple Sequence File.
 Written by Omiga 1.1

Name: 00BW0762_1	SEQ	ID NO: 636	Len: 232	Check: 3461	Weight: 1.00
Name: 00BW0768_2	SEQ	ID NO: 637	Len: 232	Check: 5650	Weight: 1.00
Name: 00BW0874_2	SEQ	ID NO: 638	Len: 232	Check: 3483	Weight: 1.00
Name: 00BW1471_2	SEQ	ID NO: 639	Len: 232	Check: 9491	Weight: 1.00
Name: 00BW1616_2	SEQ	ID NO: 640	Len: 232	Check: 1504	Weight: 1.00
Name: 00BW1686_8	SEQ	ID NO: 641	Len: 232	Check: 1380	Weight: 1.00
Name: 00BW1759_3	SEQ	ID NO: 642	Len: 232	Check: 5319	Weight: 1.00
Name: 00BW1773_2	SEQ	ID NO: 643	Len: 232	Check: 156	Weight: 1.00
Name: 00BW1783_5	SEQ	ID NO: 644	Len: 232	Check: 8063	Weight: 1.00
Name: 00BW1795_6	SEQ	ID NO: 645	Len: 232	Check: 3123	Weight: 1.00
Name: 00BW1811_3	SEQ	ID NO: 646	Len: 232	Check: 4460	Weight: 1.00
Name: 00BW1859_5	SEQ	ID NO: 647	Len: 232	Check: 9116	Weight: 1.00
Name: 00BW1880_2	SEQ	ID NO: 648	Len: 232	Check: 4302	Weight: 1.00
Name: 00BW1921_1	SEQ	ID NO: 649	Len: 232	Check: 2737	Weight: 1.00
Name: 00BW2036_1	SEQ	ID NO: 650	Len: 232	Check: 4558	Weight: 1.00
Name: 00BW2063_6	SEQ	ID NO: 651	Len: 232	Check: 1020	Weight: 1.00
Name: 00BW2087_2	SEQ	ID NO: 652	Len: 232	Check: 7532	Weight: 1.00
Name: 00BW2127_2	SEQ	ID NO: 653	Len: 232	Check: 3425	Weight: 1.00
Name: 00BW2128_3	SEQ	ID NO: 654	Len: 232	Check: 5136	Weight: 1.00
Name: 00BW2276_7	SEQ	ID NO: 655	Len: 232	Check: 3623	Weight: 1.00
Name: 00BW3819_3	SEQ	ID NO: 656	Len: 232	Check: 993	Weight: 1.00
Name: 00BW3842_8	SEQ	ID NO: 657	Len: 232	Check: 6030	Weight: 1.00
Name: 00BW3871_3	SEQ	ID NO: 658	Len: 232	Check: 3547	Weight: 1.00
Name: 00BW3876_9	SEQ	ID NO: 659	Len: 232	Check: 1951	Weight: 1.00
Name: 00BW3886_8	SEQ	ID NO: 660	Len: 232	Check: 3786	Weight: 1.00
Name: 00BW3891_6	SEQ	ID NO: 661	Len: 232	Check: 3655	Weight: 1.00
Name: 00BW3970_2	SEQ	ID NO: 662	Len: 232	Check: 8913	Weight: 1.00
Name: 00BW5031_1	SEQ	ID NO: 663	Len: 232	Check: 2223	Weight: 1.00
Name: 96BW01B21	SEQ	ID NO: 664	Len: 232	Check: 2176	Weight: 1.00
Name: 96BW0407	SEQ	ID NO: 665	Len: 232	Check: 5261	Weight: 1.00
Name: 96BW0502	SEQ	ID NO: 666	Len: 232	Check: 333	Weight: 1.00
Name: 96BW06_J4	SEQ	ID NO: 667	Len: 232	Check: 5784	Weight: 1.00
Name: 96BW11_06	SEQ	ID NO: 668	Len: 232	Check: 4950	Weight: 1.00
Name: 96BW1210	SEQ	ID NO: 669	Len: 232	Check: 6118	Weight: 1.00
Name: 96BW15B03	SEQ	ID NO: 670	Len: 232	Check: 5089	Weight: 1.00
Name: 96BW16_26	SEQ	ID NO: 671	Len: 232	Check: 3957	Weight: 1.00
Name: 96BW17A09	SEQ	ID NO: 672	Len: 232	Check: 1945	Weight: 1.00
Name: 96BWM01_5	SEQ	ID NO: 673	Len: 232	Check: 5827	Weight: 1.00
Name: 96BWM03_2	SEQ	ID NO: 674	Len: 232	Check: 2303	Weight: 1.00
Name: 98BWMC12_2	SEQ	ID NO: 675	Len: 232	Check: 2423	Weight: 1.00
Name: 98BWMC13_4	SEQ	ID NO: 676	Len: 232	Check: 4043	Weight: 1.00
Name: 98BWMC14_a	SEQ	ID NO: 677	Len: 232	Check: 3568	Weight: 1.00
Name: 98BWM014_1	SEQ	ID NO: 678	Len: 232	Check: 4909	Weight: 1.00
Name: 98BWM018_d	SEQ	ID NO: 679	Len: 232	Check: 3505	Weight: 1.00
Name: 98BWM036_a	SEQ	ID NO: 680	Len: 232	Check: 6393	Weight: 1.00
Name: 98BWM037_d	SEQ	ID NO: 681	Len: 232	Check: 1912	Weight: 1.00
Name: 99BW3932_1	SEQ	ID NO: 682	Len: 232	Check: 19	Weight: 1.00
Name: 99BW4642_4	SEQ	ID NO: 683	Len: 232	Check: 6848	Weight: 1.00
Name: 99BW4745_8	SEQ	ID NO: 684	Len: 232	Check: 938	Weight: 1.00
Name: 99BW4754_7	SEQ	ID NO: 685	Len: 232	Check: 1379	Weight: 1.00
Name: 99BWMC16_8	SEQ	ID NO: 686	Len: 232	Check: 4222	Weight: 1.00
Name: A2_CD_97CD	SEQ	ID NO: 687	Len: 232	Check: 2359	Weight: 1.00
Name: A2_CY_94CY	SEQ	ID NO: 688	Len: 232	Check: 5163	Weight: 1.00
Name: A2D_97KR	SEQ	ID NO: 689	Len: 232	Check: 9468	Weight: 1.00
Name: A2G_CD_97C	SEQ	ID NO: 690	Len: 232	Check: 4189	Weight: 1.00
Name: A_BY_97BL0	SEQ	ID NO: 691	Len: 232	Check: 2590	Weight: 1.00
Name: A_KE_Q23	SEQ	ID NO: 692	Len: 232	Check: 2652	Weight: 1.00

Name: A_SE_SE659	SEQ	ID NO: 693	Len: 232	Check: 9245	Weight: 1.00
Name: A_SE_SE725	SEQ	ID NO: 694	Len: 232	Check: 985	Weight: 1.00
Name: A_SE_SE753	SEQ	ID NO: 695	Len: 232	Check: 1638	Weight: 1.00
Name: A_SE_SE853	SEQ	ID NO: 696	Len: 232	Check: 2503	Weight: 1.00
Name: A_SE_SE889	SEQ	ID NO: 697	Len: 232	Check: 2327	Weight: 1.00
Name: A_SE_UGSE8	SEQ	ID NO: 698	Len: 232	Check: 9538	Weight: 1.00
Name: A_UG_92UG0	SEQ	ID NO: 699	Len: 232	Check: 2621	Weight: 1.00
Name: A_UG_U455	SEQ	ID NO: 700	Len: 232	Check: 2084	Weight: 1.00
Name: AC_IN_2130	SEQ	ID NO: 701	Len: 232	Check: 2406	Weight: 1.00
Name: AC_RW_92RW	SEQ	ID NO: 702	Len: 232	Check: 3441	Weight: 1.00
Name: AC_SE_SE94	SEQ	ID NO: 703	Len: 232	Check: 3488	Weight: 1.00
Name: ACD_SE_SE8	SEQ	ID NO: 704	Len: 232	Check: 3016	Weight: 1.00
Name: ACG_BE_VI1	SEQ	ID NO: 705	Len: 232	Check: 5006	Weight: 1.00
Name: AD_SE_SE69	SEQ	ID NO: 706	Len: 232	Check: 3362	Weight: 1.00
Name: AD_SE_SE71	SEQ	ID NO: 707	Len: 232	Check: 2262	Weight: 1.00
Name: ADHK_NO_97	SEQ	ID NO: 708	Len: 232	Check: 8765	Weight: 1.00
Name: ADK_CD_MAL	SEQ	ID NO: 709	Len: 232	Check: 6397	Weight: 1.00
Name: AG_BE_VI11	SEQ	ID NO: 710	Len: 232	Check: 6471	Weight: 1.00
Name: AG_NG_92NG	SEQ	ID NO: 711	Len: 232	Check: 2880	Weight: 1.00
Name: AGHU_GA_VI	SEQ	ID NO: 712	Len: 232	Check: 9053	Weight: 1.00
Name: AGU_CD_Z32	SEQ	ID NO: 713	Len: 232	Check: 523	Weight: 1.00
Name: AJ_BW_BW21	SEQ	ID NO: 714	Len: 232	Check: 3842	Weight: 1.00
Name: B_AU_VH	SEQ	ID NO: 715	Len: 232	Check: 8468	Weight: 1.00
Name: B_CN_RL42	SEQ	ID NO: 716	Len: 232	Check: 9366	Weight: 1.00
Name: B_DE_D31	SEQ	ID NO: 717	Len: 232	Check: 3989	Weight: 1.00
Name: B_DE_HAN	SEQ	ID NO: 718	Len: 232	Check: 563	Weight: 1.00
Name: B_FR_HXB2	SEQ	ID NO: 719	Len: 232	Check: 3184	Weight: 1.00
Name: B_GA_OYI	SEQ	ID NO: 720	Len: 232	Check: 5511	Weight: 1.00
Name: B_GB_CAM1	SEQ	ID NO: 721	Len: 232	Check: 4779	Weight: 1.00
Name: B_GB_GB8	SEQ	ID NO: 722	Len: 232	Check: 1128	Weight: 1.00
Name: B_GB_MANC	SEQ	ID NO: 723	Len: 232	Check: 2885	Weight: 1.00
Name: B_KR_WK	SEQ	ID NO: 724	Len: 232	Check: 9915	Weight: 1.00
Name: B_NL_3202A	SEQ	ID NO: 725	Len: 232	Check: 3135	Weight: 1.00
Name: B_TW_TWCYS	SEQ	ID NO: 726	Len: 232	Check: 2211	Weight: 1.00
Name: B_US_BC	SEQ	ID NO: 727	Len: 232	Check: 3145	Weight: 1.00
Name: B_US_DH123	SEQ	ID NO: 728	Len: 232	Check: 7019	Weight: 1.00
Name: B_US_JRCSF	SEQ	ID NO: 729	Len: 232	Check: 4099	Weight: 1.00
Name: B_US_MNCG	SEQ	ID NO: 730	Len: 232	Check: 4137	Weight: 1.00
Name: B_US_P896	SEQ	ID NO: 731	Len: 232	Check: 4405	Weight: 1.00
Name: B_US_RF	SEQ	ID NO: 732	Len: 232	Check: 450	Weight: 1.00
Name: B_US_SF2	SEQ	ID NO: 733	Len: 232	Check: 5413	Weight: 1.00
Name: B_US_WEAU1	SEQ	ID NO: 734	Len: 232	Check: 5335	Weight: 1.00
Name: B_US_WR27	SEQ	ID NO: 735	Len: 232	Check: 3720	Weight: 1.00
Name: B_US_YU2	SEQ	ID NO: 736	Len: 232	Check: 9943	Weight: 1.00
Name: BF1_BR_93B	SEQ	ID NO: 737	Len: 232	Check: 3598	Weight: 1.00
Name: C_BR_92BR0	SEQ	ID NO: 738	Len: 232	Check: 3908	Weight: 1.00
Name: C_BW_96BW0	SEQ	ID NO: 739	Len: 232	Check: 3880	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 740	Len: 232	Check: 4542	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 741	Len: 232	Check: 6118	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 742	Len: 232	Check: 5089	Weight: 1.00
Name: C_ET_ETH22	SEQ	ID NO: 743	Len: 232	Check: 744	Weight: 1.00
Name: C_IN_93IN1	SEQ	ID NO: 744	Len: 232	Check: 943	Weight: 1.00
Name: C_IN_93IN9	SEQ	ID NO: 745	Len: 232	Check: 1241	Weight: 1.00
Name: C_IN_93IN9	SEQ	ID NO: 746	Len: 232	Check: 9885	Weight: 1.00
Name: C_IN_94IN1	SEQ	ID NO: 747	Len: 232	Check: 6448	Weight: 1.00
Name: C_IN_95IN2	SEQ	ID NO: 748	Len: 232	Check: 5597	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 749	Len: 232	Check: 1052	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 750	Len: 232	Check: 744	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 751	Len: 232	Check: 1265	Weight: 1.00
Name: CRF01_AE_T	SEQ	ID NO: 752	Len: 232	Check: 697	Weight: 1.00
Name: CRF01_AE_T	SEQ	ID NO: 753	Len: 232	Check: 8468	Weight: 1.00

Name:	CRF01_AE_T	SEQ	ID NO:	754	Len:	232	Check:	9246	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	755	Len:	232	Check:	8105	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	756	Len:	232	Check:	9948	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	757	Len:	232	Check:	9460	Weight:	1.00
Name:	CRF02_AG_F	SEQ	ID NO:	758	Len:	232	Check:	925	Weight:	1.00
Name:	CRF02_AG_F	SEQ	ID NO:	759	Len:	232	Check:	9559	Weight:	1.00
Name:	CRF02_AG_G	SEQ	ID NO:	760	Len:	232	Check:	399	Weight:	1.00
Name:	CRF02_AG_N	SEQ	ID NO:	761	Len:	232	Check:	2782	Weight:	1.00
Name:	CRF02_AG_S	SEQ	ID NO:	762	Len:	232	Check:	538	Weight:	1.00
Name:	CRF02_AG_S	SEQ	ID NO:	763	Len:	232	Check:	6700	Weight:	1.00
Name:	CRF03_AB_R	SEQ	ID NO:	764	Len:	232	Check:	6784	Weight:	1.00
Name:	CRF03_AB_R	SEQ	ID NO:	765	Len:	232	Check:	3106	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	766	Len:	232	Check:	1551	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	767	Len:	232	Check:	5866	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	768	Len:	232	Check:	7925	Weight:	1.00
Name:	CRF05_DF_B	SEQ	ID NO:	769	Len:	232	Check:	3625	Weight:	1.00
Name:	CRF05_DF_B	SEQ	ID NO:	770	Len:	232	Check:	5585	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	771	Len:	232	Check:	3770	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	772	Len:	232	Check:	4202	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	773	Len:	232	Check:	5376	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	774	Len:	232	Check:	1869	Weight:	1.00
Name:	CRF11_cpx	SEQ	ID NO:	775	Len:	232	Check:	3479	Weight:	1.00
Name:	CRF11_cpx	SEQ	ID NO:	776	Len:	232	Check:	3712	Weight:	1.00
Name:	D_CD_84ZR0	SEQ	ID NO:	777	Len:	232	Check:	1380	Weight:	1.00
Name:	D_CD_ELI	SEQ	ID NO:	778	Len:	232	Check:	4418	Weight:	1.00
Name:	D_CD_NDK	SEQ	ID NO:	779	Len:	232	Check:	4588	Weight:	1.00
Name:	D_UG_94UG1	SEQ	ID NO:	780	Len:	232	Check:	2178	Weight:	1.00
Name:	F1_BE_VI85	SEQ	ID NO:	781	Len:	232	Check:	4350	Weight:	1.00
Name:	F1_BR_93BR	SEQ	ID NO:	782	Len:	232	Check:	7703	Weight:	1.00
Name:	F1_FI_FIN9	SEQ	ID NO:	783	Len:	232	Check:	5036	Weight:	1.00
Name:	F1_FR_MP41	SEQ	ID NO:	784	Len:	232	Check:	84	Weight:	1.00
Name:	F2_CM_MP25	SEQ	ID NO:	785	Len:	232	Check:	2622	Weight:	1.00
Name:	F2KU_BE_VI	SEQ	ID NO:	786	Len:	232	Check:	2193	Weight:	1.00
Name:	G_BE_DRCBL	SEQ	ID NO:	787	Len:	232	Check:	2548	Weight:	1.00
Name:	G_NG_92NG0	SEQ	ID NO:	788	Len:	232	Check:	3608	Weight:	1.00
Name:	G_SE_SE616	SEQ	ID NO:	789	Len:	232	Check:	2716	Weight:	1.00
Name:	H_BE_VI991	SEQ	ID NO:	790	Len:	232	Check:	1561	Weight:	1.00
Name:	H_BE_VI997	SEQ	ID NO:	791	Len:	232	Check:	663	Weight:	1.00
Name:	H_CF_90CF0	SEQ	ID NO:	792	Len:	232	Check:	1804	Weight:	1.00
Name:	J_SE_SE702	SEQ	ID NO:	793	Len:	232	Check:	1615	Weight:	1.00
Name:	J_SE_SE788	SEQ	ID NO:	794	Len:	232	Check:	1704	Weight:	1.00
Name:	K_CD_EQTB1	SEQ	ID NO:	795	Len:	232	Check:	4783	Weight:	1.00
Name:	K_CM_MP535	SEQ	ID NO:	796	Len:	232	Check:	2033	Weight:	1.00
Name:	N_CM_YBF30	SEQ	ID NO:	797	Len:	232	Check:	6419	Weight:	1.00
Name:	O_CM_ANT70	SEQ	ID NO:	798	Len:	232	Check:	8742	Weight:	1.00
Name:	O_CM_MVP51	SEQ	ID NO:	799	Len:	232	Check:	5835	Weight:	1.00
Name:	O_SN_MP129	SEQ	ID NO:	800	Len:	232	Check:	8625	Weight:	1.00
Name:	O_SN_MP130	SEQ	ID NO:	801	Len:	232	Check:	8793	Weight:	1.00
Name:	U_CD_83C	SEQ	ID NO:	802	Len:	232	Check:	1586	Weight:	1.00

SEQ	ID	NO	1	50
636	00BW0762_1	MGGKWSKSS.	IVGWPAVRER	IR...RTDPAAEGVG
637	00BW0768_2	MGGKWSKSSI	V.GWPEVRER	IRR..TEP..AAEGVG
638	00BW0874_2	MGGKWSKSS.	LTGWPAVRER	IR...RTEPAAEGVG
639	00BW1471_2	MGGKWSKSS.	IVGWPAVKER	IRR..TNPR.TERAAVGVG
640	00BW1616_2	MGNKWSKSS.	IVGWPAVRDR	MRR..AEP..AAEGVG
641	00BW1686_8	MGGKWSKRS.	KADWPAVREK	LR...TTEPAAEGVG
642	00BW1759_3	MGNKWSKS..	..WPVRER	IRR..TRPARGNEPAAEGVG
643	00BW1773_2	MGSKWSKSSI	V.GWPKVRET	IRR..TEP..AAEGVG
644	00BW1783_5	MGNKWSKS..	..WPAIRER	IRR..TNPAAERTRAAEGVG
645	00BW1795_6	MGGKWSKSS.	VVGWPAIRER	MRR..... .TEPAAEGVG

646	00BW1811_3	MGGKWSKSC.	KIGWPAVRER	MRR.....	TEPAVEGVG
647	00BW1859_5	MGGKWSKSG.	KVGWPEVRER	MRR..TRPAA	EGG.....	DSAAEGVG
648	00BW1880_2	MGGKWSKSS.	LVGWPAVRER	IRT..TAP..
649	00BW1921_1	MGGKWSKSS.	IVGWPAVRER	MR....KTEP	AAEGVG
650	00BW2036_1	MGGKWSKSS.	IVGWPAVRER	IRR.....	TEPAAEGVG
651	00BW2063_6	MGGKWSKSSI	I.GWPAVRER	MRK..AEP..	AAEGVG
652	00BW2087_2	MGSKWSKSS.	IVGWPAVRER	IRR..T....	RTEPAAEGVG
653	00BW2127_2	MGGKWSKSSI	I.GWPAIRER	IRR..TEP..	AAEGVG
654	00BW2128_3	MGSKWSKCSI	I.GWPAVRER	IRR..AEP..	AAVGVG
655	00BW2276_7	MGSKWSKC..	.SGWPDVRER	MRR..ATPAA	EAGRA...AP	AAEGAAPGVG
656	00BW3819_3	MGSKWSKCSI	V.GWPDVRER	MRR..ARPAV	RERRRQTEPA	AEGVAAEGVG
657	00BW3842_8	MGGKWSKGR.	IVGWPAVRER	MRR.....	TEPAAEGVG
658	00BW3871_3	MGSKWSKRS.	IVEWPAVRER	LR....KTEP	AAEGVG
659	00BW3876_9	MGGKWSKSS.	IVGWPAVRER	IRQ..TGAR.	AAEGV G
660	00BW3886_8	MGGKWSKSS.	IVGWSAVRER	MK....RTEP	AAEGVG
661	00BW3891_6	MGGKWSKSS.	IVGWPTVRER	MRR..TQP..	AAEGVG
662	00BW3970_2	MGSKWSKRS.	TAGWPAVRER	MRR..TQPAA	EG.....	TQSAAGVG
663	00BW5031_1	MGGKWSKSS.	LVGWPEVRDR	IRR..TDP..	AAEGVG
664	96BW01B21	MGGKWSKSSI	V.GWPAVRER	IRR..TEP..	AAEGVG
665	96BW0407	MGGKWSKSSI	V.GWPAVRER	MRR..AEP..	AAEGVG
666	96BW0502	MGGKWSK...	CSGWPAVRER	MRR..TRPAV	EGR.....	TESAAEGVG
667	96BW06_J4	MGGKWSKSS.	IVGWPAVRER	IR....RTDP	PAEGVR
668	96BW11_06	MGGKWSKSSI	I.GWPAIRER	IRR..TEPAA	ER.....V	GAAAGVG
669	96BW1210	MGNKWSKG..	..WPAVRDR	IRR..TEPAT	EPAAEGVG
670	96BW15B03	MGGKWSKSS.	IVGWPAVRER	IRR.....	TEPAAEGVG
671	96BW16_26	MGGKWSK...	..WPAVRER	MRR..TR...	VG
672	96BW17A09	MGXKWSKRS.	IVGWPNVRER	IRR..TNPLT	ER.....	EAERAAGVG
673	96BWMO1_5	MGSKWSKSSI	I.GWPAVRER	IRK..TEPRK	TEPAAEGVG
674	96BWMO3_2	MGGKWSKSS.	IVGWPAVRER	MRR..TRPGA	AE.....	GVG
675	98BWMC12_2	MGSKWSKSS.	IIGWPAVRER	MR....RTEP	AAEGVG
676	98BWMC13_4	MGGKWSKSS.	IIGWPAVRER	MRR.....	TEPAAEGVG
677	98BWMC14_a	MGGKWSKSS.	LVGWPDVRER	IR....KPRP	KP.....	AAEGVG
678	98BWMO14_1	MGSKLSKSK.	IVGWPAIRER	LR.....	RTEPAAEGVG
679	98BWMO18_d	MGGKWSKSS.	IVGWPAVRER	IRQ..TDPRE	RI.....R	QTEPAAEGVG
680	98BWMO36_a	MGGKWSKSSI	V.GWPAVRER	IRR..TEPRR	AEPAAEGVG
681	98BWMO37_d	MGGKWSKSS.	IVGWPEVRER	LR....RTAP	AAEGVG
682	99BW3932_1	MGGKWSKRKI	V.QWPTVRER	LRR..TEP..	AEGVG
683	99BW4642_4	MGGKWSKSS.	IVGWPAVRER	IRR..TQPAA	EG.....	VG
684	99BW4745_8	MGSKLSKSC.	TAGWPTVRER	IRQ..AEP..	AAEGVG
685	99BW4754_7	MGGKWSKSS.	IVGWANVRER	MRR.....	TEPAAVGVG
686	99BWMC16_8	MGNKWSKS..	..WPAVRER	IRR..TEPAV	RV.....R	RTEPAAEGVG
687	A2_CD_97CD	MGGKWSKRT.	IVGWPEIRER	MRR..TPPAA	EG.....VR	PTPPAAEGVG
688	A2_CY_94CY	MGGKWSKRS.	IPGWPAIRER	MRRTPTAQR	TE.....	AVSPAAPGVG
689	A2D_97KR	MGGKWSKRS.	LPGWPAIRER	MRRTPPAAER	TP.....	PAA.AAEGVG
690	A2G_CD_97C	MGSKWSKSS.	IVGWPAVRAR	IR...QTPP.	AAEGVG
691	A_BY_97BL0	XXGKWSKSS.	IXXWPQVXR	IRRAPAP...	AARXVG
692	A_KE_Q23	MGGKWSKSS.	IVGWPEIRER	MRRAPP....	AAPGVG
693	A_SE_SE659	MGGKWSKSS.	IVGWPEIRER	MRRAPS....	AAAPGVG
694	A_SE_SE725	MGSKWSKSS.	IVGWREVRER	LRQTLAAARGVG
695	A_SE_SE753	MGGRWSKSR.	IVGWPEVRER	IRRAPP....	AATGVG
696	A_SE_SE853	MGGKWSKRS.	KEGWSEVREK	IRQT.....	PPAAKGVG
697	A_SE_SE889	MGGKWSKSS.	IVGWPKVRER	MARTPP....	AAKGVG
698	A_SE_UGSE8	MGNKWSK...	..GWPEVRER	IRQARAPAHT	PAPTAATGVG
699	A_UG_92UG0	MGNKWSKSC.	IVGWPEVRER	IRQTPTAARE	RTR.....	QAPTAAGVG
700	A_UG_U455	MGGKWSKKS.	RVEWPEVRKR	MRETPA....	AAKGVG
701	AC_IN_2130	MGGKWPCKSS.	VVGWPEVRER	IRRTPA....	AAPGVG
702	AC_RW_92RW	MGSKWSKCSF	V.GWPAVRER	LRQ..TEP..	AAEGVG
703	AC_SE_SE94	MGGKWSKSS.	IIGWPOIRER	IRRTPP....	AATGVG
704	ACD_SE_SE8	MGGKWLKSSI	V.GWPAVRER	IRR..TEP..	AAEGVG
705	ACG_BE_VI1	MGGKWSKRS.	KVEWPQVRER	MRQ..TPIAA	EA.....EG	AAAGVG
706	AD_SE_SE69	MGGKWSKSS.	IVGWPAVRER	IKR..T....	DPAAEGVG

707	AD_SE_SE71	MGGKWSKSS.	IVGWPEVRER	MRRARAP...	SAAPGVG
708	ADHK_NO_97	MGGKWSKSS.	IVGWPAIRER	MRR..AEP..	AAEGVG
709	ADK_CD_MAL	MGGKWSKSS.	IVGWPKIRER	IRRTPTTETG	VGAVSQD
710	AG_BE_VI11	MGGKWSKSS.	PVGWSRVREER	MRR..TPPAA	EG.....	AAAEGVG
711	AG_NG_92NG	IGGKWSKSS.	IVGWPAVRER	IR...QTP..	PAEGVG
712	AGHU_GA_VI	MGGWSRSS.	IVGWSTIRER	MRRAP....	AAAGVG
713	AGU_CD_Z32	MGNKWSKG..	...WPAVRER	IRQ..TPPAP	P.....	AAEGVG
714	AJ_BW_BW21	MGSNWSKS.S	IIGWPQVRER	MKR.....AP	A.....P	AAEGVG
715	B_AU_VH	MGGKGSKR.I	RSEWPTVRER	IIQ..AEPAA	AG.....	VG
716	B_CN_RL42	MGGKWSKHS.	MFGWPSVRER	MKR..AEPAA	DG.....	VG
717	B_DE_D31	MGGKWSKSS.	VVGWPAIRER	MK.....	RAEPAAEGVG
718	B_DE_HAN	MGGKWSK...	CSGWPTVRER	MKQAEP....	EPAADGVG
719	B_FR_HXB2	MGGKWSKSS.	VIGWPTVRER	MR.....	RAEPAADRVG
720	B_GA_OYI	MGGKWSKCS.	MKGWPTIRER	MKR..AELQP	PE.....	PAAEGVG
721	B_GB_CAM1	MGGKWSKRS.	LGGWSAVRER	MQR..AEP..	RAEPAAEGVG
722	B_GB_GB8	MGGKLSKRS.	MFGWSRVDR	MQQ..AEP..	AAEGVG
723	B_GB_MANC	MGGKWSKSR.	KIGWPTVRER	MKQ..VDPAE	EGR.....KK	QAEPAAGVG
724	B_KR_WK	MGGKWSKRS.	VPGWNTIRKR	MRR..AEPAA	EG.....	VG
725	B_NL_3202A	MGGKWSKSS.	VVGWPAIRER	MK.....	RAEPAADGVG
726	B_TW_TWCYS	MGGKWSKRS.	IPGWSNIRER	IRQ..AEPAA	AADGVG
727	B_US_BC	MGGKWSKRM.	EGGWHAVRER	MR.....	RAEPAADGVG
728	B_US_DH123	MGGKLSKCG.	GVGWSTVRER	MRR..AEPAA	DR.....	EP.AVGVG
729	B_US_JRCSF	MGGKWSKHS.	VPGWSTVRER	MRR..AEPAT	DR.....VR	QTEPAAVGVG
730	B_US_MNCG	MGGKWSKR..	VTGWPTVRER	MRR..AEP..	AELAADGVG
731	B_US_P896	MGGKWSKRR.	AEGWQTIRER	MRRAPAA...	EPAADGVG
732	B_US_RF	MGGKWSKSK.	MGGWPAVRER	MQK..AEPAA	DG.....	VG
733	B_US_SF2	MGGKWSKRS.	MGGWSAIRER	MRR..AEP..	RAEPAADGVG
734	B_US_WEAU1	MGGIWSKRS.	GSGWPAIRER	MKR..AEPAA	EG.....	VG
735	B_US_WR27	MGGKWSKRS.	VGGWPAIRER	MX.....	RAEPAAEGVG
736	B_US_YU2	MGGKWSKRS.	MAGWPTVRER	MRR..AEPAA	ER.....MR	RAEPAADGVG
737	BF1_BR_93B	MGSKWSKSS.	IVGWPAIRER	LRQ..TP...	PAAGVG
738	C_BR_92BR0	MGNKWSKCST	V.GRPAIRER	MRR..AP..	AAEGVG
739	C_BW_96BW0	MGGKWSKSSI	V.GWPAVRER	MRR..TEP..	AAEGVG
740	C_BW_96BW1	MGGKWSKRSK	I.EWPTIRDR	MRR..TEPAA	EG.....V	GAAAGVG
741	C_BW_96BW1	MGNKWSKG..	...WPAVRDR	IRR..TEPAT	EPAAEGVG
742	C_BW_96BW1	MGGKWSKSS.	IVGWPAVRER	IRR.....	TEPAAEGVG
743	C_ET_ETH22	MGGTMSKCS	P.V.GWPAIRER	IRR..AAP..	AAEGVG
744	C_IN_93IN1	MGGKWSKCSI	V.GWPAIRER	MRR..AEP..	AAEGVG
745	C_IN_93IN9	MGGKWSKCSI	V.GWPDIRER	MRR..TQP..	AAEGVG
746	C_IN_93IN9	MGGKWSKCSI	V.GWPAVRER	MRR..TEP..	AAEGVG
747	C_IN_94IN1	MGGKWSKCSI	V.GWPEIRER	MRR..TQP..	AADGVG
748	C_IN_95IN2	MGGKWSKCSI	V.GWPDIRER	MRR..TEP..	AAEGVG
749	CRF01_AE_C	MGGKWSKN.R	IVGWPOVRER	IRR..TPAAA	EGVG
750	CRF01_AE_C	MGGKWSKSC.	IVGWPOVRER	IRQ..TPVAE	E.....R	QTPAAAEGVG
751	CRF01_AE_C	MGNKWSKS..	...WPQIRER	IRQ..TPVAT	EGVG
752	CRF01_AE_T	MGGKWSKS.S	IVGWPOVREK	IKQ..TPPAA	EGVG
753	CRF01_AE_T	MGGKWSKS.S	IVGWPOVREK	IKQ..TPPAA	EGVG
754	CRF01_AE_T	MGGKWSKS.S	IVGWPOVRER	IKQ..TPPAA	EGVG
755	CRF01_AE_T	MGAKWSKRG.	...WPQVRER	IRQ..TPPAA	EGVG
756	CRF01_AE_T	MGSKWSKS.S	IVGWPOVREK	IKQ..TPPAT	EGVG
757	CRF01_AE_T	MGNKWSKS..	...WPRVRER	IKQ..TPPAA	EGVG
758	CRF02_AG_F	MGGKWSKSS.	IVGWPKVRER	IR...QTPP.	AATGVG
759	CRF02_AG_F	MGGKWSKSS.	LVGWPKVRER	II...QTPP.	AATGVG
760	CRF02_AG_G	MGGKWSKSS.	IVGWPOVRER	IR...QTPT.	AAKGVG
761	CRF02_AG_N	MGGKWSKSS.	IVGWPKVMKR	MR...QTPT.	AATGVG
762	CRF02_AG_S	MGGKWSKSS.	IVGWPOIRDR	IR...QTPP.	AARGVG
763	CRF02_AG_S	MGGKWSKSS.	LVGWPOVRER	IRRTQPTPS.	AAIGVG
764	CRF03_AB_R	MGGKWSKSS.	IVGWPOVRER	IRRAPAP...	AARGVG
765	CRF03_AB_R	MGGKWSKSS.	IVGWPOIRER	IRRAPAP...	AARGVG
766	CRF04_cpx_	MGGKWSKSS.	IVGWPEIRER	MRR..ARAEP	ERM.....RA	QAEPAAGVG
767	CRF04_cpx_	MGGKWSKSS.	LVGWPAIRER	MRR..ARAEPAA	QAEPAAGVG

768	CRF04_cpx_	MGNKWSKS..	...WPAVRER	MRR..ARAEPA	RAEPAAVGVG
769	CRF05_DF_B	MGGKWSKSS.	VVGWPAIREK	MRR..TP...PAAEGVG
770	CRF05_DF_B	MGGKWSKNR.	IVGWPAIRER	MRR..TPPAAGAAAEVG
771	CRF06_cpx_	MGNKWSK...	..GWSQVRER	MRR..TPPTE	R.....	...AAEGVG
772	CRF06_cpx_	MGSKWSKS.S	IVGWQVVRER	IRQ..TPPTE	G.....	...AAKGVG
773	CRF06_cpx_	MGGKWSKS.S	LVGWQVVRER	IRQ..TPPTE	G.....	...AAEGVG
774	CRF06_cpx_	MGGKWSKS.S	IVGWPKVRER	MRQ..TPPAA	E.....R	QTPPAAEGVG
775	CRF11_cpx_	MGGKWSKS.S	IVGWPEIRER	LRR.....T	PPAAAADGVG
776	CRF11_cpx_	MGGNWSKS.S	IVGWPEIRER	LRR.....T	PPTAAAEVG
777	D_CD_84ZR0	MGGKWSKSS.	IVGWPAIRER	IRK..TDPRE	RR.....	RPEPAADGVG
778	D_CD_ELI	MGGKWSKSS.	IVGWPAIRER	IRR..T....NPAADGVG
779	D_CD_NDK	MGGKWSKSS.	LVGWPAIRER	IRK..T....DPAADGVG
780	D_UG_94UG1	MGGKWSKSS.	IVGWPAVRER	MRR..T....EPAAEVG
781	F1_BE_VI85	MGGKWSKSS.	IVGWPAVGER	MRQ..TP...TAAEGVG
782	F1_BR_93BR	MGGKWSKSS.	IVGWPAIRER	MRR..TPPT.PPAAEGVG
783	F1_FI_FIN9	MGGKWSKSS.	IVGWPAIRER	MRR..PP...PAAAEVG
784	F1_FR_MP41	MGGKWSKSS.	IVGWPAVRER	MRR..TP...PAAEGVG
785	F2_CM_MP25	MGGKWSKSS.	IVGWPAIRER	IRR..TP...VAAEGVG
786	F2KU_BE_VI	MGGKWSK...	..GWPSVRER	IRR..TPPAA	P.....	...AADGVG
787	G_BE_DRCBL	MGNKWSKRK.	VAGWPEVRER	LR...QHPA.AAEGVG
788	G_NG_92NG0	MGGKWSKSS.	IVGWQIRER	IR...QTPV.AAEGVG
789	G_SE_SE616	MGGKWSKSS.	IVGWPEVRER	IR...NTPT.AAEGVG
790	H_BE_VI991	MGGKWSKGC.	ISGWPAVRER	IRQ..TEP..AAEGVG
791	H_BE_VI997	MGGKWSKSS.	IVGWPAVRER	IRR..AQP..AADGVG
792	H_CF_90CF0	MGGKWSKSR.	MGGWSTIRER	MRR..AEP..VAEGVG
793	J_SE_SE702	MGNKWSKS..	...WPQVRDR	MRR..A..AP	A.....P	...AADGVG
794	J_SE_SE788	MGNKWSKS..	...WPQVRER	MRR.....AP	A.....P	...AADGVG
795	K_CD_EQTB1	MGGKWSKS.S	IVGWSTVRER	MR.....	KTPPAADGVG
796	K_CM_MP535	MGGKWSKS.S	IVGWPAIRER	MRR..ARPAA	DR.....V	GTQPAADGVG
797	N_CM_YBF30	MGKIWSKSS.	LVGWPEIRER	MRRQTQEP..AVEPAVGAG
798	O_CM_ANT70	MGNALRKKG.	FEGWAAVRER	MRTRTF...P	ESEPCAPGVG
799	O_CM_MVP51	MGNAWSKSK.	FAGWSEVRDR	MRRSSS....D	PQQPCAPGVG
800	O_SN_MP129	MGNVLGKDI.	FKGWSAVRER	MRGTS....	DPEPCAPGVG
801	O_SN_MP130	MGNVLGKDK.	FKGWSAVRER	MRKTS....P	EPEPCAPGVG
802	U_CD___83C	MGNKWSKQ..	...WPAIRER	MRR..ARPAA	E.....P	...AADGVG

51

100

00BW0762_1	AASQDLDRHG	AITSSNTPTT	NAACAWLEAQ	EEDE...VGF	PVRPQVPLRP
00BW0768_2	AASQDLDKYG	ALTSSNTANT	NAACAWLEAQ	EKEE.E.VGF	PVRPQVPLRP
00BW0874_2	EASQDLDKHG	ALTTSNTAAN	NADCAWLQAH	EEEG..EVGF	PVRPQVPLRP
00BW1471_2	AASQDLDKYG	ALTANNTPAN	NADCARLQAH	EEDN..EVGF	PVRPQVPLRP
00BW1616_2	PASQDLGRHG	ALTTSNTAHN	NADCAWLEAQ	EEEG.G.VGF	PVRPQVPLRP
00BW1686_8	AASQDLAKHG	ALTSSNTAHN	NADCAWLEAQ	EEEE...VGF	PVRPQVPLRP
00BW1759_3	AASQDLDKYG	ALTSSNTPTT	NAACAWLEAQ	EEAE.E.VGF	PVRPQVPLRP
00BW1773_2	AASQDLDKYG	ALTSSNTDTN	NADCAWLKAQ	EEEG.E.VGF	PVRPQVPLRP
00BW1783_5	AASRDLDKHG	ALTSSNTPAT	NADCAWLEAQ	EEEE.E.VGF	PVRPQVPVRP
00BW1795_6	AASQDLDKYG	ALTSSNTATN	NADCAWLEAQ	EEAD..DVGF	PVRPQVPLRP
00BW1811_3	AASQDLDRHG	ALTSSNTATN	NADCAWLEAQ	EEGE..EVGF	PVRPQVPLRP
00BW1859_5	AASRDLARHG	ALTSSNTATT	NAACAWLEAQ	EEAD..EVGS	PVRPQVPLRP
00BW1880_2AAT	NDACARLKEQ	EEEG.E.VGF	PVRPQVPVRP
00BW1921_1	AASRDLDKYG	ALTSSNTVTT	NAACAWLEAQ	EKEG..GVGF	PVRPQVPLRP
00BW2036_1	AASQDLDKHG	ALTSSNTSTT	NADCAWLEAQ	EEAD..DVGF	PVRPQVPLRP
00BW2063_6	AASQDLDKHG	ALTSSNTANN	NADCAWLEAQ	EEEE...VGF	PVKPQVPLRP
00BW2087_2	AASQDLDKHG	ALTPSNTAGN	NSTCAWLQAH	EEEE..EVGF	PVRPQVPLRP
00BW2127_2	AASQDLDKHG	ALTSSNTATN	NADCAWLQAH	EEES.EGVGF	PVRPQVPLRP
00BW2128_3	AASQDLDKYG	ALTSSNTDTN	NAACAWLRAQ	EEEE.E.VGF	PVX.....TS
00BW2276_7	AASRDLDHRG	ALTSSNTPTN	NADCAWLQAH	EEEE.EEVGF	PVRPQVPLRP
00BW3819_3	TASQDLAKHG	ALTSSNTPAN	NAACAWLQAH	EEEE.D.VGF	PVRPQVPLRP
00BW3842_8	AASRDLDKHG	ALTSSNTAEN	NADCAWLEAQ	EETE..EVGF	PVRPQVPLRP
00BW3871_3	AASQDLDKHG	ALTSSNTAQN	NAACAWLEAQ	EEAE.GEVGF	PVRPQVPLRP
00BW3876_9	AASQDLDRHG	ALTSSNTGAT	NSDVAWLEAQ	EEEG.E.VGF	PVRPQVPLGP

00BW3886_8	AASQDLDKHG	ALTSSNTPAN	NADCAWLETQ	EEAD..EVGF	PVRPQVPLRP
00BW3891_6	AASQDLDKYG	ALTSSNTADT	NADCAWLQAQ	EEEG.E.VGF	PVRPQVPLRP
00BW3970_2	AASQDLDKHG	ALTSSNTAAT	NADCAWLEAQ	EEDG..DVGF	PVRPQVPLRP
00BW5031_1	AASQDLDKHG	ALTSSNTAAT	NKDCAWLEAQ	EEEG.E.VGF	PVRPQVPLRP
96BW01B21	AASQDLDKYG	ALTSSNTDPN	NAACAWLRAQ	EEEG.E.VGF	PVRPQVPLRP
96BW0407	TASRDLDKYG	ALTSSNTPTN	NAACAWLEPQ	EEEE.E.VGF	PVRPQVPLRP
96BW0502	AASQDLDKYG	ALTSSNTSTN	NADCAWLEAQ	EEEG..DVGF	PVRPQVPLRP
96BW06_J4	APSQDLDKHG	ALTSSNTPAN	NADVAWLEPQ	EEEG..AVGF	PLRPQVPLKP
96BW11_06	AASQDLDKHG	ALTSSNTAAN	NADCAWLEAQ	EEEE...VGF	PVRPQVPLRP
96BW1210	SASKDLEKHG	ALTSSNTAAN	NPHCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
96BW15B03	AASQDLDKYG	AFTSSNTASN	NADCAWLEAQ	EEAD..EVGF	PVRPQVPLRP
96BW16_26	AEYQDLDKDR	ALTSSNTDTN	NAACAQ...Q	EEEE.E.VGF	PVRPQVPLRP
96BW17A09	AASQDLDKHG	ALTSSNTPAN	NADCAWLQAQ	EEDE..EVGF	PVRPQVPLRP
96BWM01_5	AVSQDLQDHG	AITSSNTATN	.ADCACLEAQ	EEEA.E.LGF	PVRPQMPLKP
96BWM03_2	AASQDLDKYG	ALTSSNTASN	NADCAWLEAQ	EEAN..EVGF	PVRPQVPLRP
98BWMC12_2	AASQDLDKYG	AMTSSNTAHN	NGDCAWLQAQ	EEEE..EVGF	PVRPQVPLRP
98BWMC13_4	AASQDLDKHG	ALTSSNTATT	NADCAWLEAQ	AEAE..KVGF	PVRPQVPLRP
98BWMC14_a	AASQDLDKYG	ALTSSNTATN	NAACAWLEAQ	EEAG..EVGF	PVKPQVPLRP
98BWM014_1	AASQDLDKHG	ALTSSNTASN	NAACAWLQAQ	EEDN.GDVGF	PVRPQVPLRP
98BWM018_d	AASRDLERHG	AITSSNTAAN	NPACAWLEAQ	EEDG.D.VGF	PVRPQVPLRP
98BWM036_a	AASQDLDKHG	ALTSSNTASN	NADCAWLEAQ	EEEE.E.VGF	PVKPQVPLRP
98BWM037_d	AASQDLAKHG	AITSSNTATT	NADCAWLEAQ	EEGE..EVGF	PVRPQVPLRP
99BW3932_1	AASQDLANHG	ALTSSNTATN	NADCAWLQAQ	EEEE...VGF	PVRPQVPLRP
99BW4642_4	AASQDLDRHG	AITSSNTAAT	NADCAWLEAQ	EEAD..EVGF	PVRPQX...P
99BW4745_8	AASKDLDKHG	ALTSSNTAGT	NADCAWLQAQ	EEEG.E.VGF	PVRPQVPLRP
99BW4754_7	AASQDLDKYG	ALTSSNTAAT	NADCARLEAQ	EETE..EVGF	PVRPQVPLRP
99BWMC16_8	AASKDLEKHG	ALTSSNTVHN	NPDCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
A2_CD_97CD	AVSQDLARHG	AVTSSNTAAN	NPDCAWLEAQ	EEE...EVGF	PVRPQVPLRA
A2_CY_94CY	AVSQDLATHG	AVTSSNTAAT	NPDCAWVEAQ	EEES..EVGF	PVRPQVPLRP
A2D_97KR	AVSQDLATRG	AVTINNTAAT	NADSAWLEAQ	EEEE..EVGF	PVRPQVPLRP
A2G_CD_97C	AVSQDLARHG	AITSSNTAAN	NPDCAWLEAQ	QEDS..EVGF	PVRPQVPLRP
A_BY_97BL0	PVSQDXDKHG	AVTSSNTAAN	NADCAWLEAQ	X...EXEVGF	PVRPQVPLRP
A_KE_Q23	AVSQDLDKHG	AVTSKNINH.	.PSYAWLEAQ	E...DEDVGF	PVRPQVPLRP
A_SE_SE659	AVSQDLAKHG	AVTSSNINN.	.PSCVWLEAQ	E...EEEVGF	PVRPQVPLRP
A_SE_SE725	AVSQDLEKYG	AVTSSNVNH.	.PSCAWLEAQ	E...EEEVGF	PVRPHVPLRP
A_SE_SE753	AVSQDLDKYG	AITSSNINH.	.PSCVWLEAQ	E...DEGVGF	PVRPQVPLRP
A_SE_SE853	AVSQDLDRHG	AITSSNINH.	.PSCTWLEAQ	E...DEEVGF	PVKPQVPLRP
A_SE_SE889	AVSQDLDKHG	AVTSSNINH.	.PSCAWVEAQ	E...EEEVGF	PVRPQVPLRP
A_SE_UGSE8	AVSQDLEKHG	AITSSNINH.	.PSCTWLEAQ	AQE.DEEVGF	PVRPQVPLRP
A_UG_92UG0	AVSQDLDKHG	AVTSSNVNH.	.PSCVWLEAQ	E...EEEVGF	PVRPQVPLRP
A_UG_U455	AVSQDLDKYG	AVTSSNTSST	NASCWLEAQ	E...EGDVGF	PVRPQVPLRP
AC_IN_2130	AVSQDLDKHG	AVTSSNVNH.	.PSCVWLDQAQ	E...EEEVGF	PVRPQVPLRP
AC_RW_92RW	AASQDLDKYG	ALTSSNTPSN	NADCAWLAAQ	EEEN.E.VGF	PVRPQVPLRP
AC_SE_SE94	AVSQDLDKHG	AITSSNINH.	.PSNTWLAAQ	E.E.EEEVGF	PVRPQVPLRP
ACD_SE_SE8	AASQDLDKYG	ALTSSNTVTN	NPDCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
ACG_BE_VI1	AVSQDLARHG	AVTSRNTSAT	NADCAWLEAQ	EDE...EVGF	PVRPQVPLRP
AD_SE_SE69	AASRDLGKHG	AITSSNTAQT	NPDCAWLEAQ	EED...GEVGF	PVRPQVPLRP
AD_SE_SE71	AVSQDLDKHG	AITSSNINH.	.PSCVWLEAQ	E...DEDVGF	PVRPQVPLRP
ADHK_NO_97	AASRDLDRRG	AIXINNLPN	NSDSAWLEAQ	EE...EEVGF	PVRPQVPLRP
ADK_CD_MAL	AVSQDLDKCG	AAASSSPAAN	NASCEPPEEE	EE....VGF	PVRPQVPLRP
AG_BE_VI11	AVSRDLAKHG	AITSSNTVAT	NADCAWLEAQ	KEG...EEVGF	PVRPQVPLRP
AG_NG_92NG	AAPQDLARHG	AITSSNTAQT	NPDCAWLEAQ	QENS..EVGF	PVRQQVPLRP
AGHU_GA_VI	AVSQDLDKRG	AITTNNTVKT	NADCAWLEAQ	EDE...EVGF	PVRPQLPLRP
AGU_CD_Z32	AASQDLAKHG	AISSSNTATN	NPDCAWLEAQ	EESE..EVGF	PVRPQVPLRP
AJ_BW_BW21	AVSRDLDKHG	AITSSNTPTT	NADCAWLEAQ	TEAE.DEVGF	PVKPQVPLRP
B_AU_VH	AASRDLEKHG	AITSSN..IN	NADCVWLQAQ	EEE...EVGF	PVRPQVPLRP
B_CN_RL42	AVSRDLEKHG	AITSSNTAAT	NAACAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_DE_D31	AVSRDLEKHG	AITSSNTPAT	NAACAWLEAQ	EEE...EVGF	PVKPQVPLRP
B_DE_HAN	AASRDLEKHG	AITSSNTATN	NAACAWLEAQ	EEE...EEGF	PVRPQVPLRP
B_FR_HXB2	AASRDLEKHG	AITSSNTAAT	NAACAWLEAQ	EEE...EVGF	PVTPQVPLRP
B_GA_OYI	AASRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EDE...EVGF	PVRPQVPLRP

B_GB_CAM1	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_GB_GB8	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_GB_MANC	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_KR_WK	AASRDLEQRG	AITTSNTASN	NAACAWQEAQ	EEE...EVGF	PVRPQVPLRP
B_NL_3202A	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EDE...EVGF	PVKPQVPLRP
B_TW_TWCYS	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_US_BC	AVSRDLEKHG	AITSSNTAAN	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_US_DH123	AASRDLDKGH	AITSSNTAAT	NADCAWLEAQ	QEE...EEVGF	PVRPQIPLRP
B_US_JRCSF	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAY	EDE...EVGF	PVRPQVPLRP
B_US_MNCG	AASRDLEKHG	ALTSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVKPQVPLRP
B_US_P896	AVSRDLARHG	AITSSN..TN	NADIAWLEAQ	EEG...EVGF	PVRPQVPLRP
B_US_RF	AASRDLEKHG	TITSSNTAAN	NAACTWLEAQ	EDED.EEVGF	PVRPQVPLRP
B_US_SF2	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_US_WEAU1	AVSRDLAKHG	AITSSN..EN	NADCVWLKAQ	EDE...EVGF	PVRPQVPLRP
B_US_WR27	AVSRDLEKHG	AITNSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_US_YU2	AVSRDLERHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
BF1_BR_93B	AVSQDLERRG	AITSSNTGAN	NPDLAWLEAQ	EEEE...VGF	PVRPQVPLRP
C_BR_92BR0	PASQSDSKYG	ALTSSSTPAN	NADCAWLEAQ	QEEE.E.VGF	PVRPQVPLRP
C_BW_96BW0	TASQDLDKHG	ALTTSNTAAN	NAACAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
C_BW_96BW1	AASQDLDKHG	ALTSSNTAAN	NADCAWLEAQ	EEEE...VGF	PVRPQVPLRP
C_BW_96BW1	SASKDLEKHG	ALTTSNTAAN	NPHCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
C_BW_96BW1	AASQDLDKYG	AFTSSNTASN	NADCAWLEAQ	EEAD...EVGF	PVRPQVPLRP
C_ET_ETH22	AASRDLDKYG	ALTSSNTPAN	NPDCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
C_IN_93IN1	AASQDLDKHG	ALTSSNTDTT	NADCAWLRAQ	EEEG.E.VGF	PVTPQVPLRP
C_IN_93IN9	AASQDLDKYG	ALTSSNTDIT	NPDCAWLKAQ	EEEE.E.VGF	PVRPQVPLRP
C_IN_93IN9	AASQDLDKYG	ALTSSNTDTT	NADCAWLRAQ	EEEE.E.VGF	PVRPQVPLRP
C_IN_94IN1	AASQDLDKYG	ALTSSNTDTT	NADCAWLRTQ	EEEE.E.VGF	PVRPQVPLRP
C_IN_95IN2	AASQDLDRYG	ALTSSNTDTT	NTE.....	EEE.G.VGF	PVRPQVPLRP
CRF01_AE_C	AASQDLDKHG	AITSSNMNN.	.ADCAWLEAQ	EE...EEVGF	PVRPQVPLRP
CRF01_AE_C	AVSQDLDKHG	AVTSSNINN.	.ADNVWLEAQ	EE...EEVGF	PVRPQVPLRP
CRF01_AE_C	AVSQDLDKHG	AVTSSNMNS.	.AASVWLEAQ	ED...EEVGF	PVRPQVPTRP
CRF01_AE_T	TVSQDLDKHG	AVTSSNMNN.	.DDCVWLGAQ	EE...EEVGF	PVRPQVPLRP
CRF01_AE_T	AVSQDLDKHG	AVTSSNMNN.	.ADCEWLRAQ	EE...EEVGF	PVRPQVPLRP
CRF01_AE_T	AVSQDLDKHG	AVTSSNMNN.	.ADCVWLRAQ	EE...EGVGF	PVRPQVPLRP
CRF01_AE_T	AVSRDLDKHG	AVTSSNMNN.	.ADSVWLRAQ	EED...EEVGF	PVRPQVPLRP
CRF01_AE_T	AVSQDLDKHG	AITSSNIDN.	.ADCVWLRAQ	ED...EEVGF	PVMPQVPLRP
CRF01_AE_T	AVSQDLDKHG	AVTSTNMDN.	.ADSVWLRAQ	EED...EEVGF	PVEPQVPLRP
CRF02_AG_F	AASQDLDRHG	AITSSNTADT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
CRF02_AG_F	AASQDLDRHG	AITSSNTAET	NADCAWLEAQ	EDE...EVGF	PVKPQVPLRP
CRF02_AG_G	AASQDLDKYG	AITSSNTAFT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
CRF02_AG_N	AASQDLDRHG	AITSSNTAQT	NPDCAWLEAQ	EDE...NVGF	PVRPQVPLRP
CRF02_AG_S	AASQDLDRHG	AITSSNTAAT	NAACAWLEAQ	EEE...EVGF	PVRPQVPLRP
CRF02_AG_S	AVSQDLDRHG	AITSRNTAHT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
CRF03_AB_R	PVSQDLDKYG	AVTSSNTAAN	NADCAWLEAQ	E...EEEVGF	PVRPQVPLRP
CRF03_AB_R	PVSQDLDKYG	AVTSSNTAAN	NADCAWLEAQ	K...EEEVGF	PVRPQVPLRP
CRF04_cpx_	AVSQDLDKHG	AITINNTAAT	NPDKTWLEAQ	EEEE...EVGF	PVRPQVPLRP
CRF04_cpx_	AVSRDLDKHG	AITSSNTAAT	NPDKAWLEAQ	EEDE...EVGF	PVRPQVPLRP
CRF04_cpx_	AVSQDLDKYG	AITTSNTAAT	NPDKAWLEAQ	EEEE...EVGF	PVRPQVPLRP
CRF05_DF_B	AVFQDLDRNG	AVTIRNTVAT	NPDMAWVEAQ	EEEE...VGF	PVKPQVPLRP
CRF05_DF_B	SVSQDLERRG	AITSNNTAAT	NADLAWVEAQ	EEEE...VGF	PVRPQVPLRP
CRF06_cpx_	AVSQDLDKHG	AITSSNTATT	NAACAWVEAQ	TEE...EVGF	PVRPQVPVPR
CRF06_cpx_	AVSQDLDKHG	AITSNNTPTT	NAACAWLEEQ	TED...EVGF	PVRPQVPLRP
CRF06_cpx_	AVSQDLDRHG	AITSSNTVTT	NAACAWLEAQ	TED...EVGF	PVRPQVPLRP
CRF06_cpx_	AASQDLAKHG	AITSSNTAAT	NADCAWLEAQ	SEDN.EEVGF	PVRPQVPLRP
CRF11_cpx_	AVSKDLEKFG	AITSSNTAHT	NDTCAWLEAQ	ED...EEVGF	PVRPQVPLRP
CRF11_cpx_	AASKDLERHG	AITSSNTSQN	NAACAWLEAQ	ED...EGVGF	PVRPQVPLRP
D_CD_84ZR0	AVSRDLERHG	AITSSNTATT	NAACAWVEAQ	EED...EEVGF	PVRPQVPLRP
D_CD_ELI	AVSRDLEKHG	AITSSNTAST	NADCAWLEAQ	EES...DEVGF	PVRPQVPLRP
D_CD_NDK	AVSRDLEKHG	AITSSNTAST	NDTCAWLEAQ	EES...EEVGF	PVRPQVPLRP
D_UG_94UG1	AASRDLEKHG	AITSSNTAQT	NDACAWLEAQ	EE...EEVGF	PVRPQVPLRP
F1_BE_VI85	AVSRDLDRRG	AITSSNTRTT	NPDLAWLEAQ	EEEE...VGF	PVRPQVPVPR

F1_BR_93BR	AVSQDLERRG	AITSSNTRAN	NPDLAWEAQ	EEDE...VGF	PVRPQVPLRP
F1_FI_FIN9	AVSQDLERRG	AITSSNTGAT	NPDLAWEAQ	EDEE...VGF	PVRPQVPLRP
F1_FR_MP41	AVSQDLDRRG	AVTSSNTAAT	NPDLAWEAQ	EDEE...VGF	PVRPQVPLRP
F2_CM_MP25	AVSQDLDKRG	AITNSNTGAT	NADLAWEAQ	EDEE...VGF	PVRPQVPLRP
F2KU_BE_VI	AVSQDLAKHG	AITSSNTSST	NPDCAWEAQ	EEE...EVGF	PVGPQVPLRP
G_BE_DRCBL	AVSQDLDRHG	AITSRNTAGT	NPDCAWEAQ	EEDS...EVGF	PVRPQVPLRP
G_NG_92NG0	AVSQDLARHG	AITSSNTATN	NPDCAWEAQ	EEDS...DVGF	PVRPQVPLRP
G_SE_SE616	AVSQDLDRHG	AITSSNTAAN	NPDCAWEAQ	EEDS...EVGF	PVRPQVPLRP
H_BE_VI991	AVSQDLDRRG	AVTINNIAASN	NADSAWEAQ	EEE...EEVGF	PVRPQVPLRP
H_BE_VI997	AVSRDLDRRG	AVTINNTAAT	NPDVAWEAQ	EEA...EEVGF	PVRPQVPLRP
H_CF_90CF0	AVSRDLDRRG	AVTINNTAST	NRDAAWEAQ	EDG...EEVGF	PVRPQVPLRP
J_SE_SE702	AVSQDLAKHG	AITSSNTAAT	NDDCAWEAQ	T...E.EEVGF	PVRPQXPLRP
K_SE_SE788	AVSQDLAKHG	AITSSNTAAT	NADCAWEAQ	T...E.EEVGF	PVKPQIPLRP
K_CD_EQTB1	AVSQDLDKHG	AVTSSNTAFN	NPDCAWEAQ	ED...EDVGF	PVRPQVPLRP
K_CM_MP535	AVSQDLARHG	AVTSSNTSHN	NPDCAWEAQ	EE...EEVGF	PVRPQVPLRP
N_CM_YBF30	AASQDLANRG	AITIRNTRDN	NESIAWEAQ	EEEE...EVGF	PVRPQVPLRP
O_CM_ANT70	QISRELAARG	GIPSSHTPQN	NAALAFLESH	QEEE...VGF	PVAPQVPLRP
O_CM_MVP51	AVSRELATRG	GISSSHTPQN	NAALAFLDH	KDED...VGF	PVRPQVPLRP
O_SN_MP129	QISRELAARG	GIPSSYTPQN	NAALAFLESH	QDEE...VGF	PVRPQVPLRP
O_SN_MP130	QVSRELAARG	GISNSHTPQN	NAALAFLESH	QDED...VGF	PVRPQVPLRP
U_CD___83C	AASRDLEKYG	AITSSNTAET	NEACAQLEAA	QE.D.GEVGF	PVRPQVPLRP

101			150		
00BW0762_1	MTYKGALDLG	FFLK.EKGGL	EGLIYSTKRK	EILDLWVYHT	QGYFPDWQNY
00BW0768_2	MTYKGAVDLS	WFLK.EKGGL	EGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY
00BW0874_2	MTFKGAFDLG	FFLK.EKGGL	EGLIWSQKRQ	DILDLWVYHT	QGYFPDWQNY
00BW1471_2	MTYKGAFDLG	FFLK.EKGGL	DGMIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
00BW1616_2	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKKRK	EILDLWVYHT	QGFFPDWQCY
00BW1686_8	MTYKGAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
00BW1759_3	MTYKAAFDLG	FFLK.EKGGL	EGLIHSKQRQ	DILDLWVYHT	QGYFPDWQNY
00BW1773_2	MTYKAAFDLS	FLLK.EXGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
00BW1783_5	MTYKAAFDLS	FFLK.EKGGL	EGLIHSKQRQ	DILDLWVYNT	QGYFPDWQNY
00BW1795_6	MTYKAAFDLS	FFLK.EKGGL	DGLIYSRKRQ	EILDLWVYHT	QGFFPDWQNY
00BW1811_3	MTYKAAFDLS	FFLK.EKGGL	DGLIHSKKRQ	DILDLWVYHT	QGYFPDWQNY
00BW1859_5	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
00BW1880_2	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFSDWQNY
00BW1921_1	MTYKAAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
00BW2036_1	MTYKAAIDLS	FFLK.EKGGL	DGLIYSAKRQ	EILDLWVYHT	QGFFPDWQNY
00BW2063_6	MTMKGAVDLS	FFLK.EKGGL	EGLIYSKRRQ	EILDLWVYHT	QGFFPDWQNY
00BW2087_2	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKQRQ	DILDLWVYNT	QGFFPDWQNY
00BW2127_2	MTYKAAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
00BW2128_3	GTFKAAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
00BW2276_7	MTYKAAFDLS	FFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGYFPDWQNY
00BW3819_3	MTYKGAFDLS	FFLK.EKGGL	EGLIYSKKRQ	DILDLWVYNT	QGYFPDWQSY
00BW3842_8	MTYKGAVDLS	FFLK.EKGGL	DGLIYSQKRQ	DILDLVHHT	QGYFPDWQNY
00BW3871_3	MTYKGAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
00BW3876_9	MTYKGAVDLS	FFLK.EKGGL	ERLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
00BW3886_8	MTYKGAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
00BW3891_6	MTYKGAVDLS	FFLKXEKGGL	EGLIYSKKRQ	EILDLWVYHI	QGYFPDWQNY
00BW3970_2	MTYKGAFNLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
00BW5031_1	MTYKGAFDLG	WFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
96BW01B21	MTYKGAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYNT	QGVFPDWQNY
96BW0407	MTYKAAVDLS	FFLK.EKGGL	GGIYSNKRQ	DILDLWVYNT	QGYFPDWQNY
96BW0502	MTYKGAFDLG	FFLK.EKGGL	EGLVYSKKRQ	EILDLWVYHT	QGFFPDWQNY
96BW06_J4	MTYKGAVDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
96BW11_06	MTYKAAFDLS	FFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGFFPDWHNY
96BW1210	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWQCY
96BW15B03	MTYKGAVDLS	FFLK.EKGGL	DGLIYSPKRQ	EILDLWVYHT	QGFFPDWHNY
96BW16_26	MTYKEAFDLS	FFLK.EKGGL	DGLIYSKKRQ	DILDLWVYNT	QGFLPDWQNY
96BW17A09	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
96BWM01_5	VTYKAAFDLS	FFLK.KKGGL	EGLIYSKKRQ	NILDLWVYHT	QGFFPDWHNY

96BWM03_2	MTQKGAFDLG	FFLK.EKGGL	DGLIYSRKRQ	EILDLWVYHT	QGYFPDWQNY
98BWM012_2	MTFKGALDLG	FFLK.EKGGL	DGLIHSKRRQ	DILDLWVYHT	QGYFPDWQNY
98BWM013_4	MTYKGAVDLS	FFLK.EKGGL	DGLIYSKQRQ	DILDLWVYNT	QGYFPDWQNY
98BWM014_a	MTYKAAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
98BWM014_1	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
98BWM018_d	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
98BWM036_a	ITYKAAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY
98BWM037_d	MTYKGAFDLG	FFLK.EKGGL	DGLIHSKKRQ	DILDLWVYHT	QGYFPDWQNY
99BW3932_1	MTYKAAFDLS	FFLK.EKGGL	EGLIYSKQRQ	DILDLWVYNT	QGYFPDWHNY
99BW4642_4	MTYKAAFDLS	FFLK.EKGGL	DGLIYSRKRQ	DILDLWVYHT	QGYFPDWQNY
99BW4745_8	MTYKSAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
99BW4754_7	MTYKAAFDLS	FFLK.EKGGL	DGLIHSKKRQ	EILDLWVHHT	QGYFPDWQNY
99BWM016_8	MTYKAAVDLS	WFLK.EXGGL	DGLIHSQKRQ	EILDLWVYHT	QGYFPDWQNY
A2_CD_97CD	MTYKGAVDLS	HFLK.EKGGL	DGLIYSQRRQ	DILDLWVYNT	QGYFPDWQNY
A2_CY_94CY	MTFKGAFDLG	FFLK.EKGGL	DGLIYSQKRQ	DILDMWVYHT	QGYFPDWQNY
A2D_97KR	MTYKGAFDLS	HFLR.EKGGL	DGLIHSQKRQ	DILDLWVYHT	QGYFPDWQGY
A2G_CD_97C	MTYKSAFDLS	FFLK.EKGGL	DGLIYSKQRQ	DILDLWVYNT	QGYFPDWQNY
A_BY_97BL0	MTXXXXXDXS	HFXK.EKGGL	DGXIYSKKRQ	XILDLXVYHT	QGYFPDWQNY
A_KE_Q23	MTYKGAVDLS	HFLK.KKGGL	DGLVYSRKRQ	EILDLWVYHT	QGYFPDWQNY
A_SE_SE659	MTYKAAVDLS	HFLK.EKGGL	DGLIYSRKRQ	EILDLWVHHT	QGYFPDWQNY
A_SE_SE725	MTYKGALDLS	HFLK.EKGGL	DGLIYSRRRQ	EILDLWVYNT	QGYFPDWQNY
A_SE_SE753	MTYKGALDLS	HFLK.EKGGL	DGLVYSKKRQ	EILDLWVHHT	QGYFPDWQNY
A_SE_SE853	MTYKGAFDLS	HFLK.EKGGL	DGLIYSRKRQ	EILDLWVYNT	QGYFPDWQNY
A_SE_SE889	MTYKGAVDLS	HFLK.EKGGL	DGLIYSRRRQ	EILDLWVYNT	QGYFPDWQNY
A_SE_UGSE8	MTYKGALDLS	HFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGYFPDWHNY
A_UG_92UG0	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
A_UG_U455	MTYKAAFDLS	FFLK.EKGGL	DGLIHSQKRQ	EILDLWVYHT	QGYFPDWQNY
AC_IN_2130	MTYKGALDLS	FFLK.EKGGL	DGLIYSRKRQ	EILDLWVYHT	QGYFPDWHNY
AC_RW_92RW	MTYKAAVDLS	FFLK.EKGGL	EGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
AC_SE_SE94	MTYKGALDLS	HFLK.EKGGL	DGLIYSQQRQ	DILDLWVYNT	QGYFPDWQNY
ACD_SE_SE8	MTYKAAVDLS	FFLK.EKGGL	EGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
ACG_BE_VI1	MTFKGALDLS	HFLK.EKGGL	DGLIYSRKRQ	EILDLWVYHT	QGYFPDWQNY
AD_SE_SE69	MTYKGAVDLS	HFLK.EKGGL	EGLVWSPKRQ	EILDLWVYHT	QGYFPDWQNY
AD_SE_SE71	MTYKAAVDLS	HFLK.EKGGL	DGLIYSRKRQ	DILDLWVYHT	QGYFPDWQCY
ADHK_NO_97	MTYKAAVDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVHNT	QGYFPDWQNY
ADK_CD_MAL	MTYKGAFDLS	HFLK.EKGGL	DGLVWSPKRQ	EILDLWVYHT	QGYFPDWQNY
AG_BE_VI11	MTYKAAVDLS	HFLK.EKGGL	EGLIYSQQRQ	DILDLWVYNT	QGYFPDWQNY
AG_NG_92NG	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
AGHU_GA_VI	MTFKGAFDLG	FFLK.EKGGL	DGLIHSQKRQ	DILDLWVYHT	QGYFPDWQNY
AGU_CD_Z32	MTFKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWHNY
AJ_BW_BW21	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY
B_AU_VH	MTFKAAHDLS	FFLK.EKGGL	DGLIYSQRRQ	DILDLWIYHT	QGYFPDWQNY
B_CN_RL42	MTYKGALDLS	HFLR.EKGGL	EGLIYSQRRQ	DILDLWVYHT	QGYFPDWQNY
B_DE_D31	MTYKAAVDLS	HFLK.EKGGL	EGLVHSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_DE_HAN	MTYKGALDLS	HFLK.EKGGL	EGLIYSPKRQ	EILDLWVYHT	QGYFPDWQNY
B_FR_HXB2	MTYKAAVDLS	HFLK.EKGGL	EGLIHSQRRQ	DILDLWIYHT	QGYFPD.QNY
B_GA_OYI	MTYKGALDLS	HFLK.EKGGL	EGLIYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_GB_CAM1	MTYKAAVDLS	HFLK.EKGGL	EGLIYSQRRQ	DILDLWIYHT	QGYFPDWQNY
B_GB_GB8	MTYKAAVDLS	HFLK.EKGGL	DGLIYSPKRQ	EILDLWVYHT	QGYFPDWQNY
B_GB_MANC	MTFKGALDLS	HFLR.EKGGL	EGLVYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_KR_WK	MTYKSALDLS	HFLK.EKGGL	EGLVYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_NL_3202A	MTYKGALDLS	HFLK.EKGGL	EGLIYSQRRQ	DILDLWIYHT	QGYFPDWQNY
B_TW_TWCYS	MDYKGALDLS	HFLR.EKGGL	EGLVYSQKKE	DILDLWIYHT	QGYFPDWQNY
B_US_BC	ITYKAAVDLS	HFLK.EKGGL	EGLIFSQRRQ	DILDLWYHT	QGYFPDWQNY
B_US_DH123	MTYKAAVDLS	HFLK.EKGGL	EGLIYSQKRQ	DILDLWVYNT	QGYFPDWQNY
B_US_JRCSF	MTYKAAIDLS	HFLK.EKGGL	EGLIYSQKRQ	DILDLWIYHT	QGYFPDWQNY
B_US_MNCG	MTYKAAIDLS	HFLK.EKGGL	DGLIYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_US_P896	MTYKAAVDLS	HFLK.EKGGL	EGLVHSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_US_RF	MTFKAAVDLS	HFLK.EKGGL	DGLVFSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_US_SF2	MTYKAAIDLS	HFLK.EKGGL	EGLIWSQRRQ	EILDLWIYHT	QGYFPDWQNY
B_US_WEAU1	MTYKAAHDLS	HFK.EKGGL	EGLIYSQKRQ	DILDLWVYHT	QGYFPDWQNY

B_US_WR27	MTYKAAVDLS	HFLK.EKGGL	EGLIYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_US_YU2	MTHKAAMDLS	HFLK.EKGGL	EGLIHSQQRQ	DILDLWVYHT	QGYFPDWQNY
BF1_BR_93B	MTYKGALDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
C_BR_92BR0	MTYKAVVDLS	FFLE.EKGGL	EGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
C_BW_96BW0	MTYKAAVDLS	FFLK.EKGGL	EGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
C_BW_96BW1	MTYKAAFGLS	FFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGFFPDWHNY
C_BW_96BW1	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWQCY
C_BW_96BW1	MTYKGAVDLS	FFLK.EKGGL	DGLIYSPKRQ	EILDLWVYHT	QGFFPDWHNY
C_ET_ETH22	MTYKAAFDSL	LFLK.EKGGL	EGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
C_IN_93IN1	MTYKSAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
C_IN_93IN9	MTFKEAVDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
C_IN_93IN9	MTFKGAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
C_IN_94IN1	MTFKGAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
C_IN_95IN2	MTFKGALDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF01_AE_C	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF01_AE_C	MTYKGAFDLS	FFLK.EKGGL	DGLIHSKRRQ	EILDLWVHNT	QGYFPDWQNY
CRF01_AE_C	MTYKGAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF01_AE_T	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWHNY
CRF01_AE_T	MTFKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF01_AE_T	MTYKGAFDLS	FFLK.EKGGL	EGLVYSKKRQ	EILDLWVYHT	QGFFPDWHNY
CRF01_AE_T	MTFKEAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF01_AE_T	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF01_AE_T	MTYKGAFDLS	FFLE.EKGGL	DGLVYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF02_AG_F	MTYKAAFDLG	FFLK.EKGGL	DGLVYSKKRQ	EILDLWVYHT	QGFFPDWQNY
CRF02_AG_F	MTYKGAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
CRF02_AG_G	MTYKGALDLS	HFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGFFPDWHNY
CRF02_AG_N	MTYKGAVDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF02_AG_S	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
CRF02_AG_S	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
CRF03_AB_R	MTYKGAFDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQ..
CRF03_AB_R	MTYKGAFDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF04_cpx_	MTFKGALDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWDNY
CRF04_cpx_	MTFKAALDLS	HFLK.EKGGL	DGLIYSQKRQ	DILDLWVYNT	QGYFPDWQNY
CRF04_cpx_	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY
CRF05_DF_B	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	DILDLWVYNT	QGYSPDWQNY
CRF05_DF_B	MTFKGALDLS	HFLK.EKGGL	DGLIWSRKRQ	KILDLWVYNT	QGYFPDWQNY
CRF06_cpx_	MTYKAAFDSL	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF06_cpx_	MTFKGAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF06_cpx_	MTFKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	DILDLWVYHT	QGFFPDWQNY
CRF06_cpx_	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
CRF11_cpx_	MTYKAAFDLG	FFLK.EKGGL	DGLIYSQKRQ	EILDLWVYHT	QGFFPDWQNY
CRF11_cpx_	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVHNT	QGFFPDWQNY
D_CD_84ZR0	MTYKAAVDLS	HFLR.KKGGL	EGLVYSQKRQ	DILDLWVYHT	QGFFPDWQNY
D_CD_ELI	MTYKEALDLS	HFLK.EKGGL	EGLIWSKKRQ	EILDLWVYNT	QGIFFPDWQNY
D_CD_NDK	MTYKEAVDLS	HFLK.EKGGL	EGLIWSKKRQ	EILDLWVYNT	QGIFFPDWQNY
D_UG_94UG1	MTYKEAVDLS	HFLK.EKGGL	EGLVWSPKRQ	EILDLWVYHT	QGFFPDWQNY
F1_BE_VI85	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRG	DTLWVYHT	QGYFPDWQNY
F1_BR_93BR	MTYKGAVDLS	HFLK.EKGGL	EGLIYSKRRQ	EILDLWVYHT	QGYFPDWQNY
F1_FI_FIN9	MTYKGAFDLS	QFXX.EKGGL	EGLXYSKKRQ	EILDLWLYHT	QGYFPDWQNY
F1_FR_MP41	MTFKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
F2_CM_MP25	MTYKAAVDLS	HFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGYFPDWQNY
F2_KU_BE_VI	MTYKGAFDLS	HFIK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWHNY
G_BE_DRCBL	MTYKAAFDSL	FFLK.EKGGL	DGLVYSKKRQ	EILDLWVYHT	QGFFPDWQNY
G_NG_92NG0	MTYKAAFDSL	FFLK.EKGGL	DGLIYSKRRQ	DILDLWVYNT	QGFFPDWQNY
G_SE_SE616	MTFKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY
H_BE_VI991	MTYKGAFDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYNT	QGYFPDWHNY
H_BE_VI997	MTYKAAVDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY
H_CF_90CF0	MTYKGAFDLS	HFLK.EKGGL	DGLIYSQKRQ	DILDLWVYNT	QGYFPDWQNY
J_SE_SE702	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVHNT	QGYFPDWQNY
J_SE_SE788	MTYKGAVDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVHNT	QGYFPDWQNY
K_CD_EQTB1	MTFKGAFDLG	FFLK.EKGGL	DGLIYSKRRQ	EILDLWVYHT	QGFFPDWQNY

K_CM_MP535	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
N_CM_YBF30	ITYKQAFDLS	FFLK.DKGGL	EGLVWSRKRQ	DILDLWVYHT	QGILPDWHNY
O_CM_ANT70	MTYKGAFDLS	FFLK.EKGGL	EGLIYSHKRA	EILDLWVYNT	QGFFPDWQNY
O_CM_MVP51	MTFKAAFDLS	FFLK.EKGGL	DGLIYSHKRA	EILDLWIYHT	QGFFPDWQCY
O_SN_MP129	MTYKGAFDLS	FFLK.EKGGL	DGLIYSHKRA	EILDLWVYHT	QGFFPDWQGY
O_SN_MP130	MTYKGAFDLS	FFLK.EKGGL	DGLIYSPERA	EILDLWVYHT	QGFFPDWQNY
U_CD___83C	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY

	151		200
00BW0762_1	TPGPGTRYSL	TFGWPFKLVP	VD.PKEVEEA NEGENNCLLH PMSQHRIDDD
00BW0768_2	TPGPGVRYPL	TLGWCFKLVP	VD.PREAEEE TKGENSCLLH PMSQHGMEDS
00BW0874_2	TPGPGVRYPL	TFGWPFKLVP	VD.PTEVEEA NEGENNCLLH PMSQHGMDDK
00BW1471_2	TPGPGVRYPL	TFGWCFKLVP	VD.PKEVDAN .EGENNCLLH PMSQHGMDDK
00BW1616_2	TPGPGTRLPL	TFGWCFKLVP	VD.PREVEEA NEGENNCLLH PMSQQGMEDE
00BW1686_8	TPGPGVRYPL	TFGWPFKLVP	VD.PREVQEA NKGENNCLLH PMSQHGMEDD
00BW1759_3	TPGPGIRYPL	TFGWCFKLVP	VD.PKEVEEA NEGEDNCLLH PMSLHGMEDD
00BW1773_2	TPGPGVRFPL	TFGWCFKLVP	VD.PREVEEA NEGEDNCLLH PMSQHGMEDD
00BW1783_5	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA NEGENNCLLH PMSQHGMEDA
00BW1795_6	TPGPGTRYPL	TFGWCFKLVP	VD.PREVEEA NEGENNCLLH PMSQHGIEDG
00BW1811_3	TPGPGVRYPL	TFGWCFKLVP	VD.PGEVEEA NKGENNCLLH PMSLHGAEDI
00BW1859_5	TPGPGVRYPL	TFGWCFKLVP	VD.PGEVEEA NEGEDNCLLH PISQHGMDT
00BW1880_2	TPGPGIRYPL	TFGWCFKLVP	VD.PGEVEEA NKGENNCLLH PMSQYGMDDK
00BW1921_1	TPGPGVRYPL	TFGWPFKLVP	VD.PKEVEEA NKGENNCLLH PLSQQGMEDE
00BW2036_1	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA NQGENNCLLH PMSQFGMDDK
00BW2063_6	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA NEGENNCLLH PISLHGMEDN
00BW2087_2	TPGPGVRYPL	TSGWCFKLVP	VD.PREVEEA NEGESNSLLH PISLHGMEDD
00BW2127_2	TPGPGVKYPL	TFGWCFKLEP	VD.PKEVEEA NEGDNNCLLH PMSQHGMDDK
00BW2128_3	TPGPGVRYPL	TFGWRYKLVP	VD.PQEVQQS NEGDNNCLLH PMSQHGIEDA
00BW2276_7	TPGPGIRYPL	TFGWCFKLVP	VD.PREVEEA NEGENNCLLH PRSLHGIEDA
00BW3819_3	TPGPGIRYPL	TFGWCFKLVP	VD.PREVEEN TEGENTCLLH PMSQHGMEDD
00BW3842_8	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA NQGENNCLLH PMSQHGVDDP
00BW3871_3	TPGPGVRYPL	TFGWPFKLVP	VD.PREVEED NNGENNCLLH PMSQHGMDDK
00BW3876_9	TPGPGTRFPL	TFGWCFKLVP	VD.PREVEEA NEGENSCLLH PISQHGMEDD
00BW3886_8	TPGPGVRYPL	TFGWPFKLVP	VD.PREVEEA NQGENNCLLH PMSQYGMEDD
00BW3891_6	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA NEGENNCLLH PISQHGMEDD
00BW3970_2	TPGPGVRYPL	TFGWCFKLVP	VD.PREIEEA NKGEDNCLLH PMSQHGMEDD
00BW5031_1	TPGPGVRYPL	TFGWCFKLVP	VD.PKEVEEA TEGENNCLLH PICQHGMEDD
96BW01B21	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA SEGEDNCLLH PMSQHGMEDD
96BW0407	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA NEGENNCLLH PMSLHGMEDD
96BW0502	TPGPGVKYPL	TFGWCFKLVP	VD.PGEVEEA NKGEDNCLLH PMSQHGMEDD
96BW06_J4	TPGPGITYPL	TFGWPFKLVP	VD.PREVEEA NNGENNCLLH PMSQHGMDDK
96BW11_06	TPGPGVRYPL	TFGWCFKLVP	VD.PGEVEEA NEGENNCLLH PMAQHGMEDD
96BW1210	TPGPGVRYPL	TFGWCFKLVP	VD.PGEVEEA NKGEDNCLLH PMSQHGIEDA
96BW15B03	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEN NQGENHCLLH PMSQHGMDDP
96BW16_26	TPGPGVRFPL	TFGWCFKLVP	VD.PREVEEE TEGDNNCLLH PMNQHGMDDP
96BW17A09	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEED NEGENNCLLH PMSQHGMEDA
96BWM01_5	TPGPGIRYPL	TFGWCFKLVP	VD.PREVEEA NKGENTSLLH PVSLHGMEDD
96BWM03_2	TSPPGVRYPL	TFGWCFKLVP	VD.PKEVEEA SEGENNCLLH PMNQHGMEDE
98BWMC12_2	TPGPGVRYPL	TFGWPFKLVP	VD.PKEVEEA NKGENNCLLH PMSLHGIEDA
98BWMC13_4	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA NEGENNCLLH PMSLHGIEDA
98BWMC14_a	TPGPGTRYPL	TFGWPFKLVP	VD.PREVEEA NNGENNCLLH PMSQHGMDDK
98BWM014_1	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA NEGEDNCLLH PMSQHGIEDP
98BWM018_d	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA NEGEDNCLLH PMSQHGMEDA
98BWM036_a	TPGPGTRYPI	TFGWCFKLVP	VD.PREVEEA NEGENNSLLH PVSLHGMEDD
98BWM037_d	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA TEGEDNCLLH PLSQHGIEDA
99BW3932_1	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEN NQRENSCLLH PMSQHGMEDP
99BW4642_4	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA NEGENNCLLH PMSQHGMEDA
99BW4745_8	TPGPGVRYPL	TFGWCLKLVP	VD.PREVEED NEGENNCLLH PMSQHGMEDA
99BW4754_7	TPGPGIRYPL	TFGWCFKLVP	VD.PREVQEA NEGDDNCLLH PMSQFGMDDK
99BWMC16_8	TPGPGIRYPL	TFGWCFRLVP	VD.PSEVEEA NQGENNCLLH PISQHGMEDD
A2_CD_97CD	TPGPGARFPL	TFGWCFKLVP	VD.PSEVEEA TEGENNSLLH PICQHGAEDE

A2_CY_94CY	TPGPGIRYPL	TFGWCFKLVP	VE.	PSEVEEA	TQGENNSLLH	PICQHGVDDE
A2D_97KR	TPGPGIRYPL	TFGWCFKLVP	VS.	PAEVEEA	TEGETNSLLH	PICQHGIEDP
A2G_CD_97C	TPGPGVRYPL	TFGWCFKLVP	MD.	PAEVEEA	NKEENSSLLH	PICQHGMEDE
A_BY_97BL0	TPGPXIRFPL	TFXXCYKLVP	VD.	PAEVEEA	TXGENNSLLH	PICQHGMDDE
A_KE_Q23	TPGPGTRFPL	TFGWCFKLVP	VD.	PDEVEKA	TEGENNSLLH	PICQHGMDDE
A_SE_SE659	TPGPGIRFPL	TFGWCFKLVP	VD.	PDEVEKD	TEGENNSLLH	PICQHGMDDE
A_SE_SE725	TPGPGVRYPL	TFGWCFKLVP	VD.	PDEVEQA	NEGENNSLLH	PMCQHGMDDE
A_SE_SE753	TPGPGIRYPL	TFGWCFKLVP	VD.	PDEVKKD	TEGENNSLLH	PMCQHGMDDE
A_SE_SE853	TPGPGVRYPL	TFGWCFKLVP	VE.	PEEVEKA	NEGENNSLLH	PICQHGMDDE
A_SE_SE889	TPGPGTRFPL	TFGWCFKLVP	VD.	PDEVEKA	TEGENNSLLH	PICQHGMDDE
A_SE_UGSE8	TPGPGIRYPL	TFGWCFKLVP	VD.	PDEVEKA	TEGENNSLLH	PMCQHGMDDE
A_UG_92UG0	TPGPGIRYPL	TFGWCFKLVP	VD.	EDEVEEA	TGGENNSLLH	PICQHGMDDE
A_UG_U455	TPGPGIRYPL	TFGWCFKLVP	VD.	PAEVEEA	TGGENNSLLH	PICQHGMDDE
AC_IN_2130	TPGPGVRYPL	TFGWCFKLVP	VD.	PREVEEA	TGGEDNCLLH	PVCQHGMEDE
AC_RW_92RW	TPGPGVRYPL	TFGWCFKLVP	VD.	PREVEEA	NEGEDNCLLH	PLSQHGMEDE
AC_SE_SE94	TPGPGIRYPL	TFGWCFKLVP	VN.	PDEVEEA	TKGENNSLLH	PMCQHGMDDE
ACD_SE_SE8	TPGPGTRYPL	TFGWCFKLVP	VD.	PREVEEA	NEGENNCLLH	PMSQHGIEDP
ACG_BE_VI1	TPGPGTRFPL	TFGWCFKLVP	MD.	PTVEVEEA	NEGENNCLLH	PISQHGMEDE
AD_SE_SE69	TPGPGIRYPL	IFGWCFELVP	VD.	PKEVEED	IG. ENSSLLH	PMHQHGMEDE
AD_SE_SE71	TPGPGTRFPL	TFGWCFKLVP	VD.	PDEVEKA	TEGETNTLLH	PICQHGMDDE
ADHK_NO_97	TPGPGERFPL	TFGWCFKLVP	VD.	PQEVEKA	NDGENNCLLH	PMCQHGMEDE
ADK_CD_MAL	TPGPGIRFPL	TFGWCFKLVP	MS.	PEEVEEA	NEGENNCLLH	PISQHGMEDE
AG_BE_VI11	IPGPGTRFPL	TFGWCFKLVP	MD.	PAGIEKA	NEGENNSLLH	PICQHGMDDE
AG_NG_92NG	TPGPGTRFPL	TFRWCFKLVP	MD.	PAEIEEA	NKGENNSLLH	PICQHGLED
AGHU_GA_VI	TPGPGIRYPL	CFGWCFKLVP	VD.	PKEVEEA	TEGENNCLLH	PICQHGMDDE
AGU_CD_Z32	TPGPGTRYPL	CFGWCFKLVP	VD.	PREVEEA	NTGENNCLLH	PMSQHGMDDE
AJ_BW_BW21	TPGPGTRFPL	TFGWCFKLVP	VD.	PKEVEEA	NEGENNCLLH	PLCQHGMEDE
B_AU_VH	TPGPGTRYPL	TFGWCFKLVP	VE.	PDQVEKA	NEGENISLLH	PMSLHGMEDE
B_CN_RL42	TPGPGTRFPL	TFGWCFKLVP	VD.	PEQVEEA	NEGENNCLLH	PMSQHGADDP
B_DE_D31	TPGPGTRFPL	TFGWCFKLVP	VK.	PEQVEEA	NEGENNSLLH	PMSLHGMDDE
B_DE_HAN	TPGPGVRYPL	TFGWCFKLVP	VE.	PDEEENSSLLH	PASLHGTEDE
B_FR_HXB2	TPGPGVRYPL	TFGWCFKLVP	VE.	PKIEEA	NKGENNSLLH	PVSLHGMDDE
B_GA_OYI	TPGPGIRYPL	CFGWCFKLVP	MD.	PDQVEEA	NEGENNSLLH	PISLHGMDDE
B_GB_CAM1	TPGPGIRYPL	TFGWCFKLVP	VE.	PEQVEEA	NKRENASLLH	PMSQHGMDDE
B_GB_GB8	TPGPGTRFPL	TFGWCFKLVP	VE.	PEEVEKA	NEGENNCLLH	PMSQHGIEDP
B_GB_MANC	TRGPGIRYPL	AFGWCFKLVP	VD.	PEQVEEA	NEGENNSLLH	PMSLHGMDDE
B_KR_WK	TPGPGTRFPL	TFGWCFKLVP	VE.	PEKVEEA	TVGKNNCLLH	PMNLHGMDDE
B_NL_3202A	TPGPGIRYPL	TFGWCFKLVP	VE.	QEKIEEA	NEGENNSLLH	PMSQHGMDDE
B_TW_TWCYS	TPGPGVRYPL	TFGWCFKLVP	VE.	PEQVEKA	NEGENXCLLH	PMSQHGMDDE
B_US_BC	TPGPGIRYPL	TFGWCFKLVP	VD.	PEKIEEA	NEGENNSLLH	PMSQHGMDDE
B_US_DH123	TPGPGIRYPL	TFGWCFKLVP	VD.	PEKVEEA	NEGENNCLLH	PISLHGMEDE
B_US_JRCSF	TAGPGVRFPL	TFGWCFKLVP	VD.	PEKVEEA	NEGENNCLLH	PMSQHGMDDE
B_US_MNCG	TPGPGIRYPL	TFGWCFKLVP	VE.	PEKIEEA	NKGENNCLLH	PMSQHGMDDE
B_US_P896	TPGPGIRYPL	TFGWCFKLVP	VE.	PDEGENN	RE. .DNSLLH	PANQHGVEDS
B_US_RF	TPGPGTRYPL	TFGWCFKLVP	VE.	PDKVEEA	TEGENNSLLH	PICLHGMDDE
B_US_SF2	TPGPGIRYPL	TFGWCFKLVP	VE.	PEKVEEA	NEGENNSLLH	PMSLHGMEDE
B_US_WEAU1	TPGPGTRYPL	CFGWCFKLVP	VE.	PEKVEEA	NEGENNSLLH	PMSLHGMDDE
B_US_WR27	TPGPGTRYPL	TFGWCFKLVP	LE.	PDQVEEA	NKGENNCLLH	PMSQHGMDDE
B_US_YU2	TPG. GTRWPL	TFGWCFKLVP	VE.	PEKIEEA	NAGENNCLLH	PMSQHGMDDE
BF1_BR_93B	TPGPGTRYPL	TLGWCFKLVP	VD.	PEEVEKA	NEGENNCLLH	PMSQHGMEDE
C_BR_92BR0	TPGPGVRFPL	TFGWCFKLVP	VD.	PREVEEA	NTGENNSLLH	PMSLHGMEDE
C_BW_96BW0	TPGPGVRYPL	TFGWCFKLVP	VD.	PKEVEEA	NEGENNCLLH	PMSLHGMEDE
C_BW_96BW1	TPGPGVRYPL	TFGWCFKLVP	VD.	PGEVEEA	NEGEN. CLLH	PIAQHGMEDE
C_BW_96BW1	TPGPGVRYPL	TFGWCFKLVP	VD.	PGEVEEA	NGGEDNCLLH	PMSQHGIEDA
C_BW_96BW1	TPGPGVRYPL	TFGWCFKLVP	VD.	PREVEEN	NQGENHCLLH	PMSQHGMDNP
C_ET_ETH22	TPGPGVRYPL	TFGWCFKLVP	VD.	PSEVEEI	NEGENNCLLH	PASLHGMEDE
C_IN_93IN1	TPGPGVRYPL	TFGWCFKLVP	VD.	PREVEEA	NEGEDNCLLH	PVCQHGMEDE
C_IN_93IN9	TPGPGVRYPL	TFGWCFKLVP	VD.	PREVEEA	NEGEDNCLLH	PVCQHGMEDE
C_IN_93IN9	TPGPGVRFPL	TFGWCFKLVP	VD.	PREVEEA	NEGENNCLLH	PVCQHGMEDE
C_IN_94IN1	TPGPGTRFPL	TFGWCFKLVP	VD.	PREVEEA	NEGEDNCLLH	PVCQHGMEDE
C_IN_95IN2	TPGPGVRFPL	TFGWCFKLVP	VD.	PREVEEA	NKGEDNCLLH	PVCQHGMEDE

CRF01_AE_C	TPGPGIRYPL	CFGWCYKLVP	VD.PKEVEED	NKDESNCLLH	PMSQHGVDDE
CRF01_AE_C	TPGPGVRYPL	CFGWCYKLVP	VD.PREVEED	NKGENNCLLH	PMSQHGIDDD
CRF01_AE_C	TPGPGTRYPL	CFGWCYKLVP	VD.PREVEED	NKGENNCLLH	PMSQHGIEDE
CRF01_AE_T	TPGPGIRYPL	CFGWCYKLVP	VD.PREVEED	NKGENNCLLH	PLSQHGIEDE
CRF01_AE_T	TPGPGIRYPL	CFGWCYKLVP	VD.PREVEED	NKEENNCLLH	PMSQHGIDDE
CRF01_AE_T	TPGPGIRYPL	CFGWCYKLVP	VD.PREVEED	NKGENNCLLH	PMSQHGIEDE
CRF01_AE_T	TPGPGIRFPL	CFGWCYKLVP	VD.PREVEED	NKGENNCLLH	PMSQHGMDG
CRF01_AE_T	TPGPGIRFPL	CFGWCYKLVP	VD.QREVEED	NKGENNCLLH	PMSQHGIEDE
CRF01_AE_T	TPGPGVRLPL	CFGWCYKLVP	VD.PREVEED	NKGENNCLLH	PMSQHGIEDE
CRF02_AG_F	TPGPGTRYPL	TFGWCFNLEP	ID.PAEIEEA	NKEENNCLLH	PICQHGMEDE
CRF02_AG_F	TPGPGTRYPL	TFGWCFKLEP	MD.PAEVEEA	NKGENNCLLH	PICQHGMEDE
CRF02_AG_G	TPGPGTRFPL	TFGWCFKLV	MD.PKAVEEA	TEGENNSLLH	PICQHGIEDE
CRF02_AG_N	TPGPGTRFPL	TFGWCFKLV	MD.PAEVEEA	NEGENNSLLH	PICQHGMEDD
CRF02_AG_S	TPGPGTRFPL	TFGWCFKLV	MD.PADIEKD	TEGENNSLLH	PICQHGMEDE
CRF02_AG_S	TPGPGIRYPL	TFGWYCYKLVP	MD.PAEVEEA	NQGENNSLLH	PICQHGMEDE
CRF03_AB_R	...PGIRFPL	TFGWYCYKLVP	VD.PAEVEEA	TEGENNSLLH	PICQHGMDDE
CRF03_AB_R	TPGPGIRFPL	TFGWYCYKLVP	VD.PDEVEEA	TEGENNSLLH	PICQHGMDDE
CRF04_cpx_	TPGPGERFPL	CFGWCYKLVP	VD.PQEVEEA	TEGENTCLLH	PISQHGMEDE
CRF04_cpx_	TPGPGERFPL	CFGWCYKLVP	VD.PQEVEEA	NEGENNSLLH	PISQHGMEDE
CRF04_cpx_	TPGPGTRFPL	CFGWCYKLVP	VD.PQEVEEI	TAGEDNCLLH	PISQHGMEDE
CRF05_DF_B	TPGPGIRYPL	TLGWCFKLV	VN.PEEVEKA	NEGEDNCLLH	PMSLHGMEDD
CRF05_DF_B	TPGPGTRYPL	TFGWCFKLV	VD.PEEVEKA	NEGENKCLLH	PMHQHGMDDE
CRF06_cpx_	TPGPGTRFPL	TFGWYCYKLVP	VD.PEEVEEL	TKGENNSLLH	PICQHGAEDE
CRF06_cpx_	TPGPGIRYPL	TFGWYCYKLVP	VD.PREVEEE	TKGENNSLLH	PMCQHGAEDE
CRF06_cpx_	TPGPGIRYPL	TFGWYCYKLVP	VD.PREVEED	TKGENNSLLH	PMSQHGMEDE
CRF06_cpx_	TPGPGIRYPL	TFGWYCYKLVP	VD.PKEVEEE	TKGENXSLLH	PMCQHGVDDE
CRF11_cpx_	TPGPGVRYPL	CFGWCYKLVP	VD.PREVEEA	NEGENNSLLH	PMSQHGMDDE
CRF11_cpx_	TPGPGIRYPL	CFGWCYKLVP	VD.PREVEEA	NEGENNSLLH	PMSQHGIEDE
D_CD_84ZR0	TPGPGIRYPL	TFGWCFELVP	VD.PEVVEKA	TEGEDNCLLH	PICQHGMEDE
D_CD_ELI	TPGPGIRYPL	TFGWYCYELVP	VD.PQEVEED	TEGETNSLLH	PICQHGMEDE
D_CD_NDK	TPGPGIRYPL	TFGWCFQLVP	VD.PQEVEEA	TEREDNCLLH	PMCQQGMEDP
D_UG_94UG1	TPGPGIRYPL	TFGWCFELVP	ME.PKEVEEN	TEGEDNCLLH	PINQHGMEDE
F1_BE_VI85	TPGPGIRYPL	TLGWCFKLV	VD.PEEVEKA	NEGENNSLLH	PMSQHGMEDE
F1_BR_93BR	TPGPGIRYPL	TMGWCFKLV	VD.PEEVEKA	NEGENNSLLH	PMSQHGMEDE
F1_FI_FIN9	TPGPGVRYPL	TFGWCFKLV	VE.PEEVEKA	NEGENNSLLH	PMSQHGMEDE
F1_FR_MP41	TPGPGIRFPL	TFGWCFKLV	VD.PDEVEKA	NEGENNSLLH	PMSQHGMDDE
F2_CM_MP25	TPGPGPRFPL	TFGWCFKLV	VD.PEEVEKA	NEGENNSLLH	PMSLHGMEDD
F2KU_BE_VI	TPGPGIRYPL	CFGWCYKLVP	MD.PQEVEEA	NVGENNSLLH	PICQHGIDDT
G_BE_DRCBL	TPGPGTRVPL	TFGWCFKLV	ME.PSEVEEA	NKGENNCLLH	PICQHGMEDE
G_NG_92NG0	TPGPGTRLPL	TFGWCFKLV	MD.PAEIEEA	NKGENNCLLH	PICQHGMEDE
G_SE_SE616	TPGPGTRFPL	TFGWCFKLV	MD.PAEVEEA	NKGENNCLLH	PICQHGMEDE
H_BE_VI991	TPGPGERYPL	TFGWCFKLV	VD.PQDVEKA	NEGENNSLLH	PMCQHGIEDP
H_BE_VI997	TPGPGEGYPL	TFGWCFKLIP	VD.PQEVERA	NEGENNSLLY	PICQHGMEDE
H_CF_90CF0	TPGPGERFPL	TFGWCFKLV	VN.PQEVEQA	NEGENNSLLH	PMSLHGMEDD
J_SE_SE702	TPGPGTXYPL	TFGWCFKLV	VD.PSEVEEA	NEGENNSLLH	PACQHGIEDE
J_SE_SE788	TPGPGIRYPL	TFGWYCYKLVP	VD.PSEVEEA	NEGENNSLLH	PICQHGIEDE
K_CD_EQTB1	TPGPGIRYPL	TFGWYCYKLVP	VD.PREVEEA	TEGENNSLLH	PVNQHGMEDE
K_CM_MP535	TPGPGIRYPL	TFGWYCYKLVP	VD.PAEVEET	TEGEDNCLLH	PINQHGMEDE
N_CM_YBF30	TPGPGIRYPL	TFGWCFKLV	LS.AEEVEEA	NEGDNNALLH	PICQHGADDD
O_CM_ANT70	TPGPGTRFPL	TFGWLFKLV	VSEEEAERLG	NTCERANLLH	PACAHGFEDT
O_CM_MVP51	TPGPGPRFPL	TFGWLFKLV	VSAEEAERLG	NTNEDASLLH	PACNHGAEDA
O_SN_MP129	TPGPGPRFPL	TFGWLFKLV	VSEAAEELG	NKCERASLLH	PACNHGFEDN
O_SN_MP130	TPGPGTRFPL	TFGWLFKLV	VSEAAEELG	NKCDRAKLLH	PVCNHGFEDP
U_CD_83C	TPGPGIRYPL	TFGWPFKLV	VD.PKEVEEA	NEGENNSLLH	PICQHGMDDE

	201		232
00BW0762_1	HREVLWKF	SSLARRHVAR	E.LHPEYYKD C.
00BW0768_2	EREVLWKF	SSLARRHVAR	E.LHPEYYKD C.
00BW0874_2	DREVLWQFD	SSLVRRHVAR	E.LHPEYYKD C.
00BW1471_2	DREVLWVFD	SSLARRHVAR	E.LHPEYYKD C.
00BW1616_2	DREVLWKF	SSLARRHVAR	E.LHPEYYKD C.

00BW1686_8	DREVLWKFD	SHLAYRHMAR	E.LHPEYYKD	C.
00BW1759_3	HGEVLWKFD	SALARRHMAR	E.LHPEYYKD	C.
00BW1773_2	HGEVLWKFD	SSLARRHLAR	E.KHPEFYKD	C.
00BW1783_5	DKEVLQWKFD	SSLARRHMAR	E.LHPEYYKD	C.
00BW1795_6	DREVLWKFD	SHLARRHTAR	E.LHPEFYKD	CR
00BW1811_3	HGEVLEWKFD	SMLARRHMAR	E.LHPEYYKD	C.
00BW1859_5	EREVLRWKFD	SQLARRHMAR	E.LHPEYYKD	C.
00BW1880_2	HKEVLRWKFD	SSLARRHLAR	E.LHPEYYKD	C.
00BW1921_1	DREVLWKFD	SQLARRHLAR	E.KHPEWYKD	C.
00BW2036_1	HKEVLTWKFD	SHLARRHMAR	E.LHPEYYKD	C.
00BW2063_6	HREVLQWKFD	SQLARRHIAR	E.RHPEYYKD	C.
00BW2087_2	DREVLKWVFD	SSLARRHLAR	E.KHPEFYKD	C.
00BW2127_2	EREVLQWKFD	SLLSRRHLAR	IXIHAEYYKD	C.
00BW2128_3	HGEVLWKFD	SHLAYRHMAR	E.KHPEFYKD	C.
00BW2276_7	EREVLKWKFD	SSLARRHMAR	E.LHPEYYKA	C.
00BW3819_3	EGEVLQWKFD	SLLAYRHMAR	E.QHPEYYKD	C.
00BW3842_8	DREVPMWKFD	SLLARRHMAR	E.LHPGYKD	C.
00BW3871_3	DREVLWKFD	SHLVHRHMAR	E.LHPEYYKG	C.
00BW3876_9	DREVLRWKFD	S.LARRHIAR	E.LHPEYYKN	C.
00BW3886_8	EREVLKWKFD	SQLAYRHMAR	E.IHPEYYKD	C.
00BW3891_6	DREVLRWKFD	SHLARRHMAR	E.LHPEWYKD	C.
00BW3970_2	DREVLKWQFD	ISLARRHMAR	E.LHPEWYKD	..
00BW5031_1	DREVLRWKFD	SELARRHIAR	E.RHPEFYKD	C.
96BW01B21	HREVLKWKFD	SQLARRHMAR	E.LHPEYYKD	C.
96BW0407	DREVLRWKFD	SSLARRHMAR	E.LHPEYYKD	C.
96BW0502	HGEVLKWKFD	SQLARRHMAR	E.LYPEYYKD	C.
96BW06_J4	EREVLTWKFD	SHLVHRPMAR	E.IHPEYYKD	C.
96BW11_06	HKEVLKWKFD	SQLARRHLAR	E.LHPEFYKD	C.
96BW1210	DREVLKWKFD	SSLARRHLTR	E.KHPEYYKD	C.
96BW15B03	DKEVLWKFD	SHLARRHMAR	E.LHPEYYKD	C.
96BW16_26	ERGVKWKFD	SHLARRHMAR	E.LHPEYYKD	C.
96BW17A09	DREVLKWVFD	SHLARKHMAR	E.LHPEYYKN	C.
96BWM01_5	HREVLKWKFD	SSLARRHMAR	E.LHPEFYKD	C.
96BWM03_2	HGEVLWKFD	SQLARRHMAR	E.LHPEYYKD	C.
98BWMC12_2	EREVLKWQFD	SSLARRHMAR	E.LHPEYYKD	C.
98BWMC13_4	GKEVLIWKFD	SHLARRHMAR	E.LHPEFYKD	C.
98BWMC14_a	DREVLWKFD	SQLARRHIAR	E.IHPEYYKD	C.
98BWM014_1	EKEVLKWVFD	SSLARRHVAR	E.LHPEFYKD	C.
98BWM018_d	DREVLRWKFD	SSLARRHMAR	E.LHPEYYKD	C.
98BWM036_a	DREVLKWEFD	IRLAHTHMAR	Q.LHPEFYKN	C.
98BWM037_d	DREVLKWQFD	SSLARRHVAR	E.LHPEYYKD	C.
99BW3932_1	DREVLKWKFD	SMLARRHMAR	E.LHPEFYKD	C.
99BW4642_4	DREVLWKYD	SQLARRHMAR	E.LHPDYYKD	C.
99BW4745_8	DREVLRWKFD	SHLARRHMAR	E.LHPEFYKD	C.
99BW4754_7	HKEVLKWKFD	SHLARRHMAR	E.LHPEFYKD	C.
99BWMC16_8	DREVLKWQFD	SSLARRHMAR	E.LHPEYYKD	C.
A2_CD_97CD	EREVLKWKFD	SRLALRHLAR	E.QHPEFYKD	C.
A2_CY_94CY	EREVLKWEFD	RSLARRHRAR	E.LHPEYYKD	C.
A2D_97KR	EREVLKWVFD	SHLALVHKAR	E.LHPEFYKD	C.
A2G_CD_97C	DKQVLGWRFD	SSLARRHIAR	E.KHPEYYKD	C.
A_BY_97BL0	EKEVLWKFD	SRLALKHRAR	E.LHPEFYKD	C.
A_KE_Q23	EREVLKWKFD	SRLALKHRAR	E.LHPEWYKD	C.
A_SE_SE659	EKEVLKWKFD	SRLALKHLAC	E.KHPEFYKD	C.
A_SE_SE725	EKETLRWRFD	SRLALRHRAQ	E.MHPEFYKD	C.
A_SE_SE753	EREVLKWKFD	SRLALKHRAQ	E.LHPEFYKD	C.
A_SE_SE853	ERETLMWKFD	SKLALKHRAH	E.LHPEYFKN	C.
A_SE_SE889	ERETLMWKFD	SRLALTHRAR	E.LHPEFYKD	C.
A_SE_UGSE8	ERETLMWKFD	PHLAFKHRAF	E.LHPEYYKN	..
A_UG_92UG0	EKETLRWKFD	SSLARVHKAR	E.LHPEFYKD	C.
A_UG_U455	EKEVLWKFD	STLALKHRAH	E.LHPEFYKD	..
AC_IN_2130	YGEVLQWKFD	SHLAYKHQAR	E.RHPEFYKD	C.

AC_RW_92RW	DREVLKWKFD	SHLAHRHMAR	E.LHPEYYKD	C.
AC_SE_SE94	ERETLVWRFD	SRLALKHLAR	E.KHPEFYKD	C.
ACD_SE_SE8	DKEVLRWKFD	SQLARRHMAR	E.MHPEYYKD	C.
ACG_BE_VI1	DREVLVWRFD	SRLALKHIAK	E.KHPEYFKD	C.
AD_SE_SE69	EREVLMWRFN	SRLAFEHKAH	Q.LHPEYYKD	C.
AD_SE_SE71	EKEVLKWQFD	SRLALKHLAR	E.KHPEFYKD	C.
ADHK_NO_97	EXEVLMWRFD	SRLAFKHRAR	E.LHPEFYKD	C.
ADK_CD_MAL	EREVLKWKFD	SSLALRHRAR	E.QHPEYYKD	C.
AG_BE_VI11	EREVLVWKFD	SMLAFKHRAR	E.LHPEYYKD	C.
AG_NG_92NG	DREVLVWRFD	SSLARRHIAR	E.QHPEYYKD	C.
AGHU_GA_VI	EREVLMWKFD	SSLAREHVAR	K.LYPEFFKD	C.
AGU_CD_Z32	EREVLMWKFD	SSLARKHLAR	E.MHPEFYKD	..
AJ_BW_BW21	DREVLMWKFD	SSLARRHLAR	E.KHPEFYKD	C.
B_AU_VH	EKEVLMWKFD	SRLAVHHMAR	E.LHPEYYKN	..
B_CN_RL42	EREVLMWKFD	SRLAIHHMAR	E.MHPEYHKD	C.
B_DE_D31	EREVLVWRFD	SRLAFKHMAR	E.LHPEYYKN	..
B_DE_HAN	EREVLKWKFD	SHLAFHHKAR	E.LHPEYYKD	C.
B_FR_HXB2	EREVLEWRFD	SRLAFHHVAR	E.LHPEYFKN	C.
B_GA_OYI	EKEVLVWKFD	SRLAFRHMAR	E.VHPEYYKD	C.
B_GB_CAM1	EKEVLMWKFD	SRLAFHHMAR	E.KHPEFYKD	C.
B_GB_GB8	EKEVLVWKFN	SRLAFHHMAR	E.LHPEFYKD	C.
B_GB_MANC	EKEVLVWKFD	SRLAFHHVPD	E.LHPEYYKD	C.
B_KR_WK	EGEVLVWRFD	SRLAFHHMAR	E.KHPEYYKD	C.
B_NL_3202A	EREVLEWRFD	SRLAFHHMAR	E.LHPEYYKD	C.
B_TW_TWCYS	EKEVLVWRFD	STLAFHHRAR	E.LHPEYYKX	C.
B_US_BC	EREVLEWRFD	SRLAFHHMAR	E.LHPEYYKN	R.
B_US_DH123	EKEVLLWKFD	SRLAYHHMAR	E.LHPEYYKN	C.
B_US_JRCSF	EKEVLVWKFD	SKLALHHVAR	E.LHPEYYKD	C.
B_US_MNCG	EREVLVWKS	SHLAFQHYAR	E.LHPEYYKN	C.
B_US_P896	ERQVLVWRFD	SRLAFHHVAR	E.LHPEYFKN	..
B_US_RF	EKEVLVWKFD	SRLAFHHVAR	E.KHPEYYKD	C.
B_US_SF2	EKEVLVWRFD	SKLAFHHMAR	E.LHPEYYKD	C.
B_US_WEAU1	EKEVLMWKFD	SKLAFHHVAR	E.LHPEYFKD	C.
B_US_WR27	EKEVLVWKFD	SRLAFHHKAR	E.LHPEYYKN	..
B_US_YU2	EREGLEWRFD	SRLAFHHVAR	E.LHPEYYKN	..
BF1_BR_93B	DREILQWRFD	SRLAFHHMAR	E.LHPEYYKD	C.
C_BR_92BR0	HREVLQWKFD	SLARRHMAR	E.LHPEYYKD	C.
C_BW_96BW0	DGEVLRWKFD	SHLAHRHMAR	E.LHPEYYKD	C.
C_BW_96BW1	HKEVLKWKFD	SQLARRHLAR	E.LHPEFYKD	C.
C_BW_96BW1	DREVLKWKFD	SSLARRHLTR	E.KHPEYYKD	C.
C_BW_96BW1	DKEVLMWKFD	SHLARRHMAR	E.LHPEYYKD	C.
C_ET_ETH22	DREVLKWKFD	SHLARRHMAR	E.LHPEYYKD	C.
C_IN_93IN1	HREVLKWKFD	SQLARRHMAR	E.LHPEFYKD	C.
C_IN_93IN9	HREVLQWKFD	SLAHRHRAR	E.LHPEFYKD	C.
C_IN_93IN9	HREVLQWKFD	SHLAHRHMAR	E.LHPEYYKD	C.
C_IN_94IN1	HREVLWK..	.QLAHRHIAR	E.LHPEFYKD	C.
C_IN_95IN2	HNEVLVWKFD	SQLAHKHRAR	E.LHPEFYNK	DC
CRF01_AE_C	EREVLMWKFD	SSLARRHIAR	E.LRPEYYKD	C.
CRF01_AE_C	EREVLMWKFD	SSLARRHIAR	E.LHPEYYKD	..
CRF01_AE_C	EREVLMWKFD	SSLARRHIAR	E.LHPEYYKD	C.
CRF01_AE_T	EREVLMWKFD	SALARKHTAR	E.LHPEYYKD	C.
CRF01_AE_T	EREVLWKFD	STLARKHIAR	E.QHPEFYKD	C.
CRF01_AE_T	EREVLIWKFD	SALARRHIAR	E.LRPEFYKD	C.
CRF01_AE_T	EREVLWKFD	SALARKHIAR	E.MHPEYYKD	C.
CRF01_AE_T	EREVLWKFD	SALARKHVAR	E.QHPEYYKD	C.
CRF01_AE_T	EREVLIWKFD	SSLARKHLAR	E.LHPEYYKD	C.
CRF02_AG_F	DREVLVWRFD	SSLARTHRAR	E.LHPEYYKD	C.
CRF02_AG_F	DREVLVWRFD	SSLARRHIAR	E.RHPEFYKD	C.
CRF02_AG_G	DREVLVWRFD	SSLAFTHRAR	E.MHPEFYKD	C.
CRF02_AG_N	DREVLWRFD	SRLAFRHTAR	E.LHPEYYKD	C.
CRF02_AG_S	DREVLVWRFD	SRLAFTHKAR	E.MHPEFYKD	CX

CRF02_AG_S	DKEVLVWRFD	SRLAFRHTAR	E.LHPEYYKD	C.
CRF03_AB_R	EKEVLMWKFD	SRLALTHRAR	E.LHPEFYKD	C.
CRF03_AB_R	EKEVLMWKFD	SRLALTHRAR	E.LHPEFYKD	C.
CRF04_cpx_	EREVLKWKFD	SRLAYKHVAR	E.LHPEFYKD	C.
CRF04_cpx_	EREVLKWKFD	SRLAFKHIAR	E.LHPEFYKD	C.
CRF04_cpx_	EREVLKWKFD	SLLAYRHMAR	E.LHPEFYKD	C.
CRF05_DF_B	DREVLQWKFD	SSLALRHIAR	E.RHPEFYQD	..
CRF05_DF_B	DGEVLRWKFD	SSLALKHIAR	E.RRPEFYQD	..
CRF06_cpx_	EREVLKWKFD	SSLARRHIAR	E.KHPEFYKD	C.
CRF06_cpx_	EGEVLMWKFD	SSLARRHIAR	E.LHPDFYKD	C.
CRF06_cpx_	EREVLMWKFD	SSLARRHTAR	E.MHPEFYKD	C.
CRF06_cpx_	EXEVLMWKFD	SSLARRHIAX	E.XHPEFXKD	C.
CRF11_cpx_	EREVLKWKFD	SSLARKHIAR	E.LHPDFYKD	..
CRF11_cpx_	DREVLRWKFD	SSLARRHIAR	E.LHPDFYKD	..
D_CD_84ZR0	EKEVLVWRFN	SRLAFEHKAK	E.KYPEYFKN	C.
D_CD_ELI	ERQVLKWRFN	SRLAFEHKAR	E.MHPEFYKN	..
D_CD_NDK	ERQVLMWRFN	SRLALEHKAR	E.LHPEFYKD	C.
D_UG_94UG1	EREVLVWRFN	SRLAFEHKAK	M.KHPEYYKD	C.
F1_BE_VI85	DREVLRWKFD	SSLALRHIAR	E.RHPEFYQD	..
F1_BR_93BR	DKEVLKWEFD	SRLALRHIAR	E.RHPEYYQD	..
F1_FI_FIN9	DREVLKWKFD	SRLALKHIAR	E.RHPEFYRD	..
F1_FR_MP41	DREVLRWKFD	SRLAFRHIAR	E.KHPEFYQN	..
F2_CM_MP25	DKEVLKWKFD	SRLALRHIAR	E.RHPEYYKD	..
F2KU_BE_VI	EREVLVWKFD	SRLALKHLAR	E.KHPEYYKD	C.
G_BE_DRCBL	DGEVLVWRFD	SSLARRHLAR	E.LHPEYYKD	C.
G_NG_92NG0	DREVLVWRFN	SSLARRHLAR	E.LHPEYYKD	C.
G_SE_SE616	DREVLVWRFD	SSLARRHIAR	E.LHPEYYKD	C.
H_BE_VI991	EREVLMWKFD	SRLALRHRAR	E.LHPEFYKD	C.
H_BE_VI997	EGEVLMWKFD	SRLAFTHTAR	E.KHPEFYKD	C.
H_CF_90CF0	GREVLMWKFD	SRLALTHLAR	V.KHPEY.KD	C.
J_SE_SE702	EREVLKWKFD	SSLARRHIAR	E.LHPEFYKD	C.
J_SE_SE788	EREVLQWKFD	SSLARRHIAR	E.LHPEFYKD	C.
K_CD_EQTB1	HREVLKWKFD	SSLARKHVAR	E.MHPEYYKD	..
K_CM_MP535	HREILMWKFD	SSLARRHVAR	E.LHPDYYKD	..
N_CM_YBF30	HKEVLVWRFD	SSLARRHVAR	E.LHPEFYKN	C.
O_CM_ANT70	HKEILMWKFD	RSLGNTHVAM	ITHPELFQKD	..
O_CM_MVP51	HGEILKWQFD	RSLGLTHIAL	QKHPELFPSN	..
O_SN_MP129	HGQILKWQFD	RSLGSTHVAM	VTNPELFNKD	..
O_SN_MP130	HKEMLKWQFD	RSLGSTHVAL	ITHPELFLKD	..
U_CD___83C	EKEVLMWKFD	SSLARRHLAR	E.LHPEFYKD	C.

Table 14. HIV Pol Sequence Alignment
GCG Multiple Sequence File.
Written by Omega 1.1

Name: 00BW0762_1	SEQ	ID NO: 803	Len: 1046	Check: 4376	Weight: 1.00
Name: 00BW0768_2	SEQ	ID NO: 804	Len: 1046	Check: 8430	Weight: 1.00
Name: 00BW0874_2	SEQ	ID NO: 805	Len: 1046	Check: 8925	Weight: 1.00
Name: 00BW1471_2	SEQ	ID NO: 806	Len: 1046	Check: 1324	Weight: 1.00
Name: 00BW1616_2	SEQ	ID NO: 807	Len: 1046	Check: 935	Weight: 1.00
Name: 00BW1686_8	SEQ	ID NO: 808	Len: 1046	Check: 8131	Weight: 1.00
Name: 00BW1759_3	SEQ	ID NO: 809	Len: 1046	Check: 579	Weight: 1.00
Name: 00BW1773_2	SEQ	ID NO: 810	Len: 1046	Check: 1975	Weight: 1.00
Name: 00BW1783_5	SEQ	ID NO: 811	Len: 1046	Check: 216	Weight: 1.00
Name: 00BW1795_6	SEQ	ID NO: 812	Len: 1046	Check: 5932	Weight: 1.00
Name: 00BW1811_3	SEQ	ID NO: 813	Len: 1046	Check: 6525	Weight: 1.00
Name: 00BW1859_5	SEQ	ID NO: 814	Len: 1046	Check: 2879	Weight: 1.00
Name: 00BW1880_2	SEQ	ID NO: 815	Len: 1046	Check: 7093	Weight: 1.00
Name: 00BW1921_1	SEQ	ID NO: 816	Len: 1046	Check: 2524	Weight: 1.00
Name: 00BW2036_1	SEQ	ID NO: 817	Len: 1046	Check: 8279	Weight: 1.00
Name: 00BW2063_6	SEQ	ID NO: 818	Len: 1046	Check: 3935	Weight: 1.00
Name: 00BW2087_2	SEQ	ID NO: 819	Len: 1046	Check: 7898	Weight: 1.00
Name: 00BW2127_2	SEQ	ID NO: 820	Len: 1046	Check: 728	Weight: 1.00
Name: 00BW2128_3	SEQ	ID NO: 821	Len: 1046	Check: 5356	Weight: 1.00
Name: 00BW2276_7	SEQ	ID NO: 822	Len: 1046	Check: 9456	Weight: 1.00
Name: 00BW3819_3	SEQ	ID NO: 823	Len: 1046	Check: 6369	Weight: 1.00
Name: 00BW3842_8	SEQ	ID NO: 824	Len: 1046	Check: 4573	Weight: 1.00
Name: 00BW3871_3	SEQ	ID NO: 825	Len: 1046	Check: 6948	Weight: 1.00
Name: 00BW3876_9	SEQ	ID NO: 826	Len: 1046	Check: 6609	Weight: 1.00
Name: 00BW3886_8	SEQ	ID NO: 827	Len: 1046	Check: 8244	Weight: 1.00
Name: 00BW3891_6	SEQ	ID NO: 828	Len: 1046	Check: 5718	Weight: 1.00
Name: 00BW3970_2	SEQ	ID NO: 829	Len: 1046	Check: 3940	Weight: 1.00
Name: 00BW5031_1	SEQ	ID NO: 830	Len: 1046	Check: 2442	Weight: 1.00
Name: 96BW01B21	SEQ	ID NO: 831	Len: 1046	Check: 2358	Weight: 1.00
Name: 96BW0407	SEQ	ID NO: 832	Len: 1046	Check: 8537	Weight: 1.00
Name: 96BW0502	SEQ	ID NO: 833	Len: 1046	Check: 3948	Weight: 1.00
Name: 96BW06_J4	SEQ	ID NO: 834	Len: 1046	Check: 7173	Weight: 1.00
Name: 96BW11_06	SEQ	ID NO: 835	Len: 1046	Check: 973	Weight: 1.00
Name: 96BW1210	SEQ	ID NO: 836	Len: 1046	Check: 5817	Weight: 1.00
Name: 96BW15B03	SEQ	ID NO: 837	Len: 1046	Check: 5157	Weight: 1.00
Name: 96BW16_26	SEQ	ID NO: 838	Len: 1046	Check: 3303	Weight: 1.00
Name: 96BW17A09	SEQ	ID NO: 839	Len: 1046	Check: 1256	Weight: 1.00
Name: 96BWMO1_5	SEQ	ID NO: 840	Len: 1046	Check: 5593	Weight: 1.00
Name: 96BWMO3_2	SEQ	ID NO: 841	Len: 1046	Check: 3661	Weight: 1.00
Name: 98BWMC12_2	SEQ	ID NO: 842	Len: 1046	Check: 7159	Weight: 1.00
Name: 98BWMC13_4	SEQ	ID NO: 843	Len: 1046	Check: 3254	Weight: 1.00
Name: 98BWMC14_a	SEQ	ID NO: 844	Len: 1046	Check: 5638	Weight: 1.00
Name: 98BWMO14_1	SEQ	ID NO: 845	Len: 1046	Check: 7680	Weight: 1.00
Name: 98BWMO18_d	SEQ	ID NO: 846	Len: 1046	Check: 1619	Weight: 1.00
Name: 98BWMO36_a	SEQ	ID NO: 847	Len: 1046	Check: 8852	Weight: 1.00
Name: 98BWMO37_d	SEQ	ID NO: 848	Len: 1046	Check: 4750	Weight: 1.00
Name: 99BW3932_1	SEQ	ID NO: 849	Len: 1046	Check: 5391	Weight: 1.00
Name: 99BW4642_4	SEQ	ID NO: 850	Len: 1046	Check: 1514	Weight: 1.00
Name: 99BW4745_8	SEQ	ID NO: 851	Len: 1046	Check: 52	Weight: 1.00
Name: 99BW4754_7	SEQ	ID NO: 852	Len: 1046	Check: 4905	Weight: 1.00
Name: 99BWMC16_8	SEQ	ID NO: 853	Len: 1046	Check: 1544	Weight: 1.00
Name: A2_CD_97CD	SEQ	ID NO: 854	Len: 1046	Check: 9703	Weight: 1.00
Name: A2_CY_94CY	SEQ	ID NO: 855	Len: 1046	Check: 3235	Weight: 1.00
Name: A2D_97KR	SEQ	ID NO: 856	Len: 1046	Check: 3776	Weight: 1.00
Name: A2G_CD_97C	SEQ	ID NO: 857	Len: 1046	Check: 2059	Weight: 1.00
Name: A_BY_97BL0	SEQ	ID NO: 858	Len: 1046	Check: 2724	Weight: 1.00
Name: A_KE_Q23_A	SEQ	ID NO: 859	Len: 1046	Check: 1835	Weight: 1.00

Name: A_SE_SE659	SEQ	ID NO: 860	Len: 1046	Check: 647	Weight: 1.00
Name: A_SE_SE725	SEQ	ID NO: 861	Len: 1046	Check: 263	Weight: 1.00
Name: A_SE_SE753	SEQ	ID NO: 862	Len: 1046	Check: 2271	Weight: 1.00
Name: A_SE_SE853	SEQ	ID NO: 863	Len: 1046	Check: 5036	Weight: 1.00
Name: A_SE_SE889	SEQ	ID NO: 864	Len: 1046	Check: 8414	Weight: 1.00
Name: A_SE_UGSE8	SEQ	ID NO: 865	Len: 1046	Check: 3268	Weight: 1.00
Name: A_UG_92UG0	SEQ	ID NO: 866	Len: 1046	Check: 2007	Weight: 1.00
Name: A_UG_U455_	SEQ	ID NO: 867	Len: 1046	Check: 2277	Weight: 1.00
Name: AC_IN_2130	SEQ	ID NO: 868	Len: 1046	Check: 5353	Weight: 1.00
Name: AC_RW_92RW	SEQ	ID NO: 869	Len: 1046	Check: 4695	Weight: 1.00
Name: AC_SE_SE94	SEQ	ID NO: 870	Len: 1046	Check: 4206	Weight: 1.00
Name: ACD_SE_SE8	SEQ	ID NO: 871	Len: 1046	Check: 7281	Weight: 1.00
Name: ACG_BE_VI1	SEQ	ID NO: 872	Len: 1046	Check: 1400	Weight: 1.00
Name: AD_SE_SE69	SEQ	ID NO: 873	Len: 1046	Check: 4640	Weight: 1.00
Name: AD_SE_SE71	SEQ	ID NO: 874	Len: 1046	Check: 1057	Weight: 1.00
Name: ADHK_NO_97	SEQ	ID NO: 875	Len: 1046	Check: 3502	Weight: 1.00
Name: ADK_CD_MAL	SEQ	ID NO: 876	Len: 1046	Check: 2578	Weight: 1.00
Name: AG_BE_VI11	SEQ	ID NO: 877	Len: 1046	Check: 8416	Weight: 1.00
Name: AG_NG_92NG	SEQ	ID NO: 878	Len: 1046	Check: 9397	Weight: 1.00
Name: AGHU_GA_VI	SEQ	ID NO: 879	Len: 1046	Check: 9562	Weight: 1.00
Name: AGU_CD_Z32	SEQ	ID NO: 880	Len: 1046	Check: 8398	Weight: 1.00
Name: AJ_BW_BW21	SEQ	ID NO: 881	Len: 1046	Check: 3451	Weight: 1.00
Name: B_AU_VH_AF	SEQ	ID NO: 882	Len: 1046	Check: 2033	Weight: 1.00
Name: B_CN_RL42_	SEQ	ID NO: 883	Len: 1046	Check: 1369	Weight: 1.00
Name: B_DE_D31_U	SEQ	ID NO: 884	Len: 1046	Check: 4607	Weight: 1.00
Name: B_DE_HAN_U	SEQ	ID NO: 885	Len: 1046	Check: 1771	Weight: 1.00
Name: B_FR_HXB2_	SEQ	ID NO: 886	Len: 1046	Check: 4569	Weight: 1.00
Name: B_GA_OYI_	SEQ	ID NO: 887	Len: 1046	Check: 3682	Weight: 1.00
Name: B_GB_CAM1_	SEQ	ID NO: 888	Len: 1046	Check: 3161	Weight: 1.00
Name: B_GB_GB8_A	SEQ	ID NO: 889	Len: 1046	Check: 6253	Weight: 1.00
Name: B_GB_MANC_	SEQ	ID NO: 890	Len: 1046	Check: 7670	Weight: 1.00
Name: B_KR_WK_AF	SEQ	ID NO: 891	Len: 1046	Check: 8737	Weight: 1.00
Name: B_NL_3202A	SEQ	ID NO: 892	Len: 1046	Check: 2083	Weight: 1.00
Name: B_TW_TWCYS	SEQ	ID NO: 893	Len: 1046	Check: 3056	Weight: 1.00
Name: B_US_BC_L0	SEQ	ID NO: 894	Len: 1046	Check: 3160	Weight: 1.00
Name: B_US_DH123	SEQ	ID NO: 895	Len: 1046	Check: 1102	Weight: 1.00
Name: B_US_JRCSF	SEQ	ID NO: 896	Len: 1046	Check: 5571	Weight: 1.00
Name: B_US_MNCG_	SEQ	ID NO: 897	Len: 1046	Check: 3988	Weight: 1.00
Name: B_US_P896_	SEQ	ID NO: 898	Len: 1046	Check: 2465	Weight: 1.00
Name: B_US_RF_M1	SEQ	ID NO: 899	Len: 1046	Check:	Weight: 1.00
Name: B_US_SF2_K	SEQ	ID NO: 900	Len: 1046	Check: 1754	Weight: 1.00
Name: B_US_WEAU1	SEQ	ID NO: 901	Len: 1046	Check: 2993	Weight: 1.00
Name: B_US_WR27_	SEQ	ID NO: 902	Len: 1046	Check: 4098	Weight: 1.00
Name: B_US_YU2_M	SEQ	ID NO: 903	Len: 1046	Check: 5564	Weight: 1.00
Name: BF1_BR_93B	SEQ	ID NO: 904	Len: 1046	Check: 4182	Weight: 1.00
Name: C_BR_92BR0	SEQ	ID NO: 905	Len: 1046	Check: 5481	Weight: 1.00
Name: C_BW_96BW0	SEQ	ID NO: 906	Len: 1046	Check: 6833	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 907	Len: 1046	Check: 2166	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 908	Len: 1046	Check: 5817	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 909	Len: 1046	Check: 5157	Weight: 1.00
Name: C_ET_ETH22	SEQ	ID NO: 910	Len: 1046	Check: 3509	Weight: 1.00
Name: C_IN_93IN1	SEQ	ID NO: 911	Len: 1046	Check: 5471	Weight: 1.00
Name: C_IN_93IN9	SEQ	ID NO: 912	Len: 1046	Check: 4102	Weight: 1.00
Name: C_IN_93IN9	SEQ	ID NO: 913	Len: 1046	Check: 3150	Weight: 1.00
Name: C_IN_94IN1	SEQ	ID NO: 914	Len: 1046	Check: 5157	Weight: 1.00
Name: C_IN_95IN2	SEQ	ID NO: 915	Len: 1046	Check: 4641	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 916	Len: 1046	Check: 87	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 917	Len: 1046	Check: 3758	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 918	Len: 1046	Check: 2775	Weight: 1.00
Name: CRF01_AE_T	SEQ	ID NO: 919	Len: 1046	Check: 1864	Weight: 1.00
Name: CRF01_AE_T	SEQ	ID NO: 920	Len: 1046	Check: 7414	Weight: 1.00

Name:	CRF01_AE_T	SEQ	ID NO:	921	Len:	1046	Check:	7837	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	922	Len:	1046	Check:	3529	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	923	Len:	1046	Check:	7503	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	924	Len:	1046	Check:	5730	Weight:	1.00
Name:	CRF02_AG_F	SEQ	ID NO:	925	Len:	1046	Check:	9432	Weight:	1.00
Name:	CRF02_AG_F	SEQ	ID NO:	926	Len:	1046	Check:	2064	Weight:	1.00
Name:	CRF02_AG_G	SEQ	ID NO:	927	Len:	1046	Check:	9849	Weight:	1.00
Name:	CRF02_AG_N	SEQ	ID NO:	928	Len:	1046	Check:	1793	Weight:	1.00
Name:	CRF02_AG_S	SEQ	ID NO:	929	Len:	1046	Check:	4817	Weight:	1.00
Name:	CRF02_AG_S	SEQ	ID NO:	930	Len:	1046	Check:	1764	Weight:	1.00
Name:	CRF03_AB_R	SEQ	ID NO:	931	Len:	1046	Check:	1695	Weight:	1.00
Name:	CRF03_AB_R	SEQ	ID NO:	932	Len:	1046	Check:	1425	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	933	Len:	1046	Check:	8496	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	934	Len:	1046	Check:	2074	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	935	Len:	1046	Check:	9245	Weight:	1.00
Name:	CRF05_DF_B	SEQ	ID NO:	936	Len:	1046	Check:	62	Weight:	1.00
Name:	CRF05_DF_B	SEQ	ID NO:	937	Len:	1046	Check:	3427	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	938	Len:	1046	Check:	142	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	939	Len:	1046	Check:	6688	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	940	Len:	1046	Check:	8524	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	941	Len:	1046	Check:	4725	Weight:	1.00
Name:	CRF11_cpx	SEQ	ID NO:	942	Len:	1046	Check:	2194	Weight:	1.00
Name:	CRF11_cpx	SEQ	ID NO:	943	Len:	1046	Check:	8466	Weight:	1.00
Name:	D_CD_84ZR0	SEQ	ID NO:	944	Len:	1046	Check:	515	Weight:	1.00
Name:	D_CD_ELI_K	SEQ	ID NO:	945	Len:	1046	Check:	2096	Weight:	1.00
Name:	D_CD_NDK_M	SEQ	ID NO:	946	Len:	1046	Check:	3376	Weight:	1.00
Name:	D_UG_94UG1	SEQ	ID NO:	947	Len:	1046	Check:	3505	Weight:	1.00
Name:	F1_BE_VI85	SEQ	ID NO:	948	Len:	1046	Check:	3993	Weight:	1.00
Name:	F1_BR_93BR	SEQ	ID NO:	949	Len:	1046	Check:	2251	Weight:	1.00
Name:	F1_FI_FIN9	SEQ	ID NO:	950	Len:	1046	Check:	9772	Weight:	1.00
Name:	F1_FR_MP41	SEQ	ID NO:	951	Len:	1046	Check:	1447	Weight:	1.00
Name:	F2_CM_MP25	SEQ	ID NO:	952	Len:	1046	Check:	2842	Weight:	1.00
Name:	F2KU_BE_VI	SEQ	ID NO:	953	Len:	1046	Check:	5026	Weight:	1.00
Name:	G_BE_DRCBL	SEQ	ID NO:	954	Len:	1046	Check:	5377	Weight:	1.00
Name:	G_NG_92NG0	SEQ	ID NO:	955	Len:	1046	Check:	6000	Weight:	1.00
Name:	G_SE_SE616	SEQ	ID NO:	956	Len:	1046	Check:	7901	Weight:	1.00
Name:	H_BE_VI991	SEQ	ID NO:	957	Len:	1046	Check:	9107	Weight:	1.00
Name:	H_BE_VI997	SEQ	ID NO:	958	Len:	1046	Check:	5776	Weight:	1.00
Name:	H_CF_90CF0	SEQ	ID NO:	959	Len:	1046	Check:	9201	Weight:	1.00
Name:	J_SE_SE702	SEQ	ID NO:	960	Len:	1046	Check:	9700	Weight:	1.00
Name:	J_SE_SE788	SEQ	ID NO:	961	Len:	1046	Check:	8817	Weight:	1.00
Name:	K_CD_EQTB1	SEQ	ID NO:	962	Len:	1046	Check:	3723	Weight:	1.00
Name:	K_CM_MP535	SEQ	ID NO:	963	Len:	1046	Check:	3729	Weight:	1.00
Name:	N_CM_YBF30	SEQ	ID NO:	964	Len:	1046	Check:	3336	Weight:	1.00
Name:	O_CM_ANT70	SEQ	ID NO:	965	Len:	1046	Check:	9461	Weight:	1.00
Name:	O_CM_MVP51	SEQ	ID NO:	966	Len:	1046	Check:	2986	Weight:	1.00
Name:	O_SN_99SE	SEQ	ID NO:	967	Len:	1046	Check:	377	Weight:	1.00
Name:	O_SN_99SE	SEQ	ID NO:	968	Len:	1046	Check:	9312	Weight:	1.00
Name:	U_CD_83C	SEQ	ID NO:	969	Len:	1046	Check:	1358	Weight:	1.00

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SEQ	ID	NO		1						50
803			00BW0762_1	FFRENLAFFQ	G.EAREFPPE	QT.....RANSPT	SR.....	E	
804			00BW0768_2	FFRENLAFFQ	.GEAGEFPSEQTRANSTT	SR.....	K	
805			00BW0874_2	FFRENLAFFQ	G.EAREFPPE	QA.....RAISPT	SR.....	E	
806			00BW1471_2	FFRENLAFSE	G.EARELPSE	Q.....	...ARASPT	SR.....	E	
807			00BW1616_2	FFRENLAFFQ	G.KAGEFPPE	QTRANSP...	.SSTSANSPT	SR.....	E	
808			00BW1686_8	FFRENLAFFQ	G.EAREFPSE	Q.....	...ARASPT	SR.....	E	
809			00BW1759_3	FFRENLAFFQ	.GEAREFPSEQTRANSPT	TR.....	E	
810			00BW1773_2	FFRENLAFFQ	G.EAREFPSE	QTRAN.....SPT	SR.....	E	

811	00BW1783_5	FFRENLAFFE	GGEAREFPPE	QTSRE.....	..QTRANSPT	SR.....E
812	00BW1795_6	FFRENLAFFQ	G.EAREFPSE	QT.....RANSPT	SR.....E
813	00BW1811_3	FFRENLAFFQ	G.EAREFPSE	QARANSPT..ANSPT	SR.....E
814	00BW1859_5	FFRENLAFFQ	G.KAREFSPE	QA.....RANSPT	SR.....E
815	00BW1880_2	FFRENLAFFQ	G.EAREFPPE	QT.....RADSPT	SR.....E
816	00BW1921_1	FFRENLAFFQ	G.EAREFPSE	Q.....ARANSST	SR.....E
817	00BW2036_1	FFRENLAFFQ	G.KAREFPSE	QNSP.....	..TRANSPT	SR.....E
818	00BW2063_6	FFRENLAFFQ	G.EAREFPSE	QT.....RANSPT	SR.....K
819	00BW2087_2	FFRENLAFFQ	GGEAREFPSEQTRANSPT	SR.....A
820	00BW2127_2	FFGENLAFFQ	G.EAREFPPE	QARTNSP...	..QAGAISPT	SR.....E
821	00BW2128_3	FFRENLAFFQ	.GEAREFPSE	QTRTNSPTSR	.EQTRANSPT	SG.....E
822	00BW2276_7	FFRETLAFFQ	G.KARELPSE	QDRANSPT..ANSPT	GR.....Q
823	00BW3819_3	FFRENLAFFQ	G.EAREFPPE	QARTNSP...NSPT	SR.....E
824	00BW3842_8	FFREDLAFFR	R.KAREFPSE	QNRAN.....	.SPTRANSPT	SR.....E
825	00BW3871_3	FFRENLAFFQ	G.EAREFPSE	Q.....TRANSPT	SR.....K
826	00BW3876_9	FFRENLAFFQ	G.KAREFPSE	QA.....RANSPT	GR.....E
827	00BW3886_8	FFRENLAFFQ	G.EAREFPSE	QTRANSPT..SRANSPT	SR.....E
828	00BW3891_6	FFRENLAFFQ	G.EAREFSSEQ....ARANSPT	SR.....E
829	00BW3970_2	FFREILAFPE	G.EAREFPSE	Q.....IRANSPT	SR.....E
830	00BW5031_1	FFRENLAFFQ	G.EARELPPE	Q...TRTNS.	..PTNANSPT	SR.....E
831	96BW01B21	FFRENLAFFQ	G.KAREFPSE	Q.....TR.AISPT	SR.....E
832	96BW0407	FFRENLAFFQ	G.EAREFPSE	Q.....TRANSPT	SR.....E
833	96BW0502	FFRENLAFFQ	G.EAREFPPE	QIRASSPNS.TNSPT	SR.....E
834	96BW06_J4	FFRENLAFFQ	RGEAREFPSEQARANSPT	SR.....E
835	96BW11_06	FFRENLAFFQ	G.EAREFPSEQTGANSPT	SR.....E
836	96BW1210	FFRENLAFFQ	G.EAREFPSE	QTRAIS....PT	SR.....E
837	96BW15B03	FFREDLAFFQ	G.KAREFPSE	QN.....RANSPT	SR.....E
838	96BW16_26	FFRENLAFFQ	.GEAREFPSEQTRANSPT	SG.....E
839	96BW17A09	FFRENLAFFQ	GGEAREFPSE	Q.....ARANSPT	SR.....E
840	96BWM01_5	FFRENLAFFQ	G.EAREFPSE	QT.....RANSPT	SR.....N
841	96BWM03_2	FFRENLAFFQ	G.EAREFPPE	QT.....RANSPT	SR.....A
842	98BWMC12_2	FFRETLAFFQ	G.EAREFSSE	QG.....RANSPT	SR.....E
843	98BWMC13_4	FFRENLAFFQ	G.EAREFPSE	QT.....RANSPT	SR.....K
844	98BWMC14_a	FFRENLAFFQ	G.EARELPSE	Q.....TRTISPT	SR.....E
845	98BWM014_1	FFRENLAFFQ	RGEAREFPSEKTRANSPT	SR.....E
846	98BWM018_d	FFRENLAFFQ	G.EAGKFHSE	QTSANSP...	..TSRANSPT	SR.....E
847	98BWM036_a	FFRENLAFFQ	G.EAREFPPE	QTRANSPT...	..TSRANSPT	GR.....E
848	98BWM037_d	FFRENLAFFQ	G.EAREFPSE	K.....TRANSPT	GR.....E
849	99BW3932_1	FFRENLAFFQ	G.EAREFPPE	QDSANSPTSR	ELQDRANSPT	SR.....E
850	99BW4642_4	FFRENLAFFQ	G.EAREFLPE	QD.....RANSPT	SR.....E
851	99BW4745_8	FFRENLAFFQ	G.EAREFPSE	QTRANSPT...	..TRANSPT	SR.....E
852	99BW4754_7	FFRKNLAFFQ	G.EAREFPSE	QT.....RANSPT	SR.....E
853	99BWMC16_8	FFREDLAFFQ	R.EAREFPSE	Q.TRANS...	..PTRANSPT	SR.....E
854	A2_CD_97CD	FFRENLAFFQ	R.EAREFSSEQDRANSPT	N.....
855	A2_CY_94CY	FFRENLAFFQ	R.EARKFSSEQNRANSPT	SR.....E
856	A2D_97KR	FFRENLAFFQ	R.EAREFSSEQNRTRANSPT	SR.....G
857	A2G_CD_97C	FFRENLAFFQ	R.EAREFS..	SEQDRANSPT	RR.....E
858	A_BY_97BL0	FFRKNLAFFQ	R.EARKFSSEQTRAISPT	S.....RK
859	A_KE_Q23_A	FFRENLAFFQ	G.EAREFSSEQTGTNSST	S.....RD
860	A_SE_SE659	FFRENLAFFQ	R.EARKFSSEQTRANSPT	S.....RD
861	A_SE_SE725	FFRENVAFFQ	G.EARKFSSEQTGANSPT	S.....RA
862	A_SE_SE753	FFRENLAFFQ	G.EAGKFSSEQTGANSPT	S.....RD
863	A_SE_SE853	FFRENLAFFQ	R.EARKFSSEQTRANSPT	S.....RD
864	A_SE_SE889	FFRENLAFFQ	G.EARKFSSEQTGANSPT	S.....RD
865	A_SE_UGSE8	FFRENLAFFQ	G.EAGKFSSEQTGAISPT	S.....RD
866	A_UG_92UG0	FFRENLAFFQ	R.EARKFSSEQTRTNSPT	SS.....RD
867	A_UG_U455_	FFRENLAFFQ	G.EAREFSSEQTRANSPT	SR.....N.
868	AC_IN_2130	FFRENLAFFQ	G.EAREFPSEQTRANSPA	SR.....E
869	AC_RW_92RW	FFRENLAFFQ	G.EARKFSPE	Q.....	..TGANSPT	SR.....E
870	AC_SE_SE94	FFRENLAFFQ	G.EARKFSSEQTGANSPT	S.....RD
871	ACD_SE_SE8	FFREDMAFFQ	G.KAREFPSEQTRTNSPT	S.....RE

872	ACG_BE_VI1	FFRENLAFAQQ	G.EARKFSSEQTRANSPT	SRANSPTSRE
873	AD_SE_SE69	FFRENLAFAQQ	G.KAREFPSEQTRANSPT	SR.....E
874	AD_SE_SE71	FSRENLAFAQQ	G.EARKFSSEQTGTNSST	SR.....N.
875	ADHK_NO_97	FFRENLAFAQQ	R.KARELSSEQTGAISPT	SR.....E
876	ADK_CD_MAL	FFRENLAFAQQ	G.KAREFPSEQTRANSPT	SR.....E
877	AG_BE_VI11	FFRENLAFAQQ	G.EARKFSSEQTGANSPT	S.....RE
878	AG_NG_92NG	FFRENLAFAQQ	G.EAREFS..	SEQARANSPT	RR.....E
879	AGHU_GA_VI	FFRENLAFAQQ	G.EAREFS..	PEQTRANSPT	SR.....E
880	AGU_CD_Z32	FFRENLAFAQQ	G.EAREFSSEQTRANSPT	RR.....E
881	AJ_BW_BW21	FFRENLAFAQQ	G.KAREFSPEQTRANSPT	SR.....E
882	B_AU_VH_AF	FFREDLALPQ	G.KARELSSEQTRANSPT	RR.....E
883	B_CN_RL42	FFREDLAFPQ	G.KARELSSEQTRANSPT	RG.....E
884	B_DE_D31_U	FFREDLAFPQ	G.KAREFSSEQTRANSPT	RR.....E
885	B_DE_HAN_U	FFREDLAFPQ	G.EARKFSSEQTRANSPT	RR.....E
886	B_FR_HXB2	FFREDLAFPQ	G.KAREFSSEQTRANSPT	RR.....E
887	B_GA_OYI	FFREDLAFPQ	G.KAREFSSEQTRANSPT	SR.....E
888	B_GB_CAM1	FFRENLAFAQQ	G.EAREFSSEQTRANSPT	RR.....E
889	B_GB_GB8_A	FFREDLAFPQ	G.KAREFSPE	QTRANS....	..PTRADSPT	RR.....E
890	B_GB_MANC	FFREDLALPQ	G.KAREFSSEQTRANSPT	RG.....E
891	B_KR_WK_AF	FFREDLAFPQ	G.KAREFPSEQTRAISPA	RR.....E
892	B_NL_3202A	FFREDLAFPQ	G.KAREFSSEQTRANSPT	RR.....E
893	B_TW_TWCYS	FFRENLAFAQQ	G.KARKFSSEQTRANSPT	RG.....E
894	B_US_BC_L0	FFREDLAFPQ	G.KAREFSSEQTRANSST	RR.....E
895	B_US_DH123	FFRENLAFAQQ	G.KAREFSSEQTRAISPT	RR.....E
896	B_US_JRCSF	FFREDLAFPQ	G.KAREFPSEQTRANSPT	RR.....E
897	B_US_MNCG	FFREDLAFPQ	G.KAREFSSEQTRANSPT	RR.....E
898	B_US_P896	FFRENLAFAQQ	G.KAREFSSEQTRANSPT	RR.....E
899	B_US_RF_M1	FFRENLAFAQQ	G.KARELSSEQTRANSPT	RR.....E
900	B_US_SF2_K	FFREDLAFPQ	G.KAREFSSEQTRANSPT	RR.....E
901	B_US_WEAU1	FFREDLVFPK	G.KAREFSSEQTRTNSPT	RR.....E
902	B_US_WR27	FFREXPAFPH	X.KARXFPSEQTRAISPT	SR.....E
903	B_US_YU2_M	FFREDLAFPQ	G.KARKFSSEQTRANSPI	RR.....E
904	BF1_BR_93B	FFRENLAFAQQ	G.KAREFPSEQTRANSPT	SR.....E
905	C_BR_92BR0	FFRENLAFAQQ	.GEARKSSSEQNRANSPT	RR.....E
906	C_BW_96BW0	FFRENLAFAQQ	G.EAREFPSE	Q.....	..TRANSPT	SR.....E
907	C_BW_96BW1	FFRENLAFAQQ	G.EAREFPSEQTGANSPT	SR.....K
908	C_BW_96BW1	FFRENLAFAQQ	G.EAREFPSE	QTRAIS....PT	SR.....E
909	C_BW_96BW1	FFREDLAFPQ	G.KAREFPSE	QN.....	..RANSPT	SR.....E
910	C_ET_ETH22	FFRETLAFPQ	G.KAREFPSE	QTRANSPTRE	S.QTRANSPT	TR.....E
911	C_IN_93IN1	FFRENLAFAQQ	G.EAREFPPEQTGANSPT	SR.....E
912	C_IN_93IN9	FFRENLAFAQQ	G.EAREFPPEQTRADSPT	SR.....E
913	C_IN_93IN9	FFRENLAFAQQ	G.EAREFPSE	QTRANSPTS	..QTRANSPT	SR.....E
914	C_IN_94IN1	FFRENLAFAQQ	G.EAREFPPEQTRANSPT	SR.....E
915	C_IN_95IN2	FFRENLAFAQQ	G.EAREFPPEETRANSST	SR.....E
916	CRF01_AE_C	FFRENLAFAQQ	G.EAREFSSEQTRANSPT	SR.....E
917	CRF01_AE_C	FFRENLAFAQQ	G.EARKFPSEQTRANSPT	NG.....E
918	CRF01_AE_C	FFRENLAFAQQ	G.EAREFSSEQTRANSPT	SR.....E
919	CRF01_AE_T	FFREILAFPQ	G.KAGKFSSEQTRANSPT	SR.....K
920	CRF01_AE_T	FFRENLAFAQQ	R.KAGEFSSEQTRANSPT	SR.....K
921	CRF01_AE_T	FFRENLAFAQQ	G.KAREFSSEQTGANSSA	SR.....K
922	CRF01_AE_T	FFRENLAFAQQ	G.KAGKFSSEQTRANSPT	SR.....E
923	CRF01_AE_T	FFRENLAFAQQ	G.KAGEFSSEQTRANSPT	SR.....K
924	CRF01_AE_T	FFRENLAFAQQ	G.KAGKFSSEQTRTNSPT	SR.....K
925	CRF02_AG_F	FFRENLAFAQQ	G.EARKFSSKQTGTNSPT	S.....RE
926	CRF02_AG_F	FFRENLAFAQQ	G.EARKFSSKQTGTNSPT	S.....RE
927	CRF02_AG_G	FFRENLAFAQQ	R.EARELSSEQTGAISPT	G.....RE
928	CRF02_AG_N	FFRENLAFAQQ	G.EARKFSSEQTGTNSST	S.....RE
929	CRF02_AG_S	FFRENLAFAQQ	G.EARKFSSEQTGTNSPT	S.....RE
930	CRF02_AG_S	FFRENLAFAQQ	G.EARKLSSEQTGTNSPT	S.....RE
931	CRF03_AB_R	FFRENLAFAQQ	R.EARKFSSEQTRAISPT	S.....RK
932	CRF03_AB_R	FFRENLAFAQQ	R.EARKFSSEQTRAISPT	S.....RK

933	CRF04_cpx_	FFRENVAFQQ	R.EARKFSSEQARANSPA	RG.....M
934	CRF04_cpx_	FFRENVAFQQ	R.KAGEFSSEQARANSPT	RR.....E
935	CRF04_cpx_	FFRENVAFQQ	G.EARKFSSEQDRANSPA	RR.....E
936	CRF05_DF_B	FFRESLAFQ	G.EARELPPEQTGALSPA	SR.....E
937	CRF05_DF_B	FFRESLAFQ	G.KAREFPPEQARTLSPT	SR.....E
938	CRF06_cpx_	FFRENLAFFQ	G.EAREFS..	SEQARANSPT	HR.....E
939	CRF06_cpx_	FFREDLAFQ	G.EARKFS..	SEQARANSPT	RG.....E
940	CRF06_cpx_	FFRENLAFFQ	G.EAGELS..	SEQARANSPT	RR.....E
941	CRF06_cpx_	FFRENLAFFQ	G.EAREFSPE	QAR.....	TEQARTLSPT	CR.....E
942	CRF11_cpx_	FFRENLAFFQ	R.KARELSPEQTRANSPT	SR.....E
943	CRF11_cpx_	FFRENLAFFQ	G.EAREFPTEQARANSPT	SR.....E
944	D_CD_84ZR0	FFRENLAFFQ	G.KAGELSSEQTRANSPT	S.....R
945	D_CD_ELI_K	FFRENLAFFQ	G.KAGELSPKQTRANSPT	SR.....E
946	D_CD_NDK_M	FFREDLAFQ	G.KAGEFSSEQTRANSPT	SR.....E
947	D_UG_94UG1	FFRENLAFFQ	W.KAREFPSE	QT.....	..PSRANSPT	SR.....D
948	F1_BE_VI85	FFRENLAFFQ	G.EARKFPSEQTRANSPT	SR.....E
949	F1_BR_93BR	FFRENLAFFQ	G.EARKLHPEQARAVSPA	SR.....E
950	F1_FI_FIN9	FFRENLAFFQ	G.EARKFPS.ETRANSPA	SR.....E
951	F1_FR_MP41	FFRENLAFFQ	G.EARKFSSEQARANSPA	SG.....E
952	F2_CM_MP25	FFRENVAFQQ	G.EARKFSSEQTRANSPT	SR.....E
953	F2KU_BE_VI	FFRENLAFFQ	R.EAGKFSSEQTRANSPT	SR.....E
954	G_BE_DRCBL	FFRENLAFFQ	G.EAREFP..	SEQARANSPT	RR.....E
955	G_NG_92NG0	FFRENLAFFQ	G.EARKLS..	PEQDRANSPT	SR.....E
956	G_SE_SE616	FFRENLAFFQ	G.EAREFS..	SEQDRTNSPT	CR.....K
957	H_BE_VI991	FFRENLAFFQ	G.KAREFP..	PEEARANSPT	SR.....E
958	H_BE_VI997	FFRENLAFFQ	R.EARKFS..	PEQARANSPT	SR.....E
959	H_CF_90CF0	FFRENLAFFQ	R.EARKFS..	PEQARTNSPT	SR.....E
960	J_SE_SE702	FFREDLAFQ	R.EAREFSPEQTRANSPT	SR.....E
961	J_SE_SE788	FFREDLAFQ	R.EARELSPEQTRANSPT	SR.....E
962	K_CD_EQTB1	FFREVLASQ	R.EARKFSSEQTRANSPT	SR.....E
963	K_CM_MP535	FFRENLAFFQ	G.EAREFSSEQTRANSPT	SR.....E
964	N_CM_YBF30	FFREELVSLQ	R.ETRKLPD	NN.....	..KERAHSPA	TR.....E
965	O_CM_ANT70	FFRQILASGG	H.EARQLCAE	T.....	..STPISPT	DG.....G
966	O_CM_MVP51	FFREVLASGG	H.EARQLCAE	T.....	..SVPIST	NG.....G
967	O_SN_99SE	FFREILASGG	H.EARQLCAE	T.....	..SVPIST	DD.....G
968	O_SN_99SE	FFREILASGG	H.EARQLCTE	T.....	..SVPIST	DD.....G
969	U_CD___83C	FFRENLAFFQ	G.EAREFSSEQTRANSPT	SR.....E

	51			100	
00BW0762_1	LQVR.....GDK.PHSEAG	AERQ.....	GTLNFPQITL
00BW0768_2	LQVRG.....DNN.PCSEAG	AERQ.....	GTLNCPQITL
00BW0874_2	QPARAISPTS	REPQVRRDN.SRFEAG	VEREG.....	.TLNFPQITL
00BW1471_2	LQVR.....GDN.PRSEAG	AERQG.....	.TLNLPQITL
00BW1616_2	LQVR.....GNN.PLSEAG	GERQ.....	GTLNFPQITL
00BW1686_8	LQVR.....GDN.PRSEAG	AERQ.....	GTLNLPQITL
00BW1759_3	LQVRG.....NN.PRSEAG	AERQ.....	GTLNFPQITL
00BW1773_2	LQVR.....GDN.PRSEAG	AERQ.....	GTLNFPQITL
00BW1783_5	LQVR.....GDN.PCSEAG	DERQ.....	GTLNFPQITL
00BW1795_6	LQVR.....GDN.PLSEAG	AERQ.....	GTLNFPQITL
00BW1811_3	LQVR.....GDN.PRFEAG	EKRQG.....	.NLNFPQITL
00BW1859_5	LQVR.....GDD.PRSEAG	AERQ.....	GTLNFPQITL
00BW1880_2	LQVR.....GDN.PRSEAG	AEGQ.....	GTLNFPQITL
00BW1921_1	LQVR.....GDN.PCSEAG	AERQG.....	.TLNFPQITL
00BW2036_1	LQVR.....GDN.PRSEAG	AERQ.....	GTLNFPQITL
00BW2063_6	L..R.....GDN.PCSEAG	DERQ.....	GTLNFPQITP
00BW2087_2	NSPTSREL..	...QVRGDN.PSIKAG	PERQ.....	GALNFPQITL
00BW2127_2	LQVR.....GDN.PRSEAG	AERQG.....	.SLNFPQITL
00BW2128_3	LQVR.....GDN.TRSEAG	AKKQ.....	GTLNFPQITL
00BW2276_7	LQVR.....GDN.PRAEAG	AERQG.....	.TLNFPQITL
00BW3819_3	LQVR.....GDN.PRSEAG	DERQG.....	.ALNFPQITL
00BW3842_8	LQVR.....GDN.PRSEAG	AERQGT..LQ	GTLNFPQITL

00BW3871_3	LQVR.....GDN.PRSEAG	ADRQ.....	GTLNFPQITL
00BW3876_9	LQVR.....GDN.PHSEAG	AERQ.....	GTLNFPQITL
00BW3886_8	LQVR.....GDN.PRSEAG	AERQG.....	.SLNFPQITL
00BW3891_6	LQVR.....GDN.PRSEAG	AERQG.....	.TLNFPQITL
00BW3970_2	LQVR.....GDN.PRSETG	AEGQG.....	.TFNFPQITL
00BW5031_1	LQVR.....GDN.PRSEAG	DEREG.....	.TLNFPQITL
96BW01B21	LQVR.....GDN.PRSEAG	AEGQG.....	.ALNLPQITL
96BW0407	LQVR.....GDN.PRSETR	VEGQG.....	.NFNFPQITL
96BW0502	LQVR.....GDN.PRSEAG	AEGQGT..LQ	GTLNCPQITL
96BW06_J4	LQIR.....GDN.PRFEAG	TKRQ.....	GTLNFPQITL
96BW11_06	LRG.....NN.PCSEAG	DERQ.....	GTLNFPQITL
96BW1210	LQVR.....GDN.PCSEAG	AEGQG.....	TTFSFPQITL
96BW15B03	LQVR.....GDN.PRSEAG	AERQ.....	GTLNFPQITL
96BW16_26	LQVW.....GDN.PRSETG	AKGQ.....	GTFNFPQITL
96BW17A09	LQVR.....GDN.PRSEAG	AERQG.....	.TLNFLQITL
96BWM01_5	L..R.....GDN.PCSEAG	DERQGT..LQ	GALNFPQITL
96BWM03_2	LQAR.....TNSP.TSREAG	VEGQG.....	.TLNFPQITL
98BWMC12_2	P.....	...QARGDN.TRFEAG	DEGQG.....	.TLNFPQITL
98BWMC13_4	P..R.....GDN.PCSEAG	AERQ.....	GTLNLPQITL
98BWMC14_a	LQVR.....GDN.PRSEAG	AEGQ.....	GTLNFPQITL
98BWM014_1	LQVREQTR..	...ANSSTS.RELQAG	AKRQ.....	GALNCPQITL
98BWM018_d	LQVR.....GDN.PCSEAG	AERQGS....	.TLNFPQITL
98BWM036_a	LQVR.....GDK.PRSEAG	AEGQG.....	.TLNFPQITL
98BWM037_d	LQVR.....GDN.PRSEAG	GERQG.....	.TLKFPQITL
99BW3932_1	FQVR.....GDN.PCSEAG	AERQG.....	.SLNFPQITL
99BW4642_4	LQIR.....GDD.PRSEAG	AERQ.....	RTLNFPQITL
99BW4745_8	LQVR.....GGN.PHSEAG	AERQG.....	.TLNFPQITL
99BW4754_7	LQVR.....GDN.PHSEAR	VKGQ.....	GTPNFPQITL
99BWMC16_8	LQVR.....GDK.SRSEAG	VEKQG.....	.NLNFPQITL
A2_CD_97CD	...GGR....DN.LLAEAG	E..QG...AV	HPCNFPQITL
A2_CY_94CY	LENGGR....DN.LLPEAG	TGDQG...TI	QSCNFPQITL
A2D_97KR	LWNGGG....DN.PLAEAG	AEKQG...TT	HSCNFPQITL
A2G_CD_97C	PRVRR....GDS.LLPEAG	DEG...KGAV	YPCNFPQITL
A_BY_97BL0	LD.GGR....DN.PLPETG	TERQG...TV	SSFNFPQITL
A_KE_Q23_A	LWDGGR....DS.LPSEAG	AERQGT..G.	PTLSFPQITL
A_SE_SE659	PWDRRR....DS.LPSETG	ADP.....	.TFNFPQITL
A_SE_SE725	FWDGGR....DS.LPSEAG	AERQGT..E.	LTFSFPQITL
A_SE_SE753	LWNEGR....DS.LPSEAG	AEG..T..R.	PTFSFPQITL
A_SE_SE853	LWDGGS....DN.LPSEAG	AERQGT..G.	PTLSFPQITL
A_SE_SE889	LWDGGR....DN.LPSEAG	EERQGV..GG	TTLNFPQITL
A_SE_UGSE8	..DGGR....DS.LPSEAG	AKQP.....	.TFNFPQITL
A_UG_92UG0	LWDEGR....DS.LPSEAG	AERQGP..E.	PTFSFPQITL
A_UG_U455_	LWDGGK....DD.LPCETG	AERQ...GT	DSFSFPQITL
AC_IN_2130	LQIR.....GDN.PRTEAG	AKRQG.....	.TLNFPQITL
AC_RW_92RW	LWNGG....RDS.LSSETG	AERQG.....	.TFNFPQITL
AC_SE_SE94	LRDGGR....D..NSEAG	TDRQGT..G.	PAFSFPQITL
ACD_SE_SE8	LRVWRR....DN.PLPEAG	AERQ...GT	VSFSFPQITL
ACG_BE_VI1	LWEGGR....DR.LLPEAG	TEGQG...TI	SSFNFPQITL
AD_SE_SE69	LRVWRG....DS.TFSETG	AER...QGA	VSFSFPQITL
AD_SE_SE71	LWDGGR....DS.LPSEAG	AEKQG...TG	STLNFPQITL
ADHK_NO_97	LWDRGR....DN.LLSEAG	TEGQG...TA	PSLSFPQITL
ADK_CD_MAL	LRVWGG....DK..TLSETG	AERQ...GI	VSFSFPQITL
AG_BE_VI11	LGDGGR....DN.PLSEAG	TEGHG...TI	SSLNFPQITL
AG_NG_92NG	LRVRR....GDS.PFPEAG	AEG...KGIT	SIN.LPQITL
AGHU_GA_VI	LRVRR....GDS.PLPEAG	AKG...KGA	VSNLFPQITL
AGU_CD_Z32	LRDER....GDN.LLSEAG	TEGQG...TI	PSFSFPQITL
AJ_BW_BW21	LRVWR....GDS.PLPEAG	GEGQ...GT	VSNFPQITL
B_AU_VH_AF	LQVWGR....DNN.SLSEAG	ADR...QGT	VSFSFPQITL
B_CN_RL42	LQVWGR....DNN.SISEAG	ADR...QGT	ISFSFPQITL
B_DE_D31_U	LQVWGR....DSN.SLSEAG	ADR...QGT	VSFSFPQITL
B_DE_HAN_U	LQVWG.....SNS.SLSEAG	ADR...QGT	VSLSLPQITL

B_FR_HXB2_	LQVWGR....DNN.SPSEAG	ADR....QGT	VSFNFPQVTL
B_GA_OYI_	LRVWGR....DNN.SPSEAG	ADR....QGT	VSFNLPQITL
B_GB_CAM1_	LQVWGR....ENN.SLSEAG	ADR....QGT	VSFSFPQITL
B_GB_GB8_A	LQVRGR....DNN.SLTETG	ADK....QGT	VSFSFPQITL
B_GB_MANC_	LQVWGR....DNN.SCSEAG	TDR....QGT	VSLSFPQTTL
B_KR_WK_AF	LQVWGR....DNN.SLSEAG	ANR....QGT	VSFSFPQITL
B_NL_3202A	LQVWGR....DNN.SLSEAG	AEG....QGT	VSLSLPQITL
B_TW_TWCYS	LQVWGT....DNN.SLSEAG	ADR....QGP	VSFSFPQITL
B_US_BC_L0	LQVWGG....DNN.SPSEAG	AGR....QGN	VSLSFPQITL
B_US_DH123	LQVWGG....DSN.SLSEAG	AEG.....T	ISLSLPQITL
B_US_JRCSF	LQVWGR....DSN.SLSEAG	AEAGADRQGI	VSFNFPQITL
B_US_MNCG_	LQVWGR....DNN.SLSEAG	EEAGDDRQGP	VSFSFPQITL
B_US_P896_	LQVWGG....DNN.SLSEAG	ADR....QGT	VSLSFPQITL
B_US_RF_M1	LQVWGR....DN.SLSEAG	EDR....QGT	VSFSFPQITL
B_US_SF2_K	LQVWGG....ENN.SLSEAG	ADR....QGT	VSFNFPQITL
B_US_WEAU1	LQVQGR....DNN.SLSEAG	ANR....QGA	VSFNFPQITL
B_US_WR27_	LQVWXR....DNN.SLSEAG	TDR....QGT	VSFSFPQITL
B_US_YU2_M	RQVWRR....DNN.SLSEAG	ADR....QGT	VSFSFPQITL
BF1_BR_93B	LQVWGR....GNN.SLSETG	ADR....QGD	VSFGFPQITL
C_BR_92BR0	LQVWGR....DNN.SLSEAG	DDRQG....	TALNFPQITL
C_BW_96BW0	LQVR.....GDN.PRSETR	AEGQG....	.TLNFPQITL
C_BW_96BW1	LRG.....NN.PCSEAG	DERQ.....	GTLNFPQITL
C_BW_96BW1	LQVR.....GDN.PCSEAG	AEGQG....	TTFSFPQITL
C_BW_96BW1	LQVR.....GDN.PRSEAG	AERQ.....	GTLNFPQITL
C_ET_ETH22	LQVR.....GSN.TFSEAG	AERQG....	.SLNFPQITL
C_IN_93IN1	LQVR.....GDN.PSSKAG	AERQG....	.TLNFPQITL
C_IN_93IN9	LQVR.....GDT.PSSKAG	AERQG....	.TLNFPQITL
C_IN_93IN9	LQVR.....GDN.PRSEAG	AKRQG....	.TLNFPQITL
C_IN_94IN1	LQVR.....GDT.PSSKAG	AEREG....	.TLNFPQITL
C_IN_95IN2	LQVR.....GDN.PSSEAG	AERQG....	.TFNFPQITL
CRF01_AE_C	LGDGGR....DN.LLPEAG	AERQG...TP	FSFSFPQITF
CRF01_AE_C	LGDGGR....DN.LLPEAG	AERQE...TA	SSFSFPQITL
CRF01_AE_C	LRDGGR....DN.LLLEAG	AERQG...TS	SSLSFPQITL
CRF01_AE_T	LGDGGR....DN.LLTEAG	AERQG...TS	SSFSFPQITL
CRF01_AE_T	MGDGGR....DN.LLTEAG	AERQ...GS	SSFSFPQITL
CRF01_AE_T	LGDGG....G	AERQG...TS	SSFSFPQITL
CRF01_AE_T	LGDGGR....DN.LLAETG	AERQG...TP	SSFNFPQITL
CRF01_AE_T	LGDGGR....DNG	GRDNLLEAG	AERQG...TS	SSFSFPQITL
CRF01_AE_T	LGDGGR....DN.LLPEAG	AERQG...TP	SSFSFPQITL
CRF02_AG_F	LGDGGR....DN.LPSEAG	SEGP...TI	SSLSFPQITL
CRF02_AG_F	LWDGGR....DN.LPSEAG	TEGP...TI	SPSSFPQITL
CRF02_AG_G	LWDKGR....NN.LLSAAG	TEGQG...TI	SSFNFPQITL
CRF02_AG_N	LWDGGR....DT.SLSTAG	TEGQG...AI	SSFNFPQITL
CRF02_AG_S	PWDRGR....DN.LLSEAG	TGGQG...TI	SSLSFPQITL
CRF02_AG_S	LWDGGR....DN.LLPEAG	TGGQG...TI	PSFNFPQITL
CRF03_AB_R	LWDGGR....DN.PLPETG	TEGQG...TA	SSFNFPQITL
CRF03_AB_R	LWDGGR....DN.PLPETG	TERQG...TA	SSFNLPQITL
CRF04_cpx_	LREERG....DN.LLSEAG	TEGQ...GT	ISFNFPQITL
CRF04_cpx_	LRDERG....DN.LLSEAG	TEGQ...GT	ISFNFPQITL
CRF04_cpx_	LRDERG....DN.LLSEAG	TEGQ...GT	ISHNFPQITL
CRF05_DF_B	LQVWGG....DS.LLSEAG	AEG...RGTV	PSLSFPQITL
CRF05_DF_B	LRVWRG....DN.PLAEAG	AEG...RGEV	PSLSFPQITF
CRF06_cpx_	LRFR....GDS.PLPETG	VEGEGGKGAI	SLS.LPQITL
CRF06_cpx_	LRVRR....GDS.PLPGAE	AEG...KGAI	SLN.FPQITL
CRF06_cpx_	LRVRR....GDS.PLPEAG	TEGKG.KGAI	SLS.FPQITL
CRF06_cpx_	LRVRG....GNS.PLPEAG	AEG...EGAI	SLS.FPQITL
CRF11_cpx_	LRVRR....GDS.PLPETG	AEGEGE..GA	ISFNLPQITL
CRF11_cpx_	LRVRG....GDN.PLPETG	AQGE....GT	ISYNFPQITL
D_CD_84ZR0	LRVWGG....DN.PLPETG	TEG..QRQGT	VSLSFPQITL
D_CD_ELI_K	LRVWGR....DN.PLSKTG	AE....RQGT	VSFNFPQITL
D_CD_NDK_M	LRVWGG....DN.PLSETG	AE....RQGT	VSFSFPQITL

D_UG_94UG1	LRIRGG....DN..TSSETG	AER....QGT	VSFNLPQITL
F1_BE_VI85	LRVQRG....DN..PLSEAG	AERR...GTV	PSLSFPQITL
F1_BR_93BR	LQVRGG....DN..PISEAG	AERR...GTV	PSLSFPQITL
F1_FI_FIN9	PRDQRR....GN..SLSEAG	AERR...GTV	PSLSFPQITL
F1_FR_MP41	LRVQRG....NN..PLSEAG	AEGRGT.GTV	SSLSLPQITF
F2_CM_MP25	LRVRGG....DS..SLPEAG	AERQG...TG	SSLDFFPQITL
F2KU_BE_VI	LRVWGG....DK..PLSEAG	DERQG...TG	ASFNLPQITL
G_BE_DRCBL	LRVRG....GDS.PLPEAG	AEG...KGTI	S.SIFPQITL
G_NG_92NG0	LRIRR....GDS.PLPEAG	AKG...EGAI	SLN.FPQITL
G_SE_SE616	PRVRR....GDS.PLPEAG	DEG...KGAI	S...LPQITL
H_BE_VI991	LRVRR....GDH.PLSEAG	AE.....RTG	TSFNFPQITL
H_BE_VI997	LRVRG....GDD.LLPEAG	AE.....GQG	TSLCFPQITL
H_CF_90CF0	LRVRR....GDD.PLSEAG	AAE.....GQG	TSLSFPQITL
J_SE_SE702	PRVRR....GD..PLPETG	AEGQ....GT	VSSNFPQITL
J_SE_SE788	PRARR....GD..PLPETG	AEGQ....GT	VSSNFPQITL
K_CD_EQTB1	LWVRGE....DN..PLSETG	NERSG...TG	SSFNFPQITL
K_CM_MP535	LRVRGG....DN..PLSEAG	DQRQG...TE	PSFNFPQITL
N_CM_YBF30	LWVSG....GEEH	TGEGDAGEPG	EDRE...LSV	PTFNFPQITL
O_CM_ANT70	GSEGTG....ESG.TERG	PER.....A	LSVCLPQIPL
O_CM_MVP51	GSEGTR....ESE.SEGG	SGR.....A	VPICLPQIPL
O_SN_99SE_	GNEGTR....ESG.TEGG	PER.....T	LSVCLPQIPL
O_SN_99SE_	GNEGTR....KSG.TEGG	PER.....T	LSVCLPQIPL
U_CD___83C	LRVRR....GDN.PLAEAG	AEGQG..VPL	PSFNFPQITL

101

00BW0762_1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
00BW0768_2	WQRPLVSIRV	GGQIKEALLD	TGADDTVLEE	ISLPGKWKPK	MIGGIGGFIK
00BW0874_2	WQRPLVSIKI	EGQIREALLD	TGADDTVLEE	ITLSGRWKPK	MIGGIGGFIK
00BW1471_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
00BW1616_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW1686_8	WQRPLVTIKV	GGQVKEALLD	TGADDTVLEE	ISLPGKWKPK	MIGGIGGFIK
00BW1759_3	WQRPLVSIKV	GGQVKEALLD	TGADDTVLEE	LALPGRWKPK	MIGGIGGFIK
00BW1773_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW1783_5	WQRPLVTIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
00BW1795_6	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
00BW1811_3	WQRPLVTIKV	GGQTKAALLD	TGADDTVLEE	MNLPGKWKPK	MIGGIGGFIK
00BW1859_5	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	ISLPGKWKPK	MIGGIGGFIK
00BW1880_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW1921_1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW2036_1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	MSLPGKWKPK	MIGGIGGFIK
00BW2063_6	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLLGKWKPK	MIGGIGGFIK
00BW2087_2	WQRPLVSIKI	EGQIKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
00BW2127_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW2128_3	WQRPLVSIKI	GDQVKEALLD	TGADDTVLEE	IKLPGKWKPK	MIGGIGGFIK
00BW2276_7	WQRPLVSIKV	GGQIREALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW3819_3	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLSGKWKPK	MIGGIGGFIK
00BW3842_8	WQRPLVTIKV	GGQIKEALLD	TGADDTVLEE	MNMPGKWKPK	MIGGIGGFIK
00BW3871_3	WQRPLVTIKV	GGQVKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW3876_9	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	ISLPGKWKPK	MIGGIGGFIK
00BW3886_8	WQRPLVSIKV	GGQIKEALLD	IGADDTVLEE	LSLPGKWKPK	MIGGIGGFIK
00BW3891_6	WQRPLVTIKV	GGQIKEALLD	TGADDTVLEE	ISLPGKWKPK	MIGGIGGFIK
00BW3970_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW5031_1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
96BW01B21	WQRPLVTIRV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
96BW0407	WQRPLVSIKV	GGQIREALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
96BW0502	WQRPLVSIKV	GGQIKEALLD	TGADNTVLEE	INLPGKWKPK	MIGGIGGFIK
96BW06_J4	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	MSLSGKWKPK	MIGGIGGFIK
96BW11_06	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWRPK	MIGGIGGFIK
96BW1210	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
96BW15B03	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	MSLPGKWKPK	MMGGIGGFIK
96BW16_26	WQRPLVSIKV	GGQVKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK

150

96BW17A09	WQRPLVSIKV	GGQIREALLD	TGADDAVLED	INLPGKWKPK	MIGGIGGFIK
96BWM01_5	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	VNLPGWKPK	MIGGIGGFIK
96BWM03_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
98BWMC12_2	WQRPLVSIKI	GGQIREALLD	TGADDTVLEE	LSLPGRWKPK	MIGGIGGFIK
98BWMC13_4	WQRPLVSIKV	GGQVKEALLD	TGADDTVLED	IELPGKWRPK	MIGGIGGFIK
98BWMC14_a	WQRPLVSIKV	GGQTKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
98BWM014_1	WQRPLVSIKI	GGQIKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
98BWM018_d	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
98BWM036_a	WQRPLVSIKV	GGQTKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
98BWM037_d	WQRPLVSIKV	GGQIREALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
99BW3932_1	WQRPLVPIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGLIK
99BW4642_4	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	ISLPGWKPK	MIGGIGGFIK
99BW4745_8	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
99BW4754_7	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
99BWMC16_8	WRRPLVTIKV	GGQIKEALLH	PGADDTVLEE	INLPRKWKPK	MIGGIGGFIK
A2_CD_97CD	WQRPLVTVKI	EGQLREALLD	TGADDTVLED	INLPWKWKPK	MIGGIGGFIK
A2_CY_94CY	WQRPLVTVKI	EGQLKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
A2D__97KR	WQRPLVTVKI	EGQLREALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A2G_CD_97C	WQRPLVTVKI	GGQLIEALLD	TGADDTVLED	INLPGRWKPK	MIGGIGGFIK
A_BY_97BL0	WQRPLVTVRI	GGQLKEALLD	TGADXTVLED	INLPGKWKPK	MIXGIXGFIK
A_KE_Q23_A	WQRPLVTVRI	GGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_SE_SE659	WQRPLVTVKV	GGQLREALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_SE_SE725	WQRPLVTVKI	GGQLREALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_SE_SE753	WQRPLVTVKI	EGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_SE_SE853	WQRPLVTVKV	GGQLKEALLD	TGADDTVLED	INLPGKWRPK	MIGGIGGFIK
A_SE_SE889	WQRPLVTVRI	GGMQKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_SE_UGSE8	WQRPIVTVRI	GGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_UG_92UG0	WQRPLVTVKI	GGQLKKALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_UG_U455_	WQRPLVTVKI	GGQLIEALLD	TGADDTVLED	INLPGKWKPK	IIGGIGGFIK
AC_IN_2130	WQRPLVSIRV	GGQTKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
AC_RW_92RW	WQRPLVTVKI	GGQLREALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
AC_SE_SE94	WQRPLVTVRI	GGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
ACD_SE_SE8	WQRPLVKVKI	GGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
ACG_BE_VI1	WQRPLVTVRL	GGQLIEALLD	TGADDTVLEQ	INLPGKWKPK	MIGGIGGFIK
AD_SE_SE69	WQRPLVTVKI	GGQLREALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
AD_SE_SE71	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
ADHK_NO_97	WQRPVVTVKV	GGQLKEALLD	TGADDTVLED	MNLPKWKPK	MIGGIGGFIK
ADK_CD_MAL	WQRPVVTVRV	GGQLKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
AG_BE_VI11	WQRPLVTVRI	GGQLIEALLD	TGADDTVLAE	ISLPKWKPK	MIGGIGGFIK
AG_NG_92NG	WQRPLVTVRI	GGQLIEALLD	TGADDTVLEQ	INLPGKWKPK	MIGGIGGFIK
AGHU_GA_VI	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEE	INLLGKWKPK	MIGGIGGFIK
AGU_CD_Z32	WQRPIVTVKI	GGQPIEALLD	TGADDTVLEE	IKLPKWKPK	MIGGIGGFIK
AJ_BW_BW21	WQRPLVTIRV	AGQVKEALLD	TGADDTVLEE	MELPGKWKPK	MIGGIGGFIK
B_AU_VH_AF	WQRPIVTIKI	GGQLKEALLD	TGADDTVLEE	MCLPGRWKPK	MIGGIGGFIK
B_CN_RL42_	WQRPLVTIKV	GGQLKEALLD	TGADDTVLED	MNLPGRWKPK	MIGGIGGFIK
B_DE_D31_U	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
B_DE_HAN_U	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
B_FR_HXB2_	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
B_GA_OYI__	WQRPIVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
B_GB_CAM1_	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
B_GB_GB8_A	WQRPIVTIKI	GGQLKEALLD	TGADDTVLED	MNLPGRWKPK	MIGGIGGFIK
B_GB_MANC_	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
B_KR_WK_AF	WQRPLVAIKI	GGQLKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
B_NL_3202A	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
B_TW_TWCYS	WQRPLVTIRI	GGQLKEALLD	TGADDTVLEE	MNLPKWKPK	MIGGIGGFIK
B_US_BC_L0	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
B_US_DH123	WQRPLVKIKI	GGQLKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
B_US_JRCSF	WQRPLVTIKI	GGQLKEALLD	TGADDTVLED	MDLPGRWKPK	MIGGIGGFIK
B_US_MNCG_	WQRPIVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
B_US_P896_	WQRPLVTIKV	GGQLKEALLD	TGADDTVLED	MSLPGRWKPK	MIGGIGGFIK
B_US_RF_M1	WQRPIVTVKI	GGQLKEALLD	TGADDTVLEE	MNLPKWKPK	MIGGIGGFIK

B_US_SF2_K	WQRPLVTIRI	GGQLKEALLD	TGADDTVLEE	MNLPGWKPK	MIGGIGGFIK
B_US_WEAU1	WQRPLVTIKI	EGQLKEALLD	TGADDTVLED	MNLPGWKPK	MIGGIGGFIK
B_US_WR27_	CQRPLVAIKI	GGQIKEALLD	TGADDTVLEE	MSLPGRWKPK	MVGIGGFIK
B_US_YU2_M	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
BF1_BR_93B	WQRPLVTVKI	GGQLKEALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIK
C_BR_92BR0	WQRPLVNIKV	GGQLKEALLD	TGADDTVLEE	IKLPGNWKPK	MIGGIGGFIK
C_BW_96BW0	WQRPLVSIKV	GGQIREALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
C_BW_96BW1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGWKPK	MIGGIGGFIK
C_BW_96BW1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
C_BW_96BW1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	MSLPGWKPK	MMGIGGFIK
C_ET_ETH22	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	INLPGWKPK	MIGGIGGFIK
C_IN_93IN1	WQRPLVSIRV	GGQIKEALLD	TGADDTVLEE	VNLPGWKPK	MIGGIGGFIK
C_IN_93IN9	WQRPLVSIRV	GGQIKETLLD	TGADDTVLEE	VNLPGWKPK	MIGGIGGFIK
C_IN_93IN9	WQRPLVSIKV	GGQIREALLD	TGADDTVLEE	VNLPGWKPK	MIGGIGGFIK
C_IN_94IN1	WQRPLVSIRV	GGQTREALLD	TGADDTVLEE	VNLPGWKPK	MIGGIGGFIK
C_IN_95IN2	WQRPLVSIRV	GGQIKEALLD	TGADDTVLEE	VSLPGWPK	MIGGIGGFIK
CRF01_AE_C	WQRPLVTVKI	EGQLKEALLD	TGADDTVLED	INLPGRWKPK	MIGGIGGFIK
CRF01_AE_C	WQRPLVTVKV	GGQLKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF01_AE_C	WQRPIVTVKI	GGQLKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF01_AE_T	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF01_AE_T	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF01_AE_T	WQRPLVTIKI	GGQLKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF01_AE_T	WQRPLVTIKI	GGELKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF01_AE_T	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF01_AE_T	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF02_AG_F	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEE	INLPGWKPK	MIGGIGGFIK
CRF02_AG_F	WQRPLVTVRI	GGQLIEALLD	TGADDTVLEE	INLPGWKPK	MIGGIGGFIK
CRF02_AG_G	WQRPLVTVRI	GGQLIEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF02_AG_N	WQRPLVTVRI	EGQLIEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF02_AG_S	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEE	INLPGWKPK	MIGGIGGFIK
CRF02_AG_S	WQRPLFTVRI	EGQLIKALLD	TGANDTVLEK	INLPGWKPK	MIGGIGGFIK
CRF03_AB_R	WRRPLVTVRI	GGQLKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF03_AB_R	WQRPLVTVRI	GGQLKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF04_cpx_	WQRPLVTIKL	GGQIREALLD	TGADDTVLEE	INLPGWKPK	MIGGIGGFIK
CRF04_cpx_	WQPPLVTIKI	GGQIREALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF04_cpx_	WQRPLVTIKI	GGQLREALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIK
CRF05_DF_B	WQRPVVTIRI	GGQLKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF05_DF_B	WQRPVVTIKI	EGQLKEALLD	TGADDTVLEE	MNLPGWKPK	MIGGIGGFIK
CRF06_cpx_	WQRPLVTVRI	GGQLIEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF06_cpx_	WQRPLVTVRI	GGQLIEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF06_cpx_	WQRPLVTVGI	EGQLIEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
CRF06_cpx_	WQRPLVTVKV	GEQLIEALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIK
CRF11_cpx_	WQRPIVKIKV	AGQLKEALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIK
CRF11_cpx_	WQRPVVPVKV	AGQLKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
D_CD_84ZR0	WQRPVVTIKI	GGQLKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
D_CD_ELI_K	WQRPLVAIKI	GGQLKEALLD	TGADDTVLEE	MNLPGWKPK	MIGGIGGFIK
D_CD_NDK_M	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	INLPGWKPK	MIGGIGGFIK
D_UG_94UG1	WQRPVVTVKI	GGQLKEALLD	TGADDTVLEE	INLPGWKPK	MIGGIGGFIK
F1_BE_VI85	WQRPLVTIKI	GGQIKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
F1_BR_93BR	WQRPLVTIRV	GGQLKEALLD	TGADDTVLED	VNLPGWKPK	MIGGIGGFIK
F1_FI_FIN9	WQRPLVTIKI	GGQLKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
F1_FR_MP41	WQRPLVTIRV	GGQLREALLD	TGADDTVLED	IDLPGWKPK	IIGGIGGFIK
F2_CM_MP25	WQRPVVTIKV	GGQLREALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
F2KU_BE_VI	WQRPIVTIKI	GGQLREALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
G_BE_DRCBL	WQRPIVKVRI	GGQLIEALLD	TGADDTVLEE	IDLPGWKPK	MIGGIGGFIK
G_NG_92NG0	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEG	INLPGWKPK	MIGGIGGFIK
G_SE_SE616	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIK
H_BE_VI991	WQRPIVTVKI	EGQLKEALLD	TGADDTVLED	INLPGWKPK	MIGGIGGFIK
H_BE_VI997	WQRPLVTVKI	EGQLREALLD	TGADDTVLEE	INLLGRWKPK	MIGGIGGFIK
H_CF_90CF0	WQRPLVTVKI	EGQLREALLD	TGADDTVLEE	INLPGWKPK	MIGGIGGFIK
J_SE_SE702	WQRPLVTIRI	GGQLREALLD	TGADDTVLEE	IDLPGWKPK	MIGGIGGFIK

J_SE_SE788	WQRPLVTIRI	GGQLREALLD	TGADDTVLED	IDLPRKWPK	MIGGIGGFIK
K_CD_EQTB1	WQRPVTVKV	GGQLREALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
K_CM_MP535	WQRPIVTIKV	GGQLREALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
N_CM_YBF30	WQRPVITVKI	GKEVREALLD	TGADDTVIEE	LQLEGKWPK	MIGGIGGFIK
O_CM_ANT70	WDRPIVTARV	GGHLCEVLLD	TGADDTVLENN	IQLEGKWPK	MIGGIGGFIK
O_CM_MVP51	WDRPIVTAKV	GGHLCEALLD	TGADDTVLENN	IQLEGRWTPK	MIGGIGGFIK
O_SN_99SE_	WDRPVVTARV	GGHLCEVLLD	TGADDTVLTN	IQLEGKWTPK	MIGGIGGFIK
O_SN_99SE_	WDRPIVPARV	GGHLCEVLLD	TGADDTVLENN	IQLEGKWTPK	MIGGIGGFIK
U_CD___83C	WQRPLVTVKI	GGQLKEALLD	TGADDTVVEE	MTLPGKWPK	MIGGIGGFIK

	151			200	
00BW0762_1	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW0768_2	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW0874_2	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1471_2	VRQYDQIVIE	ICGKKAIGSV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1616_2	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1686_8	VRQYDQISIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1759_3	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1773_2	VRQYDQISIE	ICGKKAIGAV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1783_5	VRQYDQILIE	ICGKKAIGSV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1795_6	VRQYDHIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	ILNFPISPIE
00BW1811_3	VRQYDEILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1859_5	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1880_2	VRQYDQILIE	ICGKRAMGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1921_1	VRQYDQITIE	ICGKKAIGAV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW2036_1	VRQYDQIPIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW2063_6	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW2087_2	VRQYDQILIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW2127_2	VRQYDQVVIE	ICGKKTIGTV	LVGPTPVNIV	GRNMLTQLGC	TLNFPISPIE
00BW2128_3	VRQYDEIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW2276_7	VRQYDQILIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3819_3	VRQYEQVPIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3842_8	VRQYDQIVIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3871_3	VRQYEQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3876_9	VRQYDQILVE	ICGKKAIGTV	SVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3886_8	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3891_6	VRQYDQIAIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3970_2	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW5031_1	VRQYDQIMIE	ICGQKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW01B21	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW0407	VRQYEQILIE	ICGKKTIGTV	LVGPTPVDII	GRNMLTQLGC	TLNFPISPIE
96BW0502	VRQYDQIVIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW06_J4	VRQYDQIPIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW11_06	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW1210	VRQYDQIVIE	ICGKKAIGSV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW15B03	VRQYDQILIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW16_26	VRQYDQITIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
96BW17A09	VRQYDQIVIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BWM01_5	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BWM03_2	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
98BWMC12_2	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
98BWMC13_4	VRQYDRIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
98BWMC14_a	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
98BWM014_1	VGQYDQIPIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
98BWM018_d	VKQYEQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLAQLGC	TLNFPISPIE
98BWM036_a	VRQYDQILIE	ICGKKAIGTV	LVGPTPINII	GRNMLTQLGC	TLNFPISPIE
98BWM037_d	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
99BW3932_1	VRQYDQVVIE	ICEKKTIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
99BW4642_4	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
99BW4745_8	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
99BW4754_7	VRQYDQIHIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE

99BWMC16_8	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTPLGC	TLNFPISPIE
A2_CD_97CD	VRQYDQIVIE	ICGKRAIGTV	LVGPTPVNII	GRNMLVQLGC	TLNFPISPIE
A2_CY_94CY	VRQYDQIAIE	ICGKRAIGTV	LVGPTPVNII	GRNMLVQLGC	TLNFPISPIE
A2D_97KR	VRQYDQITIE	ICEKRAIGTV	LVGPTPVNII	GRNMLVQLGC	TLNFPISPIE
A2G_CD_97C	VRQYDQILIE	ISGKKAIGTV	LVGPTPINII	GRNMLIQIGC	TLNFPISPIE
A_BY_97BL0	VRQYDQILVE	ICXKKAIXTV	LVGPTPXNII	XRNMLTQLGC	TLNFPISPIE
A_KE_Q23_A	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE659	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE725	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE753	VKQYDQVLIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE853	VKQYDQISIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE889	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_UGSE8	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_UG_92UG0	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTLIGC	TLNFPISPIS
A_UG_U455_	VRQYDQILIE	ICGKKTIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
AC_IN_2130	VRQYDQISIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
AC_RW_92RW	VKQYDQILIE	ICGKKAIGTV	LVGPTSVNII	GRNMLTQIGC	TLNFPISPIE
AC_SE_SE94	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
ACD_SE_SE8	VRQYDQILVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
ACG_BE_VI1	VRQYDQIMIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
AD_SE_SE69	VRQYDQILIE	ICGYKAIGTV	LVGPTPVNII	GRNLLTQIGC	ALNFPISPIE
AD_SE_SE71	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
ADHK_NO_97	VRQYDXILIE	ICGKKAIGTV	LAGPTPVNII	GRNMLTQIGC	TLNFPISPIE
ADK_CD_MAL	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
AG_BE_VI11	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
AG_NG_92NG	VKQYDQILIE	IEGKKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
AGHU_GA_VI	VRQYDQVPIE	ICGKKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
AGU_CD_Z32	VRQYDQILIE	IGEKRAIGTV	LVGPTPINII	GRNILTQIGC	TLNFPISPIE
AJ_BW_BW21	VRQYNDIHIE	VEGKKAVGTV	LIGPTPINII	GRNMLTQLGC	TLNFPISPIT
B_AU_VH_AF	VRQYDQVLVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
B_CN_RL42_	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIK
B_DE_D31_U	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_DE_HAN_U	VRQYDQILVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_FR_HXB2_	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_GA_OYI_	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
B_GB_CAM1_	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_GB_GB8_A	VKQYDQILVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
B_GB_MANC_	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_KR_WK_AF	VRQYDQVAIE	ICGHKAIGTV	LIGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_NL_3202A	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_TW_TWCYS	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPID
B_US_BC_L0	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_DH123	VRQYDQVLIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_JRCSF	VRQYDQIPID	ICGHKAVGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_MNCG_	VRQYDQITIG	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
B_US_P896_	VRQYEQIDIE	ICGHKAKGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_RF_M1	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_SF2_K	VRQYDQIPVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_WEAU1	VRQYDQVPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_WR27_	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_YU2_M	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
BF1_BR_93B	VRQYDQIPIE	ICGRKATGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
C_BR_92BR0	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
C_BW_96BW0	VRQYEQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
C_BW_96BW1	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
C_BW_96BW1	VRQYDQIVIE	ICGKKAIGSV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIK
C_BW_96BW1	VRQYDQILIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
C_ET_ETH22	VRQYDQIIIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGR	TLNFPISPIE
C_IN_93IN1	VRQYDQIPIE	ICGKKAIGTV	LVGPTPINII	GRNMLTQLGC	TLNFPISPIE
C_IN_93IN9	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
C_IN_93IN9	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE

C_IN_94IN1	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
C_IN_95IN2	VRQYEEIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
CRF01_AE_C	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_C	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_C	VRQYDQIIIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPIS.PD
CRF01_AE_T	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF02_AG_F	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_F	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_G	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_N	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_S	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_S	LRQYDQILIE	ICGKKAMGSV	LVGPTPVNII	GKNILTQIGC	TLNFPISPIE
CRF03_AB_R	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
CRF03_AB_R	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
CRF04_cpx_	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
CRF04_cpx_	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
CRF04_cpx_	VRQYDQITIE	ICGKKATGTV	LVGPTPANII	GRNMLTQLGC	TLNFPISPIE
CRF05_DF_B	VRQYDQILVE	ICGQKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
CRF05_DF_B	VRQYDQILIE	ICGHKAVGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
CRF06_cpx_	VKQYDQILIE	ICGKKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
CRF06_cpx_	VRQYDQILIE	ICGKRAMGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF06_cpx_	VRQYDQILIE	ICGKKAMGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF06_cpx_	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF11_cpx_	VKQYEEIIIE	IEGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF11_cpx_	VKQYEDITIE	IEGKKAIGTV	LIGPTPVNII	GRNMLTQIGC	TLNFPISPVD
D_CD_84ZR0	VRQYDHILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
D_CD_ELI_K	VRQYDQIPIE	ICGQKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
D_CD_NDK_M	VRQYDQILIE	ICGYKAMGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
D_UG_94UG1	VRQYDQIPLE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
F1_BE_VI85	VKQYDNILIE	ICGHKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPVSPIE
F1_BR_93BR	VKQYDSILIE	ICGHRAIGTV	LVGPTPVNII	GRNMLTQIGC	TLHFPISPIE
F1_FI_FIN9	VKQYDHILIE	ICGHKAIGTV	LVGPTPVNIV	GRNMLTQIGC	TLNFPISPIE
F1_FR_MP41	VKQYDQITID	ICGHKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
F2_CM_MP25	VRQYDQVSIE	ICGQKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
F2KU_BE_VI	VRQYDQVME	ICGQKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
G_BE_DRCBL	VRQYDQILIE	ISGKRAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
G_NG_92NG0	VRQYDQILIE	IGGKKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
G_SE_SE616	VRQYDQVPIE	ISGKKAIGTI	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
H_BE_VI991	VRQYEQVAIE	IFGKKAIGTV	LVGPTPVNII	GRNILTQMG	TLNLPISPIE
H_BE_VI997	VRQYDQVAIE	ICGKKAIGTV	LVGPTPVNII	GRNILTQIGC	TLNFPISPIE
H_CF_90CF0	VRQYEQVAIE	ICGKKAIGTV	LVGPTPVNII	GRNILTQIGC	TLNFPISPIE
J_SE_SE702	VRQYNEVPPIE	IEGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
J_SE_SE788	VRQYNEVPPIE	IEGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
K_CD_EQTB1	VRQYDQVCME	ICGQKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
K_CM_MP535	VRQYDQVLIE	ICGQKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
N_CM_YBF30	VRQYDNITVD	IQGRKAVGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
O_CM_ANT70	VKEYDNVTVE	VEGREVQGT	LVGPTPVNII	GRNILTGLGC	TLNFPISP
O_CM_MVP51	VKEYNNVTVE	VQGEVQGT	LVGPTPVNII	GRNILTGLGC	TLNFPISP
O_SN_99SE_	VKEYNQVPVE	IEGREVLGT	LVGPTPVNII	GRNILTGLGC	TLNFPISP
O_SN_99SE_	VKEYNQVPVE	IEGREVLGT	LVGPTPVNII	GRNILTGLGC	TLNFPISP
U_CD___83C	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE

201

00BW0762_1	TVPVKLKPGM	DGPKVRQWPL	TEEKIKALTA	ICDEMEKEGK	ITKIGPENPY
00BW0768_2	TVPVKLKPGM	NGPKVKQWPL	TEEKIKALTA	ICEEMEREGK	ITKIGPENPY
00BW0874_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIQALTA	ICEEMEKEGK	ITKIGPENPY

250

00BW1471_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALKA	ICEEMEKEGK	ITKIGPENPY
00BW1616_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1686_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1759_3	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1773_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1783_5	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1795_6	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEDMEKEGK	ITKIGPENPY
00BW1811_3	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1859_5	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1880_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1921_1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALKE	ICTEMEKEGK	ITKIGPENPY
00BW2036_1	TVPVRLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW2063_6	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTG	ICEEMEKEGK	ITKIGPENPY
00BW2087_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW2127_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	IEKIGPENPY
00BW2128_3	TVPLKLKPGM	DGPKVNQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW2276_7	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALME	ICAEMEKEGK	ITKIGPDNPY
00BW3819_3	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	IEKIGPENPY
00BW3842_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEDMEREKG	ISKIGPENPY
00BW3871_3	TVPVKLKPGM	DGPKVKQRPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW3876_9	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW3886_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW3891_6	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW3970_2	TVPVKLKPGM	DGPKVKQWPL	TKEKIEALTA	ICEEMEKEGK	ITKIGPENPY
00BW5031_1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW01B21	TVPVKLKPGM	DGPKVKQWPL	AEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW0407	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEDMEKEGK	ITKIGPENPY
96BW0502	TVPVKLKPGM	DGPKVKQWTL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
96BW06_J4	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICAEMEKEGK	ITKIGPENPY
96BW11_06	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW1210	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	VTKIGPENPY
96BW15B03	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW16_26	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW17A09	TIPVKLKPGM	DGPKVKQWPL	TEEKIKALKA	ICEEMEKEGK	ITKIGPENPY
96BWM01_5	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BWM03_2	TVPVKLKPGM	DGPKVKQWPL	TAEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
98BWMC12_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
98BWMC13_4	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
98BWMC14_a	TIPVKLKPGM	DGPKVKQWPL	TEEKIRALTA	ICDEMEKEGK	ITKIGPENPY
98BWM014_1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
98BWM018_d	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
98BWM036_a	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPH
98BWM037_d	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
99BW3932_1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	IEKIGPENPY
99BW4642_4	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
99BW4745_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
99BW4754_7	TVPXKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ISKIGPENPY
99BWMC16_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEEEGK	IEKIGPENPY
A2_CD_97CD	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	ISKIGPENPY
A2_CY_94CY	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	ISKIGPENPY
A2D_97KR	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	ISKIGPENPY
A2G_CD_97C	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	ISKIGPENPY
A_BY_97BL0	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALXD	ICKEXEKEGK	ISKIXPENPY
A_KE_Q23_A	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE659	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE725	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE753	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE853	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE889	TVPVTLKPGM	DGPRIKQWPL	TEEKIKALTE	ICREMEKEGK	ISKIGPENPY
A_SE_UGSE8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_UG_92UG0	TVPVKLKPGM	DGPRIKQWPL	TEEKIKALTE	ICADMEREGR	ISKIGPENPY

A_UG_U455_	TVPVKLKPEM	DGPKVKQWPL	TEEKIKALTE	ICNEMEKEGK	ISKIGPENPY
AC_IN_2130	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICDEMEKEGK	ISKIGPENPY
AC_RW_92RW	TVPVALKPGM	DGPKVKQWPL	TEEKIKALRE	ICTEMEKEGK	ISKIGPENPY
AC_SE_SE94	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	LSRIGPENPY
ACD_SE_SE8	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALIE	ICTEMEKEGK	ISRIGPENPY
ACG_BE_VI1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTD	ICKEMEKEGK	ISKIGPENPY
AD_SE_SE69	TVPVQLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	IARIGPENPY
AD_SE_SE71	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
ADHK_NO_97	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICLEMEKEGK	ISKIGPENPY
ADK_CD_MAL	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICKDMEKEGK	ILKIGPENPY
AG_BE_VI11	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
AG_NG_92NG	TVPVKLKPGI	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISKIGPENPY
AGHU_GA_VI	TVPVKLKPGI	DGPKVKQWPL	TEEKIKALTE	ICNEMEKEGK	ISRIGPENPY
AGU_CD_Z32	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
AJ_BW_BW21	TVPVNLKPGM	DGPRVRQWPL	TEEKIKALTE	IFTEMEKEGK	ISKIGPENPY
B_AU_VH_AF	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_CN_RL42_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_DE_D31_U	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_DE_HAN_U	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALIE	ICTEMEKEGK	ISKIGPENPY
B_FR_HXB2_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_GA_OYI_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKVLIE	ICTEMEKEGK	ISKVGPENPY
B_GB_CAM1_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_GB_GB8_A	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_GB_MANC_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_KR_WK_AF	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_NL_3202A	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_TW_TWCYS	TVPVKLKPGM	DGPKVKQWPL	TEEKIKVLIE	ICTEMEKEGK	ISKIGPENPY
B_US_BC_L0	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_DH123	TVPVKLKPGM	DGPRVKQWPL	SEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
B_US_JRCSF	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_MNCG_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALIE	ICTEMEKEGK	ISKIGPENPY
B_US_P896_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_RF_M1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_SF2_K	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_WEAU1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_WR27_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	VTKIGPENPY
B_US_YU2_M	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
BF1_BR_93B	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
C_BR_92BR0	TVPVKLKPGM	DGPKVKQWLL	TEEKIKALTA	ICDEMEREKG	ITKIGPENPY
C_BW_96BW0	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
C_BW_96BW1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
C_BW_96BW1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	VTKIGPENPY
C_BW_96BW1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
C_ET_ETH22	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ISRIGPENPY
C_IN_93IN1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICDEMEKEGK	ITKIGPENPY
C_IN_93IN9	TVPVKLKPGM	DGPKVKQWPL	TKEKIEALTA	ICDEMEKEGK	ITKIGPENPY
C_IN_93IN9	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICDEMEREKG	ITKIGPENPY
C_IN_94IN1	TVPVKLKPGM	DGPKVKQWPL	TKEKIEALTI	ICNEMEKEGK	ITKIGPENPY
C_IN_95IN2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICDEMEKEGK	ITKIGPENPY
CRF01_AE_C	TVPVTLKPGM	DGPKVKQWPT	..EEKIALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_C	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_C	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	TCKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF02_AG_F	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
CRF02_AG_F	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTD	ICAEMEKEGK	ISKIGPENPY
CRF02_AG_G	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTD	ICMEMEKEGK	ISKIGPENPY

CRF02_AG_N	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTD	ICTEMEKEGK	ISKIGPENPY
CRF02_AG_S	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTD	ICTEMEKEGK	ISRIGPENPY
CRF02_AG_S	TVPLKHLKPGM	DGPKVKQWPL	TEEKIKHLTD	ICAEMEKEGK	ISKIGPENPY
CRF03_AB_R	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTD	ICKEMEKEGK	ISKIGPENPY
CRF03_AB_R	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALID	ICKEMEKEGK	ISKIGPENPY
CRF04_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISKIGPENPY
CRF04_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
CRF04_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALRE	ICTEMEKEGK	ISKVGPENPY
CRF05_DF_B	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISRIGPENPY
CRF05_DF_B	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISRIGPENPY
CRF06_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	ISKIGPENPY
CRF06_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISRIGPENPY
CRF06_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
CRF06_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
CRF11_cpx_	TVPVQLKAGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
CRF11_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
D_CD_84ZR0	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISRIGPENPY
D_CD_ELI_K	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISRIGPENPY
D_CD_NDK_M	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISRIGPENPY
D_UG_94UG1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALIE	ICSELEKEGK	ISKIGPENPY
F1_BE_VI85	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICLEMEKEGK	ISKIGPENPY
F1_BR_93BR	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICMEMEKEGK	ISKIGPENPY
F1_FI_FIN9	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISRIGPENPY
F1_FR_MP41	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISKIGPENPY
F2_CM_MP25	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
F2KU_BE_VI	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICLEMEKEGK	ISKIGPENPY
G_BE_DRCBL	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICNEMEKEGK	ISKIGPENPY
G_NG_92NG0	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICKDMEKEGK	ISKIGPENPY
G_SE_SE616	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
H_BE_VI991	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	ICLEMEKEGK	ISKIGPENPY
H_BE_VI997	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICMEMEKEGK	ISKIGPENPY
H_CF_90CF0	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISRIGPENPY
J_SE_SE702	TVPVKLKPGM	DGPKIKQWPL	TEEKIKALTQ	ICAELEEEGK	ISRIGPENPY
J_SE_SE788	TVPVKLKPGM	DGPKIKQWPL	TEEKIKALTQ	ICAEEMEEGK	ISRVGPENPY
K_CD_EQTB1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
K_CM_MP535	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
N_CM_YBF30	TVPVKLKPGM	DGPKVKQWPL	TTEKIEALRE	ICTEMEKEGK	ISRIGPENPY
O_CM_ANT70	PVPVKLKPGM	DGPKVKQWPL	SKEKIEALTA	ICQEMEKEGK	ISRIGPENPY
O_CM_MVP51	PVPVKLKPGM	DGPKVKQWPL	SREKIEALTA	ICQEMEKEGK	ISRIGPENPY
O_SN_99SE_	PVPVKLKPGM	DGPKIKQWPL	SKEKIEALTA	ICQEMEKEGK	ISRIGPENPY
O_SN_99SE_	PVPVKLKPGM	DGPKIKQWPL	SKEKIEALTA	ICQEMEKEGK	ISRIGPENPY
U_CD___83C	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICLEMEKEGK	ISKIGPENPY

251

300

00BW0762_1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW0768_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW0874_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1471_2	NTPIFAIAKKK	DSTKWRKLVD	FKELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1616_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1686_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1759_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1773_2	NTPVFAIKKK	DSTKWRKLVD	FGELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1783_5	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSL
00BW1795_6	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1811_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1859_5	NTPVFAIKKK	DSTKWKKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1880_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1921_1	NTPIFAIAKKK	DSTKWRKLVD	FGELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2036_1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2063_6	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2087_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV

00BW2127_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2128_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWKVQLGIPH	PAGLKKKKSV
00BW2276_7	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3819_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKQKKSV
00BW3842_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3871_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3876_9	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3886_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3891_6	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3970_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW5031_1	NTPVSAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PVGLKKKKSV
96BW01B21	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW0407	NTPVFAIKKK	DSTKWRKLLD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW0502	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW06_J4	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW11_06	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW1210	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW15B03	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW16_26	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW17A09	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGSKKKKSV
96BWM01_5	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BWM03_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWMC12_2	NTSVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWMC13_4	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWMC14_a	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM014_1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM018_d	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM036_a	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM037_d	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
99BW3932_1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGXKKKKSV
99BW4642_4	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
99BW4745_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
99BW4754_7	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
99BWMC16_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A2_CD_97CD	NTPVFAIKKK	DSDKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A2_CY_94CY	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKAV
A2D_97KR	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKMKKSV
A2G_CD_97C	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_BY_97BL0	NTPVFAIKKK	DSTKWRKLVD	FXELNKRTQD	FXEVQLGIPH	PAGLKKKKSV
A_KE_Q23_A	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_SE_SE659	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKNSV
A_SE_SE725	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_SE_SE753	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_SE_SE853	NTPIFAIKKK	DSNRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_SE_SE889	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FW....IPH	PAGKKKK.SV
A_SE_UGSE8	NTPIFAIKKK	NSDRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_UG_92UG0	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_UG_U455_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	TAGLKKKKSV
AC_IN_2130	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
AC_RW_92RW	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
AC_SE_SE94	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
ACD_SE_SE8	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
ACG_BE_VI1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRSV
AD_SE_SE69	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
AD_SE_SE71	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
ADHK_NO_97	NTPVFAIKKK	DSTKWXKXXD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
ADK_CD_MAL	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
AG_BE_VI11	NTPIFAIKKK	GSNRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRSV
AG_NG_92NG	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRSV
AGHU_GA_VI	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FCEVQLGIPH	PAGLKKKKSV
AGU_CD_Z32	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVRLGIPH	PARLKKKRSV

AJ_BW_BW21	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_AU_VH_AF	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_CN_RL42	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEAQLGIPH	PAGLKKKKSV
B_DE_D31_U	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_DE_HAN_U	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_FR_HXB2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_GA_OYI	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_GB_CAM1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_GB_GB8_A	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PSGLKKKKSV
B_GB_MANC	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_KR_WK_AF	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_NL_3202A	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSG
B_TW_TWCYS	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_BC_L0	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_DH123	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_JRCSF	NTPVFAIKKK	DSTKWRKLVD	FRELNRRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_MNCG	NTPVFAIKKK	DSTKWRKLVD	FRELNKKTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_P896	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_RF_M1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_SF2_K	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_WEAU1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PSGLKKKKSV
B_US_WR27	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_YU2_M	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
BF1_BR_93B	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_BR_92BR0	NTPVFAIKKK	DSTKWRKLVD	FRELNKRT.D	FWEVQLGIPH	PAGLKKKKSV
C_BW_96BW0	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_BW_96BW1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_BW_96BW1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_BW_96BW1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_ET_ETH22	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_IN_93IN1	NTPIFAIKKK	DSIKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_IN_93IN9	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEIQLGIPH	PAGLKKKKSV
C_IN_93IN9	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_IN_94IN1	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_IN_95IN2	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_C	NTPVFAIKEK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGVPH	PAGLKKKKSV
CRF01_AE_C	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_C	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	DSTKWRKLVD	FRELNKGTD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	D.STKRKLVG	FRELNKRTQD	FWEVQLGIPR	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	DSTRWRKLVD	FRELNKRTQD	FWEVQLGIPR	PAGLKKKKSV
CRF02_AG_F	NTPVFGIKKR	DSTKWRKLVD	FRELNKRTQD	SWEVQLGIPH	PAGLKKKKSV
CRF02_AG_F	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQG	FWEVQLRIPH	PAGLKKKKSV
CRF02_AG_G	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF02_AG_N	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF02_AG_S	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEIQLGIPH	PAGLKKKKSV
CRF02_AG_S	NTPVFAIKRK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF03_AB_R	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF03_AB_R	NTPVFIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGLPH	PAGLKKKKSV
CRF04_cpx	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF04_cpx	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF04_cpx	NTPIFAIKKK	NSNRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF05_DF_B	NTPIFAIKKK	DSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSI
CRF05_DF_B	NTPIFAIKKK	DSTRWRKLVN	FRELNKKTD	FWEVQLGIPH	PAGLKKKKSV
CRF06_cpx	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF06_cpx	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF06_cpx	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKRKSV
CRF06_cpx	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV

CRF11_cpx_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF11_cpx_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEIQLGIPH	PAGLKKKKSV
D_CD_84ZR0	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSI
D_CD_ELI_K	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
D_CD_NDK_M	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
D_UG_94UG1	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F1_BE_VI85	NTPVFAIKKK	DSSKWRKLVD	FKELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F1_BR_93BR	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F1_FI_FIN9	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F1_FR_MP41	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F2_CM_MP25	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRSV
F2KU_BE_VI	NTPIFAIKKK	NSNRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
G_BE_DRCBL	NTPIFAIKKK	DSTRWRKLVD	FRELNKRTQD	FWEVPLGIPH	PGGLKQKRSV
G_NG_92NG0	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRSV
G_SE_SE616	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
H_BE_VI991	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
H_BE_VI997	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
H_CF_90CF0	STPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
J_SE_SE702	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
J_SE_SE788	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
K_CD_EQTB1	NTPVFAIKKK	DSTKWKI LVD	FRELNKRTPD	FWEVQLGIPH	PAGLKKKKSV
K_CM_MP535	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
N_CM_YBF30	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
O_CM_ANT70	NTPIFAIKKK	DGTKWRKLVD	FRELNKRTQE	FWEVQLGIPH	PGGLKQKQSV
O_CM_MVP51	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PGGLKQKQSV
O_SN_99SE_	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PGGLKQKQSV
O_SN_99SE_	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PGGLKQKQSV
U_CD___83C	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV

301

350

00BW0762_1	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW0768_2	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW0874_2	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLSQGWKGS
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00BW1616_2	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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00BW1759_3	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
00BW1773_2	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NEAPGIRYQY	NVLPQGWKGS
00BW1783_5	TVLDVGDAYF	SVPLHENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW1795_6	TVLDVGDAYF	SIPLDEGFRK	YTAFTIPSIN	NATPGIRYQY	NVLPQGWKGS
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00BW2063_6	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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00BW2127_2	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW2128_3	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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00BW3819_3	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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00BW3871_3	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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00BW3886_8	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
00BW3891_6	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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96BW0407	AVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NSTPGIRYQY	NVLPQGWNGS
96BW0502	TVLDMGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS

96BW06_J4	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGITYQY	NVLPQGWKGS
96BW11_06	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BW1210	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSRN	NETPGIRYQY	NVLPQGWKGS
96BW15B03	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BW16_26	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NATPGIRYQY	NVLPQGWKGS
96BW17A09	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BWM01_5	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BWM03_2	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
98BWMC12_2	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
98BWMC13_4	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
98BWMC14_a	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
98BWM014_1	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
98BWM018_d	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NATPGIRHQY	NVLPQGWKGS
98BWM036_a	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
98BWM037_d	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
99BW3932_1	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NATPGIRYQY	NVLPQGWKGS
99BW4642_4	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
99BW4745_8	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
99BW4754_7	TVLDVGDAYF	SIPLDENFRK	YTAFTIPSTN	NATPGVRYQY	NVLPQGWKGS
99BWMC16_8	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
A2_CD_97CD	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
A2_CY_94CY	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
A2D_97KR	TVLDVVDAYF	SVPLHEDFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
A2G_CD_97C	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
A_BY_97BL0	TVLDVGDAYF	SVPLDESFRK	XXAFTIPSVN	NETPXIRYQY	NVLPQGWKGS
A_KE_Q23_A	TVLDVGDAYF	SVPLHEEFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
A_SE_SE659	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSTN	NATPGIRYQX	NVLPQGWKGS
A_SE_SE725	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
A_SE_SE753	TVLDLGDAYF	SVPLHEGFRK	YTAFTIPSTN	NATPGIRYQY	NVLPQGWKGS
A_SE_SE853	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
A_SE_SE889	TVLDVGDAYF	SVPLDKNFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
A_SE_UGSE8	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
A_UG_92UG0	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
A_UG_U455_	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
AC_IN_2130	TVLDVGDAYF	SVPLYEEFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
AC_RW_92RW	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AC_SE_SE94	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
ACD_SE_SE8	TILDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
ACG_BE_VI1	TVLDVGDAYF	SVPLDKEFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
AD_SE_SE69	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AD_SE_SE71	TVLDVGDAYF	SVPLHEEFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
ADHK_NO_97	TVLDVGDAYF	SVPLAEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
ADK_CD_MAL	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AG_BE_VI11	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AG_NG_92NG	TVLDVGDAYF	SIPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AGHU_GA_VI	TVLDVGDAYF	SVPLYEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AGU_CD_Z32	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AJ_BW_BW21	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
B_AU_VH_AF	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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B_DE_D31_U	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
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B_GB_MANC_	TVLDVGDAYF	SVPLYEDFRK	YTVFTIPSIN	NEAPGVRYQY	NVLPQGWKGS
B_KR_WK_AF	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
B_NL_3202A	TALDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
B_TW_TWCYS	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_BC_LO	TVLDVGDRYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS

B_US_DH123	TVLDVGDAYF	SIPLDEDFRK	YTAFTIPSVN	NAAPGIRYQY	NVLPQGWKGS
B_US_JRCSF	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_MNCG	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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B_US_WEAU1	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_WR27	TVLDVGDAXF	SVXLDXEXRK	YTAFTIPSH	NETPGIRYQY	NVLPQGWKGS
B_US_YU2_M	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSIN	NETPGTRYQY	NVLPQGWKGS
BF1_BR_93B	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGLRYQY	NVLPQGWKGS
C_BR_92BR0	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
C_BW_96BW0	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NSTPGIRYQY	NVLPQGWKGS
C_BW_96BW1	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
C_BW_96BW1	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSRN	NETPGIRYQY	NVLPQGWKGS
C_BW_96BW1	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
C_ET_ETH22	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
C_IN_93IN1	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
C_IN_93IN9	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
C_IN_93IN9	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSRN	NETPGIRYQY	NVLPQGWKGS
C_IN_94IN1	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
C_IN_95IN2	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF01_AE_C	TVLDVGDAYF	SVPLYEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF01_AE_C	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
CRF01_AE_C	TVLDVGDAYF	SVPLHE.SRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF01_AE_T	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	DETPGIRYQY	NVLPQGWKGS
CRF01_AE_T	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF01_AE_T	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF01_AE_T	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF01_AE_T	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF01_AE_T	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF01_AE_T	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF02_AG_F	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF02_AG_F	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
CRF02_AG_G	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF02_AG_N	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
CRF02_AG_S	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF02_AG_S	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
CRF03_AB_R	TVLDVGDAYF	SVPLDQDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF03_AB_R	TVLDVGDAYF	SVPLDQDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF04_cpx	TVLDVGDAYF	SVPLDPEFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF04_cpx	TVLDVGDAYF	SVPLDPAFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
CRF04_cpx	TVLDVGDAYF	SVPLDPEFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF05_DF_B	TVLDVGDAYF	SVPLDKEFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF05_DF_B	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSIN	NETPGFRYQY	NVLPQGWKGS
CRF06_cpx	TVLDVGDAYF	SIPLDEKFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF06_cpx	TVLDVGDAYF	SIPLDKDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF06_cpx	TVLDVGDAYF	SVPLGENFRK	YTAFTIPSLN	NETPGIRYQY	NVLPQGWKGS
CRF06_cpx	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF11_cpx	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
CRF11_cpx	TVLDVGDAYF	SVLLDESFRK	YTAFTIPSLN	NETPGIRYQY	NVLPQGWKGS
D_CD_84ZR0	TVLDVGDAYF	SIPLCEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
D_CD_ELI_K	TVLDVGDAYF	SVPLDEDFRK	YTAFTISSIN	NETPGIRYQY	NVLPQGWKGS
D_CD_NDK_M	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
D_UG_94UG1	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
F1_BE_VI85	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
F1_BR_93BR	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
F1_FI_FIN9	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
F1_FR_MP41	TVLDVGDAYF	SVPLDKEFRK	YTAFTIPSLN	NETPGIRYQY	NVLPQGWKGS
F2_CM_MP25	TVLDVGDAYF	SVPLDKEFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
F2KU_BE_VI	TVLDVGDAYF	SVPLDPEFRK	YTAFTIPSVN	NETPGVRYQY	NVLPQGWKGS
G_BE_DRCBL	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSTN	NETPGIRYQY	...PQGWKGS
G_NG_92NG0	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS

G_SE_SE616	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
H_BE_VI991	SVLDVGGAYF	SVPLHEDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
H_BE_VI997	SVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
H_CF_90CF0	SVLDVGDAYF	SVPLDKEFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
J_SE_SE702	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
J_SE_SE788	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
K_CD_EQTB1	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
K_CM_MP535	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
N_CM_YBF30	TVLDVGDAYF	SCPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
O_CM_ANT70	TVLDVGDAYF	SCPLDPDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
O_CM_MVP51	TVLDVGDAYF	SCPLDPDFRK	YTAFTIPSVN	NETPGVRYQY	NVLPQGWKGS
O_SN_99SE_	TVLDVGDAYF	SCPLDPDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
O_SN_99SE_	TVLDVGDAYF	SCPLDPDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
U_CD___83C	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS

	351			400	
00BW0762_1	PAIFQSSMTR	ILEPFRTQNP	EIVIIYQYMDD	LYVGSdleig	QHRVKIEELR
00BW0768_2	PAIFQDSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSNLEIG	QHRAKIEELK
00BW0874_2	PAIFQSSMTR	ILEPFRAQNP	ELViiYQYMDD	LYVGSdleig	QHRAKIEELR
00BW1471_2	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMDN	LYVRSdleig	QHRAKIEELR
00BW1616_2	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHREKIEELR
00BW1686_8	PAIFQSTMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
00BW1759_3	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
00BW1773_2	PSIFQSSMTK	ILEPFRTQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEGLR
00BW1783_5	PAIFQSSMTK	ILGPFRTQNP	DIVIIYQYMDD	LYVGSdleig	KHRAKIEELR
00BW1795_6	PAIFQSSMTR	ILEPFRTQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEKLR
00BW1811_3	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
00BW1859_5	PAIFQSSMTR	ILEPFRTQNP	EIVIIYQYMDD	LYVESdleig	QHRAKIEELK
00BW1880_2	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdlKIG	QHRAKIEELR
00BW1921_1	PAIFQSSMTK	ILEPFRAQNP	DIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
00BW2036_1	PAIFQSSMTK	ILEPFRAQNP	ELViiYQYMDD	LYVGSdleig	QHRAKIEELR
00BW2063_6	PAIFQSSMTK	ILEPFRAQNP	DIVIIYQYMDD	LYVGSdlDIG	QRREKIEDLR
00BW2087_2	PAIFQCSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
00BW2127_2	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
00BW2128_3	PSIFQSSMTK	ILKPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIQELR
00BW2276_7	PAIFQSSMTR	ILEPFRAQNP	DIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
00BW3819_3	PAIFQCSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
00BW3842_8	PAIFQSSMTK	ILEPFRAQNP	DIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
00BW3871_3	PAIFQSSMTR	ILEPFRTQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
00BW3876_9	PAVFQSSMTK	ILEPFRTQNP	EIVVYQYMDD	LYVGSdleig	QHRAKIEELR
00BW3886_8	PAIFQCSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
00BW3891_6	PAIFQSSMTR	ILEPFRAQNP	GIVIIYQYMDD	LYVGSNLEIG	QHRAKIEELR
00BW3970_2	PAIFQSSMTX	ILEPFRAQNP	DIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
00BW5031_1	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleIV	QHRAKVEELR
96BW01B21	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
96BW0407	PAIFQSSMTK	ILEPFRTKNP	DILIIYQYMDD	LYVGSdlQIG	QHRAKIEELT
96BW0502	PAIFQSSMTK	ILEPFRLQNP	EIVIIYQYMDD	LYVGSdleig	QRRAQIEELR
96BW06_J4	PAIFQSSMTR	ILEPFRTQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
96BW11_06	PSIFQSSMTK	ILEPFRAQNP	ELViiYQYMDD	LYVGSdleig	QHRAKIEELR
96BW1210	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHTAKIEELR
96BW15B03	PSIFQSSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
96BW16_26	PAIFQSSMTK	ILEPFRAQNP	GIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
96BW17A09	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGXdleig	QHRAKIEELR
96BWM01_5	PAIFQSSMTK	ILELFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
96BWM03_2	PAIFQASMIK	ILEPFRAQNP	EMViiYQYMDD	LYVGSdleig	QHRAKIEELR
98BWMC12_2	PAIFQSSMTR	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdlDIG	QHRAKIEELR
98BWMC13_4	PAIFQCSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	KHRAKIEELR
98BWMC14_a	PAIFQSSMTK	ILEPFRAQNP	DIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
98BWM014_1	PAIFQCSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
98BWM018_d	PAIFQSSMTK	ILEPFRTQNP	DIVIIYQYMDD	LYVGSdleig	QHRAKIEELR
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98BWM037_d	PAIFQCSMTR	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRakIEELR
99BW3932_1	PAIFQSSMTK	ILKPFREQNP	EMViiYQYMDD	LYVGSdleig	QHTakIEELR
99BW4642_4	PAIFQSSMTK	ILEPFRIQNP	EIVIIYQYMDD	LYVGSdleig	QHRakIEELR
99BW4745_8	PAIFQSSMTK	ILEPFRAKNP	EIVIIYQYMDD	LYVGSdleig	QHRakIEELR
99BW4754_7	PAIFQSSMTK	ILEPFRAQNP	DIViiYQYMDD	LYVGSdleig	QHRakIEKLr
99BWMc16_8	PAIFQSSMTK	ILEPFRTKNP	DIViiYQYMDD	LYVGSdleig	QHRakIEELR
A2_CD_97CD	PAIFQSSMTK	ILDPFRARNP	EMViiYQYMDD	LYVGSdleID	QHRakIEELR
A2_CY_94CY	PAIFQSSMTK	ILEPFRSKNT	ELIIYQYMDD	LYVGSdleIS	QHRVKIEELR
A2D_97KR	PAIFQSSMTK	ILEPFRKQNP	EIVIIYRYMDD	LYVGSdleig	QHRTKIEELR
A2G_CD_97C	PAIFQSSMTK	ILEPFRADNP	EIVIIYQYMDD	LYVGSdleig	QHRakIEELR
A_BY_97BL0	PSIFQSSMTK	ILEPFRLKNP	EIVIIYQYXDD	LYVGSdLETG	QHRTKIEELR
A_KE_Q23_A	PAIFQSSMTK	ILEPFRSKNP	EIVIIYQYMDD	LYVGSdleig	QHRakIEELR
A_SE_SE659	PAIFQSSMTK	ILEPFRSKNP	DIIIIYQYMDD	LYVGSdleig	QHRakIEELR
A_SE_SE725	PAIFQSSMTK	ILEPFRLKNP	EIIIIYQYMDD	LYVGSdleig	QHRTKIEELR
A_SE_SE753	PAIFQSSMTK	ILEPFRERNP	EVIIYQYMDD	LYVGSdleig	QHRTKIEELR
A_SE_SE853	PSIFQSSMTK	ILEPFRSKNP	EIIIIYQYMDD	LYVGSdleig	QHRTKIEELR
A_SE_SE889	PAIFQSSMIK	ILEPFRVQNP	EIIIIYQYMDD	LYVGSdleig	QHRakVEELR
A_SE_UGSE8	PAIFQSSMTK	ILEPFRSKNP	EIIIIYQYMDD	LYVGSdleIE	QHRTKIEELR
A_UG_92UG0	PAIFQASMTK	ILEPFRSKNP	DIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
A_UG_U455_	PSIFQSSMTK	ILEPFRSQHP	DIVIIYQYMDD	LYVGSdleig	QHRakIEELR
AC_IN_2130	PAIFQASMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdLKIG	QHRakIEELR
AC_RW_92RW	PAIFQNSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHRakIEELR
AC_SE_SE94	PAIFQSSMTK	ILAPFRSKNP	EIIIIYQYMDD	LYVGSdleig	QHRTKIEELR
ACD_SE_SE8	PAIFQSSMTK	ILEPFRSKNP	DMIIYQYMDD	LYVGSdleig	QHRTKIEELR
ACG_BE_VI1	PAIFQASMTK	ILDPFRRENp	EIVIIYQYMDD	LYVGSdleig	QHRakIEELR
AD_SE_SE69	PAIFQSSMTK	ILEPFRKQNP	EMViiYQYMDD	LYVGSdleig	QHRIKIEELR
AD_SE_SE71	PAIFQSSMTK	ILEPFRSKNP	ELIIYQYMDD	LYVGSdleig	QHRIKIEELR
ADHK_NO_97	PAIFQCSMTK	ILEPFRAKNP	EIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
ADK_CD_MAL	PAIFQSSMTK	ILEPFRTKNP	EIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
AG_BE_VI11	PAIFQASMTK	ILEPFRTENP	KIVIIYQYMDD	LYVGSdleig	QHRakIDELR
AG_NG_92NG	PAIFQSSMTK	ILEPFRTENP	EIVIIYQYMDD	LYVGSdLETG	QHRakIEELR
AGHU_GA_VI	PAIFQSSMTK	ILEPFRKQNP	EMViiYQYMDD	LYVGSdleig	QHRakIEELR
AGU_CD_Z32	PAIFQSSMTK	ILEPFRTKNP	EIVIIYQYMDD	LYVGSdleig	QHRakIEELR
AJ_BW_BW21	PAIFQYSMTK	ILEPFRANNP	EIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
B_AU_VH_AF	PAIFQSSMTK	ILEPFRKQNP	DVVIYQYMDD	LYVGSdleig	QHRTKIEELR
B_CN_RL42_	PAIFQCSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRakIEELR
B_DE_D31_U	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
B_DE_HAN_U	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleIE	QHRTKIEELR
B_FR_HXB2_	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
B_GA_OYI_	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
B_GB_CAM1_	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
B_GB_GB8_A	PAIFQSSMTK	ILEPFRKQNP	EIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
B_GB_MANC_	PAIFQSSMTK	ILEPFRKQNP	DVVIYQYMDD	LYVGSdleig	QHRTKIEELR
B_KR_WK_AF	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRIKIEELR
B_NL_3202A	PAIFQCSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
B_TW_TWCYS	PAIFQSSMTR	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRIKVEELR
B_US_BC_L0	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
B_US_DH123	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleIE	QHRTKIEELR
B_US_JRCSF	PAIFQSSMTK	ILEPFRKQNP	DIIIIYQYMDD	LYVGSdleig	QHRTKIEELR
B_US_MNCG_	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRakIEELR
B_US_P896_	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRakIEDLR
B_US_RF_M1	PAIFQSSMTK	ILEPFKKQNP	EIVIIYQYMDD	LYVGSdleig	QHRIKIEELR
B_US_SF2_K	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
B_US_WEAU1	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
B_US_WR27_	PTIFPSSMTQ	ILEPFRKPNP	EIVIIYQYMDD	LYVGSNLEIG	QHRTKIEELR
B_US_YU2_M	PAIFQSSMTT	ILEPFRKQNP	DLViiYQYMDD	LYVGSdleig	QHRTKIEELR
BF1_BR_93B	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMDD	LYVGSdleig	QHRTKIEELR
C_BR_92BR0	PSIFQSSTTK	ILEPFRAQNP	EIIIIYQYMDD	LYVGSdleig	QHRakIEELR
C_BW_96BW0	PAIFQSSMIK	ILEPFRTKNP	DIVIIYQYMDD	LYVGSdleig	QHRakIEELR
C_BW_96BW1	PSIFQSSMTK	ILEPFRAKNP	ELViiYQYMDD	LYVGSdleig	QHRarIEELR
C_BW_96BW1	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMDD	LYVGSdleig	QHTakIEELR

C_BW_96BW1	PSIFQSSMTK	ILEPFRARNP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR
C_ET_ETH22	PPIFQSSMPQ	ILEPFRAPNP	EIVIIYQYMD	LYVGSLEIG	QHRAPIEELR
C_IN_93IN1	PAIFQSSMIR	ILEPFRAQNP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR
C_IN_93IN9	PAIFQSSMTR	ILEPFRARNP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR
C_IN_93IN9	PAIFQASMTK	ILEPFRAQNP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR
C_IN_94IN1	PAIFQSSMTK	ILEPFRGRNP	EIDIIYQYMD	LYVGSLEIG	QHRAKIEELR
C_IN_95IN2	PAIFQNSMTR	ILEPFRAQNP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR
CRF01_AE_C	PAIFQSSMTK	ILEPYRAKNP	EIVIIYQYMD	LYVGSLEIG	QHRTKIEELR
CRF01_AE_C	PAIFQSSMTK	ILEPFRARNP	EIVIIYQYMD	LYVGSLEIG	QHRTKVEDLR
CRF01_AE_C	PAIFQCSMTK	ILEPFRAKNP	EIVIIYQYMD	LYVGSLEIG	QHGTKIEELR
CRF01_AE_T	PAIFQSSMTK	ILEPFRIKNP	EMVIIYQYMD	LYVGSLEIG	QHRTKIEELR
CRF01_AE_T	PAIFQSSMTK	ILEPFRIKNP	EMVIIYQYMD	LYVGSLEIG	QHRKIEELR
CRF01_AE_T	PAIFQSSMTK	ILEPFRIKNP	EMVIIYQYMD	LYVGSLEIG	QHRTKIEELR
CRF01_AE_T	PAIFQSSMTK	ILEPFRIKNP	EMVIIYQYMD	LYVGSLEIG	QHRTKIEELR
CRF01_AE_T	PAIFQSSMTK	ILEPFRIKNP	EMVIIYQYMD	LYVGSLEIG	QHRTKIEELR
CRF01_AE_T	PAIFQCSMTK	ILEPFRTKNP	EIVIIYQYMD	LYVGSLEIG	QHRTKIEELR
CRF02_AG_F	PAIFQASMTN	ILEHYRIKNP	EIMIIYQYMD	LYVGSLEIE	QHRAKIEELR
CRF02_AG_F	PAIFQASMTK	ILEPFRIKNP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR
CRF02_AG_G	PAIFQSSMTK	ILEPYRIKNP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR
CRF02_AG_N	PAIFQASMTK	ILEPFRTKNP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR
CRF02_AG_S	PAIFQASMTK	ILEPFRTKNP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR
CRF02_AG_S	PAIFQASMTK	ILEPFRTKNP	ELVIIYQYMD	LYVGSLEIG	QHRAKIEELR
CRF03_AB_R	PAIFQSSMTK	ILEPFRKQNP	EIVIIYQYMD	LYVGSLEIG	QHRTEIEELR
CRF03_AB_R	PAIFQSSMTK	ILEPFRKQNP	EIVIIYQYMD	LYVGSLEIG	QHRKIEELR
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CRF04_cpx_	PAIFQCSMTK	ILEPFRTKNP	EMVIIYQYMD	LYVGSLEIG	QHKAKIEELR
CRF05_DF_B	PAIFQCSMTK	ILEPFRKQNP	EVVIIYQYMD	LYVGSLEIG	QHRAKIEELR
CRF05_DF_B	PAIFQCSMTK	ILEPFRKQNP	EMVIIYQYMD	LYVGSLEIG	QHRTKIEELR
CRF06_cpx_	PAIFQSSMIK	ILEPFRIKNP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR
CRF06_cpx_	PAIFQCSMTK	ILDPFRIKNP	ELVIIYQYMD	LYVGSLEIG	QHRAKIEELR
CRF06_cpx_	PAIFQSSMIK	ILEPFRTKNP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR
CRF06_cpx_	PAIFQSSMIK	ILEPFRQKNP	EIVIIYQYMD	LYVGSLEIG	QHREKVEELR
CRF11_cpx_	PAIFQSSMTK	ILEPFRTQNP	EIVIIYQYMD	LYVGSLEIG	QHREKVEELR
CRF11_cpx_	PAIFQSSMTK	ILEPFRTQNP	EVVIIYQYMD	LYVGSLEIG	QHREKVEELR
D_CD_84ZR0	PAIFQSSMIK	ILEPFRKQNP	EVVIIYQYMD	LYVGSLEIG	QHRAKIEELR
D_CD_ELI_K	PAIFQSSMTK	ILEPFRKQNP	EMVIIYQYMD	LYVGSLEIG	QHRTKIEELR
D_CD_NDK_M	PAIFQSSMTK	ILEPFRKQNP	EIVIIYQYMD	LYVGSLEIG	QHRTKIEELR
D_UG_94UG1	PAIFQSSMTK	ILEPFRKQNP	EMIYYQYMD	LYVGSLEIG	QHRKIEELR
F1_BE_VI85	PAIFQCSMTK	ILEPFRMKNP	DIVIIYQYMD	LYVGSLEIG	QHRTKIEELR
F1_BR_93BR	PAIFQYSMTK	ILDPFRAKNP	DIVIIYQYMD	LYVGSLEIG	QHRTKIEELR
F1_FI_FIN9	PAIFQCSMTK	ILEPFRTKNP	DIVIIYQYMD	LYVGSLEIG	QHRTKIEELR
F1_FR_MP41	PAIFQSSMTK	ILEPFRAKNP	DIVIIYQYMD	LYVGSLEIG	QHRMKEELR
F2_CM_MP25	PAIFQSSMIK	ILEPFRKENP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR
F2KU_BE_VI	PAIFQYSMTK	ILEPFRTKNP	EMVIIYQYMD	LYVGSLEIG	QHRTKIEELR
G_BE_DRCBL	PAIFQSSMTK	ILEPFRTQNP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR
G_NG_92NG0	PAIFQSSMTK	ILEPSRTKNP	EMVIIYQYMD	LYVGSLEIG	QHRAKIEELR
G_SE_SE616	PAIFQSSMTR	ILEPFRANNP	EMVIIYQYMD	LYVGSLEIG	QHRAKIEELR
H_BE_VI991	PAIFQSSMTK	ILEPFRKQNP	EVIIYQYMD	LYVGSLEIG	QHREKIEELR
H_BE_VI997	PAIFQSSMTK	ILEPFRKQNP	EIIYYQYMD	LYVGSLEIG	QHRAKIEELR
H_CF_90CF0	PAIFQSSMTK	ILAPFREQNP	EMVIIYQYMD	LYVGSLEIG	QHRAKIEELR
J_SE_SE702	PAIFQCSMTK	ILKPFRRNP	EIVIIYQYMD	LYVGSLEIE	QHRRKIKELR
J_SE_SE788	PAIFQCSMTK	ILKPFRRNP	EIVIIYQYMD	LYVGSLEIE	QHRRKIKELR
K_CD_EQTB1	PAIFQCSMTK	ILEPFRKNP	DMVLYQYMD	LYVGSLEIG	QHRAKIEELR
K_CM_MP535	PAIFQHSMTK	ILEPFRIKNP	EMVIIYQYMD	LYVGSLEIG	QPRTKIEELR
N_CM_YBF30	PAIFQSTMTK	ILEPFREKHP	EIIYYQYMD	LYVGSLELA	QHREAVEDLR
O_CM_ANT70	PAIFQSSMTK	ILDPFRRDNP	ELEICQYMD	LYVGSLEPLT	EHRKRIELLR
O_CM_MVP51	PAIFQSSMTK	ILDPFRRKSNP	EVEIYYQYMD	LYVGSLEPLA	EHRKRVELLR
O_SN_99SE_	PAIFQSSMTK	ILDPFRRKSNP	ELEICQYMD	LYVGSLEPLT	EHRKRVELLR
O_SN_99SE_	PAIFQSSMTK	ILDPFRRKSNP	ELEICQYMD	LYVGSLEPLT	EHRKRVELLR
U_CD_83C	PAIFQSSMTK	ILEPFRKENP	EIVIIYQYMD	LYVGSLEIG	QHRAKIEELR

00BW0762_1	RHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
00BW0768_2	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKNSWTVND
00BW0874_2	AHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1471_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1616_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1686_8	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQTIQL	PTKESWTVND
00BW1759_3	NHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1773_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PDKDSWTVND
00BW1783_5	NHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
00BW1795_6	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
00BW1811_3	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKD .STVND
00BW1859_5	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1880_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
00BW1921_1	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIIL	PEQESWTVND
00BW2036_1	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKESWTVNG
00BW2063_6	NHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
00BW2087_2	GHLLQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW2127_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKGTVQPIQL	PEKDSWTVND
00BW2128_3	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW2276_7	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW3819_3	GHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW3842_8	AHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKESWTVND
00BW3871_3	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQKIQL	PTKDSWTVND
00BW3876_9	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKESWTVND
00BW3886_8	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW3891_6	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWAVQPIQL	PEKDSWTVND
00BW3970_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW5031_1	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
96BW01B21	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPINL	PEKESWTVND
96BW0407	EHLLIWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
96BW0502	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
96BW06_J4	NHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PTKDSWTVND
96BW11_06	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIKL	PEKESWTVND
96BW1210	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
96BW15B03	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKESWTVND
96BW16_26	THLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
96BW17A09	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
96BWM01_5	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DQWTVQPIQL	PEKESWTVND
96BWM03_2	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	AEKDSWTVND
98BWMC12_2	IHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTIQPIQL	PEKDSWTVND
98BWMC13_4	RHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
98BWMC14_a	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PTKDSWTVND
98BWM014_1	GHLLQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
98BWM018_d	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
98BWM036_a	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
98BWM037_d	QHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
99BW3932_1	DHLLGWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
99BW4642_4	GHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
99BW4745_8	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
99BW4754_7	EHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
99BWMC16_8	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PTKDSWTVND
A2_CD_97CD	AHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKDSWTVND
A2_CY_94CY	AHLLKWGFYT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKDSWTVND
A2D___97KR	NHLLKWGFYT	PDKKHQKEPP	FLWMEYELHP	DKWTVQPIKL	PEKDSWTVND
A2G_CD_97C	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
A_BY_97BL0	AHLLSWGFTT	PDKKHQKEPP	FLWXXYEXHP	DKWTVQPIML	PDKDSWTVND
A_KE_Q23_A	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKDSWTVND
A_SE_SE659	SHLLSWGFTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKESWTVND
A_SE_SE725	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKESWTVND

A_SE_SE753	EHLLSWGFTT	PDKKHQKEPP	FLWMGYEVHP	DKWTVQPIVL	PEKESWTVND
A_SE_SE853	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPINL	PEKESWTVND
A_SE_SE889	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKENWTVND
A_SE_UGSE8	AHLLSWGFTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKESWTVND
A_UG_92UG0	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKESWTVND
A_UG_U455_	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AC_IN_2130	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AC_RW_92RW	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AC_SE_SE94	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
ACD_SE_SE8	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIKL	PEKESWTVND
ACG_BE_VI1	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AD_SE_SE69	GHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPITL	PEKESWTVND
AD_SE_SE71	EHLLKWGFYT	PDQKHQKEPP	FLWMGYELHP	DRWTVQPIKL	PEKESWTVND
ADHK_NO_97	EHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
ADK_CD_MAL	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
AG_BE_VI11	EHLLRWGLTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AG_NG_92NG	NHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKESWTVND
AGHU_GA_VI	AHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQTVKL	PEKDSWTVND
AGU_CD_Z32	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
AJ_BW_BW21	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKEAWTVND
B_AU_VH_AF	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_CN_RL42_	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHL	DKWTVQPIML	PEKDSWTVND
B_DE_D31_U	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPITL	PEKDSWTVND
B_DE_HAN_U	QHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_FR_HXB2_	QHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_GA_OYI_	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PEKDSWTVND
B_GB_CAM1_	QHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PEKDSWTVND
B_GB_GB8_A	QHLLRWGFST	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_GB_MANC_	QYLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPITL	PEKDSWTVND
B_KR_WK_AF	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_NL_3202A	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_TW_TWCYS	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_BC_L0	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_DH123	QHLLRWGLFT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_JRCSF	QHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_MNCG_	RHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_P896_	QHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_RF_M1	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_SF2_K	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PEKDSWTVND
B_US_WEAU1	QHLLRWGFTT	PDKKHQKDEPP	FLWMGYELHP	DKWTVQPIKL	PEKESWTVND
B_US_WR27_	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKDSWTVND
B_US_YU2_M	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
BF1_BR_93B	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
C_BR_92BR0	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_BW_96BW0	EHLLKWGLTT	PYKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVHD
C_BW_96BW1	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIKL	PEKESWTVND
C_BW_96BW1	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
C_BW_96BW1	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKESWTVND
C_ET_ETH22	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_93IN1	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_93IN9	GHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_93IN9	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_94IN1	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_95IN2	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF01_AE_C	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_C	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIVL	PEKDSWTVND
CRF01_AE_C	AHLLSWGFTT	PDKKHQKESP	FLWMGYELHP	DRWTVQPIQL	PDKESWTVDD
CRF01_AE_T	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PDQKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND

CRF01_AE_T	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PGKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF02_AG_F	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF02_AG_F	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF02_AG_G	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PEKDSWTVND
CRF02_AG_N	GHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPVEL	PEKDSWTVND
CRF02_AG_S	EHLLRWGFTT	PDEKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
CRF02_AG_S	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF03_AB_R	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
CRF03_AB_R	DHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
CRF04_cpx_	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQP	AEKDSWTVND
CRF04_cpx_	EHLLRWGFYT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF04_cpx_	EHLLRWGFTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIQL	VEKESWTVND
CRF05_DF_B	EHLLOWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
CRF05_DF_B	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKDSWTVND
CRF06_cpx_	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
CRF06_cpx_	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKESWSIND
CRF06_cpx_	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
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CRF11_cpx_	KHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKECWTVND
CRF11_cpx_	KHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
D_CD_84ZR0	EHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSITL	PEKESWTVND
D_CD_ELI_K	EHLLRWGFTR	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIKL	PEKESWTVND
D_CD_NDK_M	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPINL	PEKESWTVND
D_UG_94UG1	GHLLKWGFTT	PDKKYQKEPP	FLWMGYELHP	DKWTVQPIHL	PEKESWTVND
F1_BE_VI85	EHLLRWGFTT	PDKKHQKEPP	FLWMGHELHP	DKWTVQPIQL	PNKDSWTVND
F1_BR_93BR	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
F1_FI_FIN9	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVDD
F1_FR_MP41	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
F2_CM_MP25	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQAIQL	PDKSSWTVND
F2KU_BE_VI	EHLLRWGFTT	PDEKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKEDWTVND
G_BE_DRCBL	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKENWTVND
G_NG_92NG0	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
G_SE_SE616	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
H_BE_VI991	AHLLRWGFTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPVKL	PEKDSWTVND
H_BE_VI997	AHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPVKL	PEKDSWTVND
H_CF_90CF0	AHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQTVKL	PEKDSWTVND
J_SE_SE702	EHLLKWGFYT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
J_SE_SE788	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
K_CD_EQTB1	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
K_CM_MP535	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
N_CM_YBF30	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKDVWTVND
O_CM_ANBT70	EHLYQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIQL	PNKDVWTVND
O_CM_MVP51	EHLYQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKEVWTVND
O_SN_99SE_	EHLYQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKEEWTVND
O_SN_99SE_	EHLYQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKEEWTVND
U_CD_83C	AHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKDDWTVND

451

00BW0762_1	IQKLVGKLNW	ASQIYPGIKV
00BW0768_2	IQKLVGKLNW	ASQIYPGIKV
00BW0874_2	IQKLVGKLNW	ASQIYPGIKV
00BW1471_2	IQKLVGKLNW	ASQIYAGIKV
00BW1616_2	IQKLVGKLNW	ASQIYPGVKV
00BW1686_8	IQKLVGKLNW	ASQIYSGIKV
00BW1759_3	IQKLVGKLNW	ASQIYPGIKV
00BW1773_2	IQKLVGKLNW	ASQIYPGIKV
00BW1783_5	IQKLVGKLNW	ASQIYPGIKV
00BW1795_6	IQKLVGKLNW	ASQIYPGIKV
00BW1811_3	IQKLVGKLNW	ASQIYSGIKV
00BW1859_5	IQKLVGKLNW	ASQIYAGIKV

500

RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
RQLCRLLRGA	KVLTDIVPLT	EEAELELAEN
RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
TQLCKLLRGA	KALTDIVPLT	DEAELELAEN
RQLCKLLRGT	KALTDIVPLT	DEAELELAEN
KQLCKLLRGA	KALTDIVPLT	EEAELELAEN

00BW1880_2	IQKLVGKLNW	ASQIYKGIKV	KQLCKLLRGA	KALTDIVPLP	EEAELELAEN
00BW1921_1	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
00BW2036_1	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW2063_6	IQKLVGKLNW	ASQIYPGIKV	TQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW2087_2	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
00BW2127_2	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW2128_3	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTDIIPLT	EEAELELAEN
00BW2276_7	IQKLVGKLNW	VSQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW3819_3	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW3842_8	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIIPLT	EEAELELAEN
00BW3871_3	LQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
00BW3876_9	IQKLVGKLNW	ASQIYPGIKV	RHLCKLLRGA	KALTEIVPLT	EEAELELAEN
00BW3886_8	IQKLVGKLNW	ASQIYTGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW3891_6	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW3970_2	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
00BW5031_1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
96BW01B21	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
96BW0407	IQKLVGKLNW	ASQIYPGIRV	RHLCKLLRGA	KALTDIVPLT	EEAELELAEN
96BW0502	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDVVPLT	EEAELELAEN
96BW06_J4	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTDVVPLN	EEAELELAEN
96BW11_06	IQKLVGKLNW	ASQIYPGVKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
96BW1210	IQKLVGKLNW	ASQIYPGIKV	RQLCKILRGV	KALTDIVTLT	EEAELELAEN
96BW15B03	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAED
96BW16_26	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIIPLT	EEAELELAEN
96BW17A09	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
96BWM01_5	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	DEAELELAEN
96BWM03_2	VQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
98BWMC12_2	IQRLVGKLNW	ASQIYSGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
98BWMC13_4	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
98BWMC14_a	IQKLVGKLNW	ASQNYPGIKV	RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
98BWM014_1	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
98BWM018_d	IQKLVGKLNW	ASQIYPGIKV	RQLCKLIRGT	KKLTDIVPLT	EEAELELAEN
98BWM036_a	IQKLVGKLNW	ASQIYPGIKV	KNLCKLLRGA	KALTDIVPLT	EEAELELAEN
98BWM037_d	IQELVGKLNW	ASQIYSGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
99BW3932_1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
99BW4642_4	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
99BW4745_8	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
99BW4754_7	IQKLVGKLNW	ASQIYPGIQV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
99BWMC16_8	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
A2_CD_97CD	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGT	KALTDIVPLT	REAELELEEN
A2_CY_94CY	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVTLT	KEAELELEEN
A2D_97KR	IQKLVGKLNW	ASQIYAEIKV	KQLCKLLRGA	KALTDIVPLT	KEAELELEEN
A2G_CD_97C	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTEIVSLT	AEAELELAEN
A_BY_97BL0	IQKLXGKLNW	ASQIYPEIKV	RQLCKLLXGA	KALTDIVTLT	EEAELELAEN
A_KE_Q23_A	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDVVTLT	EEAELELAEN
A_SE_SE659	IQKLVGKLNW	ASQIYPGIKV	KQLCRLLRGA	KALTDIVELT	EEAELELAEN
A_SE_SE725	IQKLVGKLNW	ASQIYAGIKV	KQLCRLLRGA	KALTDIVTLT	EEAELELAEN
A_SE_SE753	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTDIVTLT	EEAELELAEN
A_SE_SE853	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
A_SE_SE889	IQKLVGKLNW	ASQIYVGIKV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
A_SE_UGSE8	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
A_UG_92UG0	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTDIVTLT	EEAELELAEN
A_UG_U455_	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
AC_IN_2130	IQKLVGKLNW	ASQIYPGIKV	RQLCRLLRGA	KALTDIVPLT	EEAELELAEN
AC_RW_92RW	IQKLVGKLNW	ASQIYPGVKV	RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
AC_SE_SE94	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KSLTDVVTLT	EEAELELAEN
ACD_SE_SE8	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDVVTLT	EEAELELAEN
ACG_BE_VI1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
AD_SE_SE69	IQKLVGKLNW	ASQIYPGIKV	RQLCKCIRGA	KALTEVVPLT	EEAELELAEN
AD_SE_SE71	IQKLVGKLNW	ASQIYAGIKV	KQLCKCLRGA	KALTEIVPLT	EEAELELAEN
ADHK_NO_97	IQKLVGKLNW	ASQIYPGIKV	RQLCRLLRGT	KALTDIVPLT	AEAELELAEN

ADK_CD_MAL	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	AEAELELAEN
AG_BE_VI11	IQKLVGKLNW	ASQIYAGIRV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
AG_NG_92NG	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
AGHU_GA_VI	IQKLVGKLNW	ASQIYSGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
AGU_CD_Z32	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	AEAELELAEN
AJ_BW_BW21	IQKLVGKLNW	ASQIYPGIQV	RHLCRLLRGA	KALTDIVPLT	AEAELELAEN
B_AU_VH_AF	IQKLVGKLNW	ASQIYSGIKV	RQLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_CN_RL42	IQKLVGKLNW	ASQIYAGIKV	KELCKLLRGT	KALTEVIPLT	EEAELELAEN
B_DE_D31_U	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTEVIPLT	KEAELELAEN
B_DE_HAN_U	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGP	KALTEVIPLT	KEAELELAEN
B_FR_HXB2	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_GA_OYI	IQKLVGKLNW	ASQIYAGIKV	KNLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_GB_CAM1	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
B_GB_GB8_A	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTEVITLT	EEAELELAEN
B_GB_MANC	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTEVIPLT	KEAELELAEN
B_KR_WK_AF	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
B_NL_3202A	IQKLVGKLNW	ASQIYAGIKV	RHLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_TW_TWCYS	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGT	KALTEVVPLT	KEAELELAEN
B_US_BC_L0	IQKLVGKLNW	ASQIYSGIKV	KQLCKLLRGT	KALTEVVTLT	EEAELELAEN
B_US_DH123	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTEVIPLT	EEAELELAEN
B_US_JRCSF	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVIPLT	KEAELELAEN
B_US_MNCG	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_US_P896	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
B_US_RF_M1	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVQLT	KEAELELAEN
B_US_SF2_K	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_US_WEAU1	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEIIPIT	EEAELELAEN
B_US_WR27	IQKLVGKLNW	XSQIYAGIKV	XQLCKLLRGT	KALTEVVPLT	EEAELELAGN
B_US_YU2_M	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGT	KALTEVIPLT	EEAELELAEN
BF1_BR_93B	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGT	KALTEVVPLT	AEAELELAEN
C_BR_92BR0	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_BW_96BW0	IQKLVGKLNW	ASQIYPGIRV	KHLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_BW_96BW1	IQKLVGKLNW	ASQIYPGVKV	RQLCKLLRGA	KALTDIVPPT	EEAELELAEN
C_BW_96BW1	IQKLVGKLNW	ASQIYPGIKV	RQLCKILRGV	KALTDIVTLT	EEAELELAEN
C_BW_96BW1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAED
C_ET_ETH22	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVTLT	EEAELELAEN
C_IN_93IN1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_IN_93IN9	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_IN_93IN9	IQKLVGKLNW	ASQIYPGIKV	KQLCRLLRGA	KVLTDIVPLT	EEAELELAEN
C_IN_94IN1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_IN_95IN2	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
CRF01_AE_C	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTEVVPLT	EEAELELAEN
CRF01_AE_C	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTDIVTLT	EEAELELAEN
CRF01_AE_C	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYAGIKV	KQLCKPLRGT	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELEEN
CRF01_AE_T	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF02_AG_F	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF02_AG_F	IQKLVGKLNW	ASQIFAGIKV	KQLCRLLRGA	KALTDIVPLT	EEAELELAEN
CRF02_AG_G	IQKLVGKLNW	ASQIYAGIKV	KELCKLLRGA	KALTDIVTLT	EEAELELAEN
CRF02_AG_N	IQKLVGKLNW	ASQIYAGIKI	KQLCRLLRGA	KALTDIVALT	EEAELELAEN
CRF02_AG_S	IQKLVGKLNW	QVRIYAGIKV	KQLCKLLRGA	KTLDIVTLT	EEAELELAEN
CRF02_AG_S	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
CRF03_AB_R	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTEVIPLT	AEAELELAEN
CRF03_AB_R	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTEIIPIT	AEAELELAEN
CRF04_cpx	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	TEAELELAEN
CRF04_cpx	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	TEAELELAEN
CRF04_cpx	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	TEAELELAEN
CRF05_DF_B	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTEVIPLT	EEAELELAEN

CRF05_DF_B	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
CRF06_cpx_	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	AEAELELAEN
CRF06_cpx_	IQKLVGKLNW	ASQIYSGIKV	RQLCKLLRGA	KALTDIVPLT	AEAELELAEN
CRF06_cpx_	IQKLVGKLNW	ASQIYPGIKV	KHLCKLLRGA	KALTDIVPLT	AEAELELAEN
CRF06_cpx_	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	AEAELELAEN
CRF11_cpx_	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	AEAELELAEN
CRF11_cpx_	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	AEAELELAEN
D_CD_84ZR0	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTEVIPLT	EEAELELAEN
D_CD_ELI_K	IQNLVERLNW	ASQIYPGIKV	RQLCKLLRGT	KALTEVIPLT	EEAELELAEN
D_CD_NDK_M	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
D_UG_94UG1	IQKLVGKLNW	ASQIYPGIKV	RQLCKCLRGA	KALTEVIPLT	AEAELELAEN
F1_BE_VI85	IQKLVGKLNW	ASQIYPGIKV	RPLCKLLRGA	KALTDIVPLT	AEAELELAKN
F1_BR_93BR	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	TEAELELAEN
F1_FI_FIN9	IQKLVGKLNW	ASXIYPGIKV	RQLCKLLRGA	KALTDIVPLT	AEANLELAEN
F1_FR_MP41	IQKLVGKLNW	ASQIYPGIKI	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
F2_CM_MP25	IQKLVGKLNW	ASQIYPGIRV	KHLCKLLRGT	KALTDVVPLT	AEAELELAEN
F2KU_BE_VI	IQKLVGKLNW	ASQIYPGIKV	KQLCKLIRGA	KTLTDIVPLT	AEAELELAEN
G_BE_DRCBL	IQKLVGKLNW	ASQIYPGIKV	KQLCKLIRGA	KALTDIVSMT	AEAELELAEN
G_NG_92NG0	IQKLVGKLNW	ASQIYPGIKV	KHLCKLLRGA	KALTDIVPLT	AEAELELAEN
G_SE_SE616	IQKLVGKLNW	ASQIYPGIKV	THLCKLLRGA	KALTDIVSLT	AEAELELAEN
H_BE_VI991	IQKLVGKLNW	ASQIYPGIKV	KQLCXLLRGA	KALTEIVPLT	KEAELELAEN
H_BE_VI997	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDVVPLT	KEAELELAEN
H_CF_90CF0	IQKLVGKLNW	ASQIYPNIKV	KQLCKLLRGA	KALTDIIPLT	KEAELELAEN
J_SE_SE702	IQKLVGKLNW	ASQIYPGIKI	KELCKLIRGA	KALTDIVPLT	REAELELAEN
J_SE_SE788	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLKGA	KALTDIVPLT	REAELELAEN
K_CD_EQTB1	IQKLVGKLNW	ASQIFPGIKV	KQLCKLLRGV	KALTDIVPLT	AEAELELAEN
K_CM_MP535	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGV	KALTDIVPLT	AEAELELAEN
N_CM_YBF30	IQKLVGKLNW	ASQIYPGIRV	KQLCKLIRGT	KALTEVVNFT	EEAELELAEN
O_CM_ANT70	IQKLIGKLNW	ASQIYQGIRV	RELCKLIRGT	KSLTEVVPLS	REAELELEEN
O_CM_MVP51	IQKLVGKLNW	ASQIYQGIRV	KELCKLIRGT	KSLTEVVPLS	KEAELELEEN
O_SN_99SE_	IQKLVGKLNW	ASQIYQGIRV	KELCKLIRGA	KSLTEIVPLS	KEAELELEEN
O_SN_99SE_	IQKLVGKLNW	ASQIYQGIRV	KELCKLIRGT	KSLTEVVPLS	KEAELELEEN
U_CD___83C	IQKLVGKLNW	ASQIYPGIQV	RQLCKLLRGT	KALTDIVPMT	KEAELELAEN

501

00BW0762_1	R.EILKEPVH	GVYYDPSKDL	IADIQKQGND	QWTYQIYQEP	FKNLKTGKYA
00BW0768_2	R.EILREPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
00BW0874_2	R.EILREPVH	GVYYDPSKDL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
00BW1471_2	R.KILKEPVH	GVYYDPSKDL	IAEIQKQGHE	QWTYQIYQEP	FKNLKTGKYA
00BW1616_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
00BW1686_8	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
00BW1759_3	R.EILKEPVH	GVYYDPSKEL	IAELQKQGND	QWTYQIYQEP	FKNLKTGKYA
00BW1773_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
00BW1783_5	R.EILKEPVH	GVYYDPSKDL	KAEIQKQGND	QWTYQIYQEP	FKNLKTGKYA
00BW1795_6	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
00BW1811_3	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
00BW1859_5	R.EILKEPVH	EVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
00BW1880_2	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGDD	QWTYQIYQEP	LKNLKTGKYA
00BW1921_1	R.EILKEPVH	GVYYDPSKEL	IAEIQKQGQD	QWSYQIYQEP	FKNLKTGKYA
00BW2036_1	R.EILRGPVH	GVYYDPSKDL	VAEIQKQGHG	QWTYQIFQEP	FKNLKTGKYA
00BW2063_6	R.EILREPVH	GVYYDPSKDL	VAEIQKQGND	QWTYQIYQEP	FKNLKTGKYA
00BW2087_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
00BW2127_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGND	QWTYQIYQEP	FKNLKTGKYA
00BW2128_3	R.EILKEPVH	GVYYDSSKEL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
00BW2276_7	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
00BW3819_3	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
00BW3842_8	R.EILREPVH	GVYYDPSKDL	VAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
00BW3871_3	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGND	QWTYQIYQEP	FKNLKTGKYA
00BW3876_9	RXEILKEPVH	GVYYDPSKDL	IAEIQKQGYD	QWTYQIYQEP	YKNLKTGKYA
00BW3886_8	R.EILKGPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
00BW3891_6	R.EILKEPVH	GVYYDPSKDL	IAEIQKQNGG	.QTYQIYQEP	FKNLKTGKYA

550

00BW3970_2	R.EILREPVH	GVYYDPSKDL	IAEIQKQGND	QWTYQIYQEP	FKNLKTGKYA
00BW5031_1	R.EILREPVH	GVYYDPSKDL	IAEIQKQGDD	QWTYQIYQEP	FKNLKTGKYA
96BW01B21	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
96BW0407	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGHY	QWTYQIYQEP	FKNLKTGKYA
96BW0502	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
96BW06_J4	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
96BW11_06	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
96BW1210	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
96BW15B03	R.EILREPVH	GVYYDPSKDL	VAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
96BW16_26	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
96BW17A09	R.EILKEPVH	GAYYDPSKDL	IAEIQKQNG	QWTYQIYQEP	FKNLKTGKYA
96BWM01_5	R.EILREPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
96BWM03_2	R.EILKEPVH	GVYYDPSKEL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
98BWM012_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGYD	QWTYQIYQEP	FKNLKTGKYA
98BWM013_4	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGLD	QWTYQIYQEP	FKNLKTGKYA
98BWM014_a	R.EILKEPVH	GVYYDPSKDL	IAEIQKQNGD	QWTYQIYQEP	FKNLKTGKYA
98BWM014_1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
98BWM018_d	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
98BWM036_a	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
98BWM037_d	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
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99BWM016_8	R.EILKEPVH	GVYYDPSKEL	IAEIQKQGND	QWTYQIYQEP	FKNLKTGKYA
A2_CD_97CD	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGG	QWSYQIYQEP	FKNLKTGKYA
A2_CY_94CY	R.EILKTPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
A2D_97KR	R.EILKDPVH	GVYYDPSKDL	IAEVQKQGGD	QWTYQIYQEP	FKNLKTGKYA
A2G_CD_97C	R.EILKEPVH	GAYYEPSKEL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
A_BY_97BL0	R.EILKXPVH	XVYYDPSKDL	VAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
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A_SE_SE659	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
A_SE_SE725	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGLD	QWTYQIYQEP	FKNLKTGKYA
A_SE_SE753	R.EILKDPVH	GAYYDPSKDL	IVEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
A_SE_SE853	R.EILKAPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
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A_SE_UGSE8	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
A_UG_92UG0	R.EILKDPVH	GAYYDPSKDL	IAEIQKQGGD	QWIYQIYQEP	FKNLKTGKYA
A_UG_U455_	R.EILKDPVH	GVYYDPSKDL	VAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
AC_IN_2130	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
AC_RW_92RW	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
AC_SE_SE94	R.EILRDPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
ACD_SE_SE8	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGG	QWTYQIYQEP	FKNLKTGKYA
ACG_BE_VI1	R.EILKEPVH	GVYYDPAKDL	VAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
AD_SE_SE69	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
AD_SE_SE71	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGGD	QWSYQIYQEP	FKNLKTGKYA
ADHK_NO_97	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGRG	QWTYQIYQEP	FKNLKTGKYA
ADK_CD_MAL	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGG	QWTYQIYQEP	FKNLKTGKYA
AG_BE_VI11	R.EILKEPVH	GVYYDPGKEL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
AG_NG_92NG	R.EILKEPVH	GVYYDPSKDL	IAELQKQGGD	QWTYQIYQEP	FKNLKTGKYA
AGHU_GA_VI	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGGD	QWTYQIYQEP	FKNLKTGKYA
AGU_CD_Z32	R.EILKEPVH	GVYYDSSKEL	IAEVQKQGLN	QWTYQIYQEP	FKNLKTGKYA
AJ_BW_BW21	R.EILKEPVH	GVYYDSAKEL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
B_AU_VH_AF	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGG	QWTYQIYQEP	FKNLKTGKYA
B_CN_RL42_	R.EILKESVH	GVYYDPSKDL	IAEIQKQGLG	QWTYQIYQEP	FKNLKTGKYA
B_DE_D31_U	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGG	QWTYQIYQEP	FKNLKTGKYA
B_DE_HAN_U	R.EILKEPVH	GVYCDPSKDL	VAEIQKQGG	QWTYQIYQEP	FKNLKTGKYA
B_FR_HXB2_	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGG	QWTYQIYQEP	FKNLKTGKYA
B_GA_OYI_	R.EILKEPVH	GVYYDPSKDL	VAELQKQGG	QWTYQIYQEP	FKNLKTGKYA
B_GB_CAM1_	R.EILKEPVH	GVYYDPSKDL	IAELQKQGG	QWTYQIYQEP	FKNLKTGKYA
B_GB_GB8_A	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGLG	QWTYQIYQEP	FKNLKTGKYA

B_GB_MANC_	R.EILKVPVH	GVYYDPSKDL	TAEIQKQGQG	QWTYQIYQEP	FBSLKTGKYA
B_KR_WK_AF	R.EILKEPVH	GVYYDPAKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_NL_3202A	R.EILKEPVH	GVYYDPSKEL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_TW_TWCYS	R.EILKQPVH	GAYYDPSKDL	VAEIQKQGQG	QWTYQIYQET	FKNLKTGKYA
B_US_BC_L0	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTAKYA
B_US_DH123	R.EILKEPVH	GVYYDPSKDI	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_US_JRCSF	R.EILKEPVH	GVYYDPSKDL	IVEIQKQGQG	QWTYQIFQEP	FKNLKTGKYA
B_US_MNCG_	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_US_P896_	R.EILKEPVH	GVYYDPTKDL	IAELQKQGQG	QWTYQIYQEP	YKNLKTGKYA
B_US_RF_M1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_US_SF2_K	R.EILKEPVH	EVYYDPSKDL	VAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_US_WEAU1	R.EILKEPVH	GVYYDPSKDL	IAELQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_US_WR27_	R.EILKEPVH	GVYYDPSKDL	VAELQKQGQG	QWTYQIYQEP	FIXLXTGKYA
B_US_YU2_M	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
BF1_BR_93B	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	YKNLKTGKYA
C_BR_92BR0	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQN	QWTYQIYQEP	FKNLKTGKYA
C_BW_96BW0	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGHD	QWTYQIYQEP	FKNLKTGKYA
C_BW_96BW1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
C_BW_96BW1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHD	QWTYQIYQEP	FKNLKTGKYA
C_BW_96BW1	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGHD	QWTYQIYQEP	FKNLKTGKYA
C_ET_ETH22	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGND	QWTFQFYQEP	FKNLKTGKFA
C_IN_93IN1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
C_IN_93IN9	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQVYQEP	FKNLKTGKYA
C_IN_93IN9	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
C_IN_94IN1	R.EILKEPIH	GVYYDPSKDL	IAEIQKQGQD	QWTYQVYQEP	FKNLKTGKYA
C_IN_95IN2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_C	R.EILKNPVH	GVYYDPSKEL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_C	R.EILKTPVH	GVYYDPSKDL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_C	R.EILKNPVH	GVYYDPSKDL	VAEIQKQGHN	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_T	R.EILKTPVH	GVYYDPSKDL	VAEVQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_T	R.EILRTPVH	GVYYDPSKDL	VAEVQKQGQD	QWTYQIYQEP	FKNLKTGKYA
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CRF02_AG_F	R.EILKEPVH	GVYYDPAKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_F	R.EILKEPVH	GVYYDPAKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_G	R.EILKEPVH	GVYYDPTKDL	IAEIQKQGQD	QWTFQIYQEP	FKNLKTGKYQ
CRF02_AG_N	R.EILKEPVH	GVYYDPTKDL	VAELQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_S	R.EILKEPVH	GVYYDPTKDL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_S	R.EILKEPVH	GVYYDPTKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF03_AB_R	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
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CRF04_cpx_	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGLG	QXTYQIYQEP	YKNLKTGKYA
CRF05_DF_B	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGLG	QWTYQIYQEP	FKNLKTGKYA
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CRF06_cpx_	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGYG	QWTYQIYQEP	HKNLKTGKYA
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D_CD_84ZR0	R.EILKEPMH	GVYYDPSKDL	IAELQKQGQG	QWTYQIYQEP	FKNLKTGKYA
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D_CD_NDK_M	R.EILKEPVH	GVYYDPSKDL	IAELQKQGDG	QWTYQIYQEP	FKNLKTGKYA
D_UG_94UG1	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGQD	QWTYQIYQEQ	YKNLKTGKYA
F1_BE_VI85	R.EILREPVH	GVYYDPSKDL	IAEIQKQGDG	QWTYQIYQNP	FKNLKTGKYA
F1_BR_93BR	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
F1_FI_FIN9	R.EILKEPVH	GVYYDPSKDL	IPKLQKQGQG	QWTYQIYREP	FKNLKTGKYA

F1_FR_MP41	R.EILKEPVH	GVYYDPSKDL	IAELQKQGQG	QWTYQIYQEP	FKNLKTGKYA
F2_CM_MP25	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	HKNLKTGKYA
F2KU_BE_VI	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	YKNLKTGKYA
G_BE_DRCBL	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGLG	QWTYQVYQEP	YKNLKTGKYA
G_NG_92NG0	R.EILKEPVH	GVYHDPSKEL	IAEVQKQGGPD	QWTYQIYQEP	YKNLKTGKYA
G_SE_SE616	R.EILREPVH	GVYYDPSKEL	IAEVQKQGLD	QWTYQIYQEP	YKNLKTGKYA
H_BE_VI991	R.EILKEPVH	GAYYDPSKEL	IAEIQKQGGPD	QWTYQIYQEP	FKNLKTGKYA
H_BE_VI997	R.EILREPVH	GVYYDPSKDL	IAEIQKQGGPD	QWTYQIYQEP	FKNLKTGKYA
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J_SE_SE702	K.EILKEPVH	GVYYDPAREL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
J_SE_SE788	K.EILKEPVH	GVYYDSAKEL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
K_CD_EQTB1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	YKNLKTGKYA
N_CM_MP535	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGND	QWTYQIYQEP	HKNLKTGKYA
N_CM_YBF30	R.EILKEPLH	GVYYDPGKEL	VAEIQKQGQG	QWTYQIYQEL	HKNLKTGKYA
O_CM_ANT70	R.ERLQKPVH	GVYYQPDKDL	WVNIQKQGGE	QWTYQIYQEE	HKNLKTGKYT
O_CM_MVP51	R.EKLKEPVH	GVYYQPDKDL	WVSIQKHGEG	QWTYQVYQDE	HKNLKTGKYA
O_SN_99SE_	R.EKLKEPVH	GVYYQPDKDL	WVNIQKQGWG	QWTYQIYQDE	HKNLKTGKYT
O_SN_99SE_	R.EKLKEPVH	GVYYQPDKDL	WVNIQKQGGK	QWTYQIYQDE	HKNLKTGKYT
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00BW3819_3	KMKSAHTNDV	KQLTEAVQKI	VMESIVIWG. KAPKFRLPVQ KETWETWWTD
00BW3842_8	KMRTAHTNDV	KQLTEAVXKI	AMECIVIWG. KTPKFRLPIQ KETWETWWTD
00BW3871_3	KMRNAHTNDV	KQLTEAVQKI	AQESIVIWG. KTPKFRLPIQ KETWETWWTD
00BW3876_9	RMRSAHTNDV	KQLAEAVQRI	AKESIVIWG. KTPKFRLPIQ KETWETWWTD
00BW3886_8	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG. KTPKFRLPIQ KETWEIWWTD
00BW3891_6	KIRTAHTNDV	KQLTEVVQKI	AQESIVIWG. KTPKFRLPIQ KETWEIWWTE
00BW3970_2	KRRTAHTNDV	RQLAEAVQKI	TMESIVIWG. KTPRFRLPVQ KETWETWWTD
00BW5031_1	KIRTAHTNDV	RQLTEAVQKI	ALESIVIWG. KIPKFRLPIQ KETWETWWTD
96BW01B21	KMRTAHTNDV	KQLTEAVQKI	ATESIVIWG. KXPKFRLPIQ KETWETWWTD
96BW0407	KMRTAHTNDV	KQLTEVVQKI	AMESIVIWG. KTPKFRLPIQ KDTWETWWTD
96BW0502	KMRTAHTNDV	KQLTEAVQKI	AQESIVIWG. KTPKFRLPIQ KETWETWWTD
96BW06_J4	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG. KTPKFRLPIQ KEIWETWWTD
96BW11_06	KMRTAHTNDV	KQLTEAVQKI	SMESIVIWG. KIPKFRLPIQ KEAWEAWWTD
96BW1210	KLRTAHTNDV	RQLTEAVQKI	AQECIVIWG. KTPKFRLPIQ KETWEAWWTD
96BW15B03	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG. KTPKFRLPIQ KETWETWWTD
96BW16_26	KMRTAHTNDV	KQLAEAVQKI	TMESIVLWG. KTPKFRLPIQ KETWETWWTD
96BW17A09	KKKSTHTNDV	KQLTDAVQKI	TMESIVIWG. KTPKFRLPIQ KETWDTWWTE
96BWM01_5	KRRTAHTNDV	KQLTEAVQKI	ALESTVIWG. KIPKFRLPIQ KETWDTWWTD
96BWM03_2	KMRTAHTNDV	RQLTEAVQKI	AMESIVIWG. KTPKFRLPIQ KETWETWWTD
98BWMC12_2	KMRTAHTNDV	KQLAEAVQKI	AQESIVIWG. KTPKFRLPIQ KETWETWWTD

98BWMC13_4	KRKTAHTNDV	KQLTEAVQKI	ALESIVIWG.	KIPKFRLPIQ	KETWETWWTD
98BWMC14_a	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTE
98BWM014_1	KMRTAHTNDV	KQLTEAVQKI	AIESIVIWG.	KTPKFRLPIQ	KETWETWWTD
98BWM018_d	KMRTAHTNDV	RQLTEAVQKI	TMESIVIWG.	KTPKFRLPIQ	KDTWETWWTD
98BWM036_a	KRRTAHTNDV	KQLTEVVQKI	TMESIVIWG.	KTPKFRLPIQ	KDTWETWWTD
98BWM037_d	KRRTAHTNDV	RQLTEAVQKI	TMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
99BW3932_1	KMRSAPNDV	KQLTEAVHKK	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
99BW4642_4	KMRTAHTNDV	KQLAEAVQKI	AVESIVIWG.	KTPKFRLPIQ	KETWETWWTD
99BW4745_8	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
99BW4754_7	KMRTAHTNDV	KQLAEAVQKV	AIESIVIWG.	KIPKFRLPIQ	KETWETWWTD
99BWMC16_8	KIRTAHTNDV	RQLTEAVQKI	TMESIVIWG.	KTPKFRLSIQ	KDTWETWWTD
A2_CD_97CD	KRKSTHTNDV	KQLTEAVQKI	ATESIVIWG.	KIPKFRLPIQ	KETWETWWTE
A2_CY_94CY	KRRSTHTNDI	KQLTEAVQKI	TMESIVIWG.	KTPKFRLPIQ	KETWETWWAE
A2D_97KR	KRRSTHTNDV	KQLTEAVQKI	VMESIVIWG.	KIPKFRLPIQ	KETWETWWTE
A2G_CD_97C	KRGSHTNDV	KQLTEVVQKI	ATESIVIWG.	KTPKFRLPIR	KETWEVWWTE
A_BY_97BL0	KXXSAHTNXV	KQLTAVVQKV	ATESXILXG.	KTPKFRLPIQ	XETXEXWXM
A_KE_Q23_A	RKRSHTNDV	RQLAEVVQKV	VMESIVIWG.	KTPKFRLPIQ	KETWDTWWMD
A_SE_SE659	RKRSVHTNDV	KQLAEMVQKV	VTESIVIWG.	KTPKFRLPIQ	KETWETWWMD
A_SE_SE725	RKRSHTNDV	RQLAEVVQKV	VMESIVIWG.	KTPKFRLPIQ	KETWETWWMD
A_SE_SE753	RKRSHTNDV	KQLAEVVQKV	AMESIVIWG.	KTPRSKLPIQ	KETWETWWID
A_SE_SE853	RKRSHTNDV	KQLAEVVQKV	VMESIVIWG.	KTPKFRLPIQ	KETWETWWME
A_SE_SE889	RKRSHTNDV	RQLVEVVQKV	VMESIVIWG.	KTPKFRLPIQ	KETWETWWMD
A_SE_UGSE8	RKKSHTNDV	RQLAEVVQKV	VMESIVIWG.	KTPKFRLPIQ	KDTWDTWWMD
A_UG_92UG0	RKRSHTNDV	KQLAEVVQKV	VMESIVIWG.	KTPKFRLPIQ	KETWETWWMD
A_UG_U455_	RKRSHTNDV	KQLTEVVQKV	STESIVIWG.	KIPKFRLPIQ	KETWEAWWME
AC_IN_2130	KMRTAHTNDV	KQLTETVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
AC_RW_92RW	KRRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
AC_SE_SE94	KKRSHTNDV	RQLAEVVQKV	VMESIIWG.	KTPKFRLPIQ	KETWETWWMD
ACD_SE_SE8	KKRSHTNDV	KQLAEVVQKV	VMESIVIWG.	KAPKFRLPIQ	KETWETWWMD
ACG_BE_VI1	KRSAAHTNDV	KQLTEAVQKI	AQESIVIWG.	KTPKFRLPIQ	RETWEAWWME
AD_SE_SE69	KVRGTHNTDI	KQLTAAVQKI	AQECIVIWG.	KTPKFRLPIQ	KETWETWWTE
AD_SE_SE71	KLRGTHNTDI	KQLTAAVQKI	AQECIVIWG.	KTPKFRLPIQ	KETWETWWTE
ADHK_NO_97	RMKSAHTNDV	KQLTEAVQKI	SIESIVIWG.	KTPKFRLPIQ	KETWETWWTE
ADK_CD_MAL	RIKSAHTNDV	KQLTEAVQKI	AQESIVIWG.	KTPKFRLPIQ	KETWEAWWTE
AG_BE_VI11	KRKSHTNDV	KQLVEVVQKV	ATESVVIWG.	KTPKFRLPIQ	RETWEAWWRE
AG_NG_92NG	KRGSHTNDV	KQLTEAVQKI	ATESIVIWG.	KVPKFRLPIR	KETWEVWWTE
AGHU_GA_VI	KKRSHTNDV	KQLTEAVQKI	ATESIVIWG.	KIPKFRLPIQ	KETWETWWTD
AGU_CD_Z32	RRRTAHTNDV	RQLAEVVQKI	ASESIVIWG.	KTPKFRLPIQ	KETWETWWAD
AJ_BW_BW21	KRRAAHTNDV	KQLAEVVQKI	ALESIVIWG.	KTPKFRLPIQ	KETWETWWTE
B_AU_VH_AF	RMKGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWEAWWME
B_CN_RL42_	RMGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWEAWWTE
B_DE_D31_U	RMGAHTNDV	KQLTEAVQKI	TTESIVIWG.	KTPKFRLPIQ	KETWEAWWTE
B_DE_HAN_U	RMGAHTNDI	KQLTEAVQKI	ATEGIVIWG.	KTPKFRLPIQ	KETWEAWWTE
B_FR_HXB2_	RMGAHTNDV	KQLTEAVQKI	TTESIVIWG.	KTPKFRLPIQ	KETWETWWTE
B_GA_OYI_	RMGAHTNDV	KQLTEAVQKI	TQESIVIWG.	KTPKFRLPIQ	KETWEAWWTE
B_GB_CAM1_	KMRGTHNTDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWDWWID
B_GB_GB8_A	KMRGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWEAWWME
B_GB_MANC_	KMRGTHNTDV	KQLTEAVQKV	TTESIIWG.	KIPKFRLPIQ	KETWDWWTE
B_KR_WK_AF	RMGAHTNDV	KQLTEAVQKV	AIESIVIWG.	KTPKFRLPIQ	KETWEAWWTE
B_NL_3202A	RMGAHTNDV	KQLTEAVQKI	TTESIVIWG.	KTPKFRLPIQ	KETWEAWWTE
B_TW_TWCYS	RTRGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWEAWWTE
B_US_BC_L0	RTRGAHTNDV	KQLTEAVQKI	TTECIIWG.	KTPKFRLPIQ	KETWETWWTE
B_US_DH123	RTRGAHTNDV	KQLTEVVQKV	TTECIVIWG.	KTPKFRLPIQ	KETWETWWTE
B_US_JRCSE	RTRGAHTNDV	KQLTEAVQKI	ANESIVIWG.	KIPKFRLPIQ	KETWETWWTE
B_US_MNCG_	RMGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWTE
B_US_P896_	RMGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWEAWWTD
B_US_RF_M1	RMGAHTNDV	KQLTEAVQKV	ATESIVIWG.	KTPKFRLPIQ	KETWEAWWTE
B_US_SF2_K	RMGAHTNDV	KQLTEAVQKV	STESIVIWG.	KIPKFRLPIQ	KETWEAWWME
B_US_WEAU1	RVRGAHTNDV	KQLTEAVQKI	TTESIVIWG.	KTPKFRLPIQ	KETWETWWTE
B_US_WR27_	RTRGAHTNDV	XQLXEAVQKX	ATXSIVIWG.	KTPKFRLPIQ	KETWESRWTE
B_US_YU2_M	RTRGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWTE

BF1_BR_93B	RMGAHTNDV	KQLTEAVQKI	TTESIVIWG.	KIPKFKLPIQ	KETWEAWWIE
C_BR_92BR0	KMRTAHTNDV	QQLTEAVQKI	ALESIIIWG.	KTPKFRLPIQ	KETWEAWWTD
C_BW_96BW0	KMRTAHTNDV	KQLTEVVQKI	TMESIVIWG.	KTPKFRLPIQ	KDTWETWWTD
C_BW_96BW1	KMRTAHTNDV	KQLTEAVQKI	SMESIVIWG.	KIPKFRLPIQ	KEAWEAWWTD
C_BW_96BW1	KLRTAHTNDV	QQLTEAVQKI	AQECIVIWG.	KTPKFRLPIQ	KETWEAWWTD
C_BW_96BW1	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
C_ET_ETH22	KRGTAHTNDV	KQLTAVVQKI	ALESIVIWG.	KTPKFRLPIQ	KETWEAWWTD
C_IN_93IN1	KRRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
C_IN_93IN9	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
C_IN_93IN9	KMRTAHTNDV	KQLAEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWEAWWTD
C_IN_94IN1	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
C_IN_95IN2	KMRTAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWTD
CRF01_AE_C	RKRSAHTNDV	RQLAEVVQKV	ATESIVIWG.	KTPKFRLPIQ	RETWETWWAE
CRF01_AE_C	RKRSAHTNDV	RQLAEVVQKV	ATESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_C	RQSAHTNDV	RQLVEVVQKV	STESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_T	RKRSAHTNDV	RQLTEVVQKI	ATESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_T	RKRSAHTNDV	RQLTEVVQKI	ATESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_T	RKRSAHTNDV	RQLTEVVQKI	ATESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_T	RKRSAHTNDV	RQLTEVVQKI	ATESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_T	RNRSHTNDV	RQLTEVVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWME
CRF01_AE_T	RRGSAHTNDV	RQLTEVVQKV	ATESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_T	RKRSAHTNDV	RQLTEVVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWME
CRF02_AG_F	KRRAHTNDV	KQLAEVVQKV	VTESIVIWG.	KTPKFRLPIQ	RETWEAWWME
CRF02_AG_F	KRRAHTNDV	KQLTEVVQKV	ATESIVIWG.	KTPKFSLPIQ	RETWEAWWME
CRF02_AG_G	ERVAPYDL SI	TELTEVVQKV	TTESIIIWG.	KTPKFRLPIQ	RETWEAWWME
CRF02_AG_N	KKRSAHTNDV	KQLTEVVQKV	AMESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF02_AG_S	KKRSAHTNDV	KQLTEVVQKV	ATESIVIWG.	KTPKFRLPIQ	RETWEAWWME
CRF02_AG_S	KKRSAHTNDV	KQLTEVVQKV	ATESIVVWG.	KTPKFRLPIQ	RETWEAWWME
CRF03_AB_R	RLRGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFKLPIQ	KETWETWWTE
CRF03_AB_R	RLRSAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFKLPIQ	KETWETWWAE
CRF04_cpx_	RTRSAHTNDV	RQLTEAVQKI	AMECIVIWG.	KTPKFRLPIQ	KETWDTWWTE
CRF04_cpx_	KTRSAHTNDV	RQLTEVVQKI	AMECIVIWG.	KTPKFRLPIQ	KETWDTWWTE
CRF04_cpx_	KTRSAHTNDV	RQLTEAVQKI	AMECIVIWG.	KTPKFRLPIQ	KETWDTWWME
CRF05_DF_B	RARGVHTNDV	KQLAEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWEIWWTE
CRF05_DF_B	RTRNAHTNDV	KQLAEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWTE
CRF06_cpx_	RIKSAHTNDV	KQLTEAVQKI	ALESIVIWG.	KTPKFRLPIQ	KETWETWWTE
CRF06_cpx_	KIKSTHTNDV	KQLTEAVQKI	ARESIVIWG.	KTPKFRLPIQ	KETWETWWTE
CRF06_cpx_	RMRSAHTNDI	KQLTEAVQKI	ALEAIVIWG.	KIPKFRLPIQ	KETWETWWTE
CRF06_cpx_	RTKSAHTNDV	RQLTEAVQKI	ALESIVIWG.	KTPKFRLPIH	KETWETWWTE
CRF11_cpx_	KRRAAHTNDV	RQLTEVIQKI	CLEAIVIWG.	KTPKFRLPIQ	RETWETWWTD
CRF11_cpx_	KRRTAHTNDV	RQLAEVVQKI	ALEGIVIWG.	KIPKFRLPIQ	KETWETWWTD
D_CD_84ZR0	RMGAHTNDV	KQLTEAVQKI	AIESIVIWG.	KTPKFRLPIQ	KETWETWWID
D_CD_ELI_K	RMGAHTNDV	KQLAEAVQRI	STESIVIWG.	RTPKFRLPIQ	KETWETWWAE
D_CD_NDK_M	RTRGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFKLPIQ	KETWETWWIE
D_UG_94UG1	KMRGTHTNDV	KQLTEAVQKI	AQECIVIWG.	KTPKFRLPIQ	KETWETWWTE
F1_BE_VI85	KVRSHTNDV	KQLTEAVQKI	ALESIVIWGK	RSPKFKLPIL	KETWDTWWTD
F1_BR_93BR	KMRSAHTNDV	KQLTEAVQKI	SLESIVIWG.	KTPKFRLPIL	KETWDTWWTE
F1_FI_FIN9	KMRSAHTNDV	KQLTEAVQKI	ALESIVIWG.	KTPKFKLPIL	KETWDTWWTE
F1_FR_MP41	KTRSAHTNDI	KELTDAVQKV	ARECIVIWG.	KSPKFRLPIQ	KETWEAWWTD
F2_CM_MP25	RRKSAHTNDV	KQLTEVVQKV	ATEGIVIWG.	KVPKFRLPIQ	KETWEIWWTE
F2KU_BE_VI	RMRSAHTNDV	KQLTEAVQKI	ATEGIVIWG.	KTPKFRLPIQ	KETWETWWTE
G_BE_DRCBL	KGSAHTNDV	KQLTEVVQKI	ATEGIIIWG.	KIPKFKLPIK	KETWEVWWTE
G_NG_92NG0	KRGSHTNDV	KQLTEVVQKI	ATEGIVIWG.	KIPKFKLPIR	KETWEVWWTE
G_SE_SE616	KRGSHTNDV	KQLTEVVQKI	ATESIVIWG.	KTPKFKLPIR	KETWEIWWTD
H_BE_VI991	KMRSAHTNDV	KQLTEVVQKI	ATESIVIWG.	KIPKFRLPIQ	KETWETWWTE
H_BE_VI997	KMRNAHTSDV	KQLTEAVQKI	ATESIVIWG.	KIPKFKLPIQ	KETWETWWTE
H_CF_90CF0	KMRTAHTNDI	KQLTEAVQKI	STESIVIWG.	KIPKFRLPIQ	KETWETWWTE
J_SE_SE702	KRRSAHTNDV	KQLSQVVQKI	ALEAIVIWG.	KTPKFRLPIQ	KETWETWWTD
J_SE_SE788	KRRSAHTNDV	KQLAEVVQKI	ALEAIVIWG.	KTPKFRLPIQ	RETWETWWTD
K_CD_EQTB1	RIRSAHTNDV	KQLTEVVQKV	AMESIVIWG.	KTPKFRLPIQ	KETWGTWWTE
K_CM_MP535	RMRSAHTNDV	KQLTEAVQKI	ATEGIVIWG.	KTPKFRLPIQ	KETWETWWTE
N_CM_YBF30	KMRSAHTNDI	KQLVEVVQKV	ATESIVIWG.	KTPKFRLPVQ	KEVWEAWWTD

O_CM_ANT70	RQKASHTNDI	RQLAEVIQKV	SQESIIIWG.	KLPKFKLPVT	RETWETWWAD
O_CM_MVP51	RQKASHTNDI	RQLAEVVQKV	SQEAIIVIWG.	KLPKFRLPVT	RETWETWWAE
O_SN_99SE_	RQKASHTNDI	RQLAEVLQRV	SQEAIIIIWG.	KLPKFKLPIT	RETWETWWAD
O_SN_99SE_	KQKASHTNDI	RQLAEVLQKV	SQEAIIIIWG.	KLPKFKLPIT	RETWETWWAD
U_CD___83C	KRRSAHTNDV	KQLTEAVQKI	SMESIVIWG.	KIPKFKLPIQ	KETWESWWT

601

650

00BW0762_1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPL	VGVEFYVDG	AANRDTKIGK
00BW0768_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	LGAETFYVDG	AANRETKKGK
00BW0874_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AANRETKLGK
00BW1471_2	YWQATWIPEW	EFVNAPPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
00BW1616_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	IGIETFYVDG	AANRETKLGK
00BW1686_8	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKAGK
00BW1759_3	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AANRDTKKGK
00BW1773_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGVETFYVDG	AANRETKIGK
00BW1783_5	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETYYVDG	AANRETKMGR
00BW1795_6	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPV	AGVETFYVDG	AANRETKMGK
00BW1811_3	YWQATWIPEW	EFVNTPLPVK	LWYQLEEEPI	AGAETFYVDG	AANRETKIGK
00BW1859_5	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AAHRETKVEK
00BW1880_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPM	MGVETFYVDG	AANRETKIGK
00BW1921_1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
00BW2036_1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGK
00BW2063_6	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	LGVETFYVDG	AANRETKMGK
00BW2087_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AANRETKIGK
00BW2127_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGVETFYVDG	AVNRETKVGK
00BW2128_3	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKKGK
00BW2276_7	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AANRETKIGK
00BW3819_3	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGVETFYVDG	AANRDTKVGK
00BW3842_8	YWQATWIPDW	EFVNTLPLVK	LWYQLEKEPI	IGAETFYVDG	AANRDTKIGK
00BW3871_3	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKAGK
00BW3876_9	YWQATWIPDW	EFVNTPLPVK	LWYQLEKEPI	VRAETFYVDG	AANRETKIGK
00BW3886_8	YWQATWIPEW	EFVNTPLPVK	LRVQLEKEPI	AGVETFYVDG	AANRETKVGK
00BW3891_6	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	AEVETFYVDG	AANRETKRGK
00BW3970_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPM	AGVETFYVDG	AANRETKIGR
00BW5031_1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPV	AGVETFYVDG	AANRETKIGK
96BW01B21	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKIGK
96BW0407	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AANRETKLGK
96BW0502	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	PGVETFYVDG	AANRETKLGK
96BW06_J4	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	MGAETFYVDG	AANRETKAGK
96BW11_06	Y.QATWIPEW	EFVNTPLPVK	LWYQLETEPM	AGAETFYVDG	AANRETKIGK
96BW1210	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGVETFYVDG	AANRETKMGK
96BW15B03	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	IGAETFYVDG	AANRETKIGK
96BW16_26	YWQATWIPKW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
96BW17A09	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
96BWM01_5	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	LGAETFYVDG	AANRETKMGK
96BWM03_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKGPI	AGAETFYVDG	ASNRETKLGK
98BWMC12_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETLYVDG	AANRETKLGK
98BWMC13_4	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	LGVETFYVDG	AANRETKLGK
98BWMC14_a	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	IGVETFYVDG	AANRETKAGK
98BWM014_1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	PGAETFYVDG	AANRETKTGK
98BWM018_d	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	GGAETFYVDG	AANRETKMGK
98BWM036_a	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AASRETKKGK
98BWM037_d	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGVETFYVDG	AASRDTKIGK
99BW3932_1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	GGVETFYVDG	AANRETKVGK
99BW4642_4	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKKGK
99BW4745_8	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGVETFYVDG	ATNRETKRGN
99BW4754_7	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGVEFYVDG	AANRDTKLGK
99BWMC16_8	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKKGK
A2_CD_97CD	WWQATWIPEW	EFVNTPLPVK	LWYQLETEPI	AGAETFYVDG	AANRETKLGK
A2_CY_94CY	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AANRETKLGK
A2D___97KR	YWQATWIPEW	EFVNTPLPVK	LWYQLETEPI	TGAETFYVDG	AANRETKLGK

A2G_CD_97C	YWQATWIPDW	EFVNTPLPLVK	LWYRLETEPI	PGAETYYVEG	AANRETKLGK
A_BY_97BL0	XWQATXIPE.	EFVNTPLPLVK	LWYQLEKEPI	VRAETFYVDR	AANRETKIGK
A_KE_Q23_A	YWQATWILEW	EFVNTPLPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
A_SE_SE659	YWQATWIPDW	EFVNTPLPLVL	WWYLLLEEDPI	VGADSFVEG	AAKEKTLXGT
A_SE_SE725	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
A_SE_SE753	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGK
A_SE_SE853	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
A_SE_SE889	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGK
A_SE_UGSE8	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	AGVETFYVDG	AANRETKLGK
A_UG_92UG0	YWQAT.IPEW	EFVNTPLPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
A_UG_U455_	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
AC_IN_2130	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPM	AGAETFYVDG	AANRETKIGK
AC_RW_92RW	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	LGAETFYVDG	AANRETKIGK
AC_SE_SE94	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	IGAETFYVDG	AANRETKLGK
ACD_SE_SE8	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	IGAETFYVDG	AANRETKLGK
ACG_BE_VI1	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AASRETKLGK
AD_SE_SE69	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPM	VGAETFYVDG	AANRETKLGK
AD_SE_SE71	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	AGVETFYVDG	AANRETKLGK
ADHK_NO_97	YWQATWIPDW	EFVNTPLPLVK	LWYQLETEPI	VGAETFYVDG	AANRETKKGGK
ADK_CD_MAL	YWQATWIPDW	EFVNTPLPLVK	LWYQLETEPI	VGAETFYVDG	AANRETKKGGK
AG_BE_VI11	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
AG_NG_92NG	YWQATWIPDW	EFVNTPLPLVK	LWYRLETEPI	PGAETYYVDG	AANKETKLGK
AGHU_GA_VI	HWQATWIPDW	EFVNTPLPLVK	LWYQLETEPI	VGAETFYVDG	AANRETKQGGK
AGU_CD_Z32	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKQGGK
AJ_BW_BW21	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	ASNRETKLGK
B_AU_VH_AF	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_CN_RL42_	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	EEAETFYVDG	AANRETKLGK
B_DE_D31_U	YWQATWIPDW	EFVNTPLPLVK	LWYQLETEPI	VGAETFYVDG	AANRETKLGK
B_DE_HAN_U	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_FR_HXB2_	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_GA_OYI_	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGK
B_GB_CAM1_	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_GB_GB8_A	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGK
B_GB_MANC_	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_KR_WK_AF	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_NL_3202A	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_TW_TWCYS	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGK
B_US_BC_L0	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	EGAETFYVDG	AANRETKLGK
B_US_DH123	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AASRETRLGK
B_US_JRCSF	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_US_MNCG_	YT.ATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKKGGK
B_US_P896_	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRDTKSGK
B_US_RF_M1	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGK
B_US_SF2_K	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_US_WEAU1	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANKETKLGK
B_US_WR27_	YWQATWIPDW	EXVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AASRETKLGK
B_US_YU2_M	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGK
BF1_BR_93B	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
C_BR_92BR0	YWQAT.IPEW	EFVNTPLPLVK	LWYQLEKEPI	AGAETFYVDG	AANREIKMGK
C_BW_96BW0	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	AGAETFYVDG	AANRETKLGK
C_BW_96BW1	YWQATWIPDW	EFVNTPLPLVK	LWYQLETEPM	AGAETFYVDG	AANRETKIGK
C_BW_96BW1	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	AGVETFYVDG	AANRETKMGK
C_BW_96BW1	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKIGK
C_ET_ETH22	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	AGVETFYVDG	AANRETKIGK
C_IN_93IN1	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	AGVETFYVDG	AANRETKLGK
C_IN_93IN9	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	AGVETFYVDG	AANRETKKGGK
C_IN_93IN9	YWQATWIPDW	EFVNTPLPLVK	LWYRLEKEPI	AGVETFYVDG	AANRETKIGK
C_IN_94IN1	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	AGAETFYVDG	AANRDTKIGK
C_IN_95IN2	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKEPI	AGAETFYVDG	AANRETKIGK
CRF01_AE_C	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	AGAETLYVDG	AASRENKLGK
CRF01_AE_C	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	MGAETFYVDG	AASRETKQGGK

CRF01_AE_C	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	AGAETFYVDG	AASRETKLGG
CRF01_AE_T	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AASRETKLGG
CRF01_AE_T	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AASRETKLGG
CRF01_AE_T	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AASRETKLGG
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CRF01_AE_T	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AASRETKLGG
CRF02_AG_F	YWQATWIPDW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF02_AG_F	YWQATWIPDW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANKETKLGG
CRF02_AG_G	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF02_AG_N	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF02_AG_S	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF02_AG_S	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF03_AB_R	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF03_AB_R	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF03_AB_R	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF04_cpx_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF04_cpx_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF04_cpx_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
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CRF05_DF_B	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
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CRF06_cpx_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
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CRF06_cpx_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF06_cpx_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF11_cpx_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF11_cpx_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
D_CD_84ZR0	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
D_CD_ELI_K	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
D_CD_NDK_M	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
D_UG_94UG1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
F1_BE_VI85	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	ASNRETKLGG
F1_BR_93BR	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	ASNRETKLGG
F1_FI_FIN9	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	ASNRETKLGG
F1_FR_MP41	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	ASNRETKLGG
F2_CM_MP25	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
F2KU_BE_VI	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
G_BE_DRCBL	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
G_NG_92NG0	YWQAAWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
G_SE_SE616	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
H_BE_VI991	HWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
H_BE_VI997	HWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
H_CF_90CF0	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
J_SE_SE702	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	ASNRETKLGG
J_SE_SE788	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	ASNRETKLGG
K_CD_EQTB1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
K_CM_MP535	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
N_CM_YBF30	HWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
O_CM_ANT70	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
O_CM_MVP51	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
O_SN_99SE_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
O_SN_99SE_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
U_CD_83C	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG

	651			700
00BW0762_1	AGYVTDKGRR	KVITLTETTN	QKTELQAIQL	ALQDSGPEVN
00BW0768_2	AGYVTDGRGRQ	KIVPLTETTN	QKTELHAIQL	ALQDSGSEVN
00BW0874_2	AGYVTDGRGRQ	KIVSLTETTN	QKTELQAIHL	ALQDSGSEVN
00BW1471_2	AGYVTDKGRQ	KVVSILTETTN	QKTELQAIKL	ALQDSGSEVN
00BW1616_2	AGYVTDGRGRQ	KIVSLAETTN	QKTELQAIQL	ALQDSGSEVN
00BW1686_8	AGYVTDGRGRQ	KVISITETTN	QKTELQAIQL	ALQDSGSEVN
00BW1759_3	AGYVTDGRGRQ	KIVSLTETTN	QKTELQAIQL	ALQDSGLEVN

00BW1773_2	AGYVTDGRGRQ	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1783_5	AGYVTDGRGKQ	KVISLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1795_6	AGYVTDGRGRQ	KIISLTETTN	QKAEHLHAIQL	ALQDSGPEVN	IVTDSQYALG
00BW1811_3	AGYVTDKGRQ	KTVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1859_5	AGYVTDGRGRQ	KIVNLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1880_2	AGYVTDGRGRQ	KVVTLTETTN	QKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
00BW1921_1	AGYVTDKGRQ	KVITLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2036_1	AGYVTDGRGRQ	KIISLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2063_6	AGYVTDGRGRQ	KVVSLTGTTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2087_2	AGYVTDKGRQ	KIVCLNETTN	QKAEHLHAIQL	ALQDSGLEVN	IVTDSQYALG
00BW2127_2	AGYVTDGRGRQ	KVISINETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2128_3	AGYVTDKGRQ	KVVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2276_7	AGYVTDGRGRQ	KIVSLSETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3819_3	AGYVTDGRGRQ	KIVSINGTTN	QKTELRAIYL	ALQDSGSEVN	IVTDSQYALG
00BW3842_8	AGYVTDGRGRQ	KVVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3871_3	AGYVTDGRGRQ	KVISLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3876_9	AGYVTDGRGRQ	KIVSLTETTN	QKSELQAIHL	ALQDSGSEVN	IVTDSQYALG
00BW3886_8	AGYVTDGRGRQ	KVITLTETTN	QKAEHLHAIQL	ALQDSGSEAN	IVTDSQYALG
00BW3891_6	AGYVTDGRGRQ	KIVSLTETTN	QKAEHLHAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3970_2	AGYVTDGRGRQ	KIITLNETTN	QKTELQAIKL	ALQDSGSEVN	IVTDSQYALG
00BW5031_1	AGYVTDGRGRQ	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW01B21	AGYVTDGRGRQ	RIISLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW0407	AGYVTNKGGRQ	KIVPLTETTN	QKAEHLHAIQL	ALQDSGSEVN	IVTDSQYALG
96BW0502	AGYVTDGRGRQ	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW06_J4	AGYVTDGRGRQ	KVISLTETTN	QKTELQAIQL	ALQDSGLEVN	IVTDSQYALG
96BW11_06	AGYVTDKGRQ	KVVTLTETTN	QKAEHLHAIQL	ALQDSGPEVN	IVTDSQYALG
96BW1210	AGYVTDGRGRQ	KIVSLNETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW15B03	AGYVTDGRGRQ	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW16_26	AGCVTDGRGRQ	KIVSLTETTN	QKAEHLHAIQL	ALQDSGAEVN	IVTDSQYALG
96BW17A09	AGYVTDKGRQ	KVVSLTETTN	QKTELQAIKL	ALQDSGSEVN	IVTDSQYALG
96BWM01_5	AGYVTDGRGRQ	KVVPLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALK
96BWM03_2	AGYVTDGRGRQ	KVVSLNETTN	QKTELQAIQL	ALQDSGTEVN	IVTDSQYALG
98BWMC12_2	AGYVTDKGRQ	KVVSLTETTN	QKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
98BWMC13_4	AGYITDRGRQ	KVVSLTETTN	QKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
98BWMC14_a	AGYVTDGRGRQ	KVISLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
98BWM014_1	AGYVTDKGRQ	KIVSLNETTN	QKAEHLHAIQL	ALQDSGLEVN	IVTDSQYALG
98BWM018_d	AGYVTDKGRQ	KIVALTETTN	QKAEHLHAIQL	ALQDSGSEVN	IVTDSQYALG
98BWM036_a	AGYVTDGRGRQ	KCVTLTETTN	QKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
98BWM037_d	AGYVTDGRGKQ	KIITLTETTN	QKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
99BW3932_1	AGYVTDKGRQ	KVITINETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
99BW4642_4	AGYVTDGRGRQ	RIVNLTETTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
99BW4745_8	AGYVTDGRGRQ	KIVSLTETTN	QKAEHLHAIQL	ALQDSGSEVN	IVTDSQYALG
99BW4754_7	AGYVTDGRGRQ	KVVSLTETTN	QKTELQAIHL	ALQDSGPEVN	IVTDSQYALG
99BWMC16_8	AGYVTDGRGRQ	KVVTLTETTN	QKTELQAIQL	ALQDSESEVN	IVTDSQYALG
A2_CD_97CD	AGYVTDGRGRQ	KIVPLTETTN	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
A2_CY_94CY	AGYVTDGRGRQ	KIVSLTETTN	QKTELHAIYL	ALQDSGLEVN	IVTDSQYALG
A2D_97KR	AGYVTDKGRQ	KIVSLTDTTN	QKTELHAIYL	ALQDSGLEVN	IVTDSQYALG
A2G_CD_97C	AGYVTDKGRQ	KIINLTETTN	QKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
A_BY_97BL0	AGYVTDGRGRQ	KVVPLTETTN	QKTELHAIHL	VLQDSGSEVD	IVTDSQYALG
A_KE_Q23_A	AGYVTDKGRQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
A_SE_SE659	GWFAEGGRQ	VVVPLAKTTH	QTTELPALHP	SLQDSGSVVI	IVNDSQSAGG
A_SE_SE725	AGYVTDGRGRQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
A_SE_SE753	AGYVTNRGRQ	KVVSLTETTN	QKTELHAILL	ALQDSGSEVN	IVTDSQYALG
A_SE_SE853	AGYVTDGRGRQ	KVVSLTETTN	QKTEVHAIHL	ALQDSGSEVN	IVTDSQYALG
A_SE_SE889	AGYVTDGRGRQ	KVVTLAETTN	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
A_SE_UGSE8	AGYVTDGRGRQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
A_UG_92UG0	AGYVTDGRGRQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
A_UG_U455_	AGYVTDGRGRQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
AC_IN_2130	AGYATDRGRQ	KIVTLTETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
AC_RW_92RW	AGYVTDGRGRQ	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
AC_SE_SE94	AGYVTDGRGRQ	KVVSLTETTN	QKTELHAIQL	ALQDSGSEVN	IVTDSQYALG

ACD_SE_SE8	AGYVTDGRGQ	KVVSLETETT	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
ACG_BE_VI1	AGYVTDGRGQ	KAITLTETT	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
AD_SE_SE69	AGYVTDGRGQ	KVVPLTETT	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
AD_SE_SE71	AGYITDRGRQ	KVVSLETETT	QKTELQAINL	ALQDSGPEVN	IVTDSQYALG
ADHK_NO_97	AGYVTDGRGQ	KVVFLTETT	QKTELQAIHL	ALQDSGSEVN	IVTDSQYALG
ADK_CD_MAL	AGYVTDGRGQ	KVVSLETETT	QKTELQAIHL	ALQDSGSEVN	IVTDSQYALG
AG_BE_VI11	AGYVTDGRGQ	KAVSLTETT	QKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
AG_NG_92NG	AGYVTDGRGQ	KIITIQUETT	QKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
AGHU_GA_VI	AGYVTDGRGQ	KIVSLTETT	QKTELQAIHL	ALQDSGPEVN	IVTDSQYALG
AGU_CD_Z32	AGYITDKGRQ	KVITLTETT	QKTELEAIHL	ALQDSGLEVN	IVTDSQYALG
AJ_BW_BW21	AGYVTDGRGQ	KIVSLTETT	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
B_AU_VH_AF	AGYVTDGRGQ	KVVPLSDTT	QKTELQAIQL	ALQDSGLEVN	IVTDSQYALG
B_CN_RL42	AGYVTNKGRQ	KVVTLTDTT	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
B_DE_D31_U	AGYVTDGRGQ	KVVSLETETT	QKTELQAIHL	ALQDSGLEVN	IVSDSQYALG
B_DE_HAN_U	AGYVTDGRGQ	KVVSLENDTT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_FR_HXB2	AGYVTNRGRQ	KVVTLTDTT	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
B_GA_OYI	AGYVTDGRGQ	KVVSLETETT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_GB_CAM1	AGYVTDGRGQ	KVVPLTDTT	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
B_GB_GB8_A	AGYVTDGRGQ	KVVPLTDTT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_GB_MANC	AGYVTDGRGQ	KVISLETETT	QKTELQAIHL	ALQDSGLEVN	IVSDSQYALG
B_KR_WK_AF	AGYVTDGRGQ	KVVPLTDTT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_NL_3202A	AGYVTDGRGQ	KVVSLENDTT	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
B_TW_TWCYS	AGYVTDKGRQ	KVVSLETETT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_BC_L0	AGYVTNKGRQ	KVVTLTDTT	QKTELEAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_DH123	AGYVTNRGRQ	KVVSLETETT	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
B_US_JRCSF	AGYVTSRGRQ	KVVSLETETT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_MNCG	AGYVTNRGRQ	KVVSLETETT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_P896	AGYVTDGRGQ	KVVSLEADTT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_RF_M1	AGYVTDGRGQ	KVVSLETETT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_SF2_K	AGYVTDGRGQ	KVVSLEADTT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_WEAU1	AGYVTNRGRQ	RVVSLETETT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_WR27	AGYVTDGRGQ	KVVSLENDTT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_YU2_M	AGYVTNKGRQ	KVVSLETETT	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
BF1_BR_93B	AGYVTDGRGQ	KVVPLTDTT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
C_BR_92BR0	AGYVTDGRGQ	KIVSITETT	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_BW_96BW0	AGYVTDKGRQ	KIVPLTETT	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_BW_96BW1	AGYVTDKGRQ	EVVTLTETT	QKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
C_BW_96BW1	AGYVTDGRGQ	KIVSLNETTT	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_BW_96BW1	AGYVTDGRGQ	KIVSLTETT	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_ET_ETH22	AGYVTDGRGQ	KIVSLTETT	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_IN_93IN1	AGYVTDGRGQ	KIVSLTETT	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
C_IN_93IN9	AGYVTDGRGQ	KIVSLTETT	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
C_IN_93IN9	AGYVTDGRGQ	KIVPLTETT	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
C_IN_94IN1	AGYVTDGRGQ	KIVSLTETT	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
C_IN_95IN2	AGYVTDKGRN	KIVSLTETT	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_C	AGYVTDGRGQ	KVVSLETETT	QKTELHAIHL	ALQDSGSDVN	IVTDSQHALG
CRF01_AE_C	AGYVTDGRGQ	KVVSLETETT	QKTELHAIHL	ALQDSGPEVN	IVTDSQYALG
CRF01_AE_C	AGYATDRGRH	KVVSLETETT	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLETETT	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLETETT	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVISLETETT	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLETETT	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLETETT	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTNRGRQ	KVVSLETETT	QKSELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_F	AGYVTDGRGQ	KVVSLETETT	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_F	AGYVTDGRGQ	KVVSLETETT	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_G	AGYVTDGRGQ	KVVSLETETT	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_N	AGYVTDGRGQ	KVVSLETETT	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_S	AGYVTDGRGQ	KVVSLEAETT	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_S	AGYVTDGRGQ	NVVSLETETT	QKTELHAILL	ALQESGSEVN	IVTDSQYALG
CRF03_AB_R	AGYVTDGRGQ	KVVSLETETT	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG

CRF03_AB_R	AGYVTDGRGRQ	KVVS LTDITN	QKTELHAIHL	ALQDSGLEVN	IVTDSQYALG
CRF04_cpx_	AGYVTDGRGRQ	KVVS LSETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYAIG
CRF04_cpx_	AGYVTDGRGRQ	KVVS LSETTN	QKTELQAIYL	ALKDSGSEVN	IVTDSQYAIG
CRF04_cpx_	AGYVTDGRGRQ	KVITLPETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYAMG
CRF05_DF_B	AGYITDKGRQ	KAVSLTETTN	QKAEHQAIHL	ALQDSGLEVN	IVTDSQYALG
CRF05_DF_B	AGYVTDKGRQ	KAVSLTETTN	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
CRF06_cpx_	AGYVTDGRGRQ	KVVTLTETTN	QKTELQAINL	ALQDSGPEVN	IVTDSQYALG
CRF06_cpx_	AGYVTDGRGRQ	KVVS LAETTN	QKTELQAINL	ALQDSGSEVN	IVTDSQYALG
CRF06_cpx_	AGYVTDKGRQ	RVISLTETTN	QKTELQAINL	ALQDSGSEVN	IVTDSQYALG
CRF06_cpx_	AGYVTDGRGRQ	KVVS LTETTN	QKTELQAINL	ALQDSGSEVN	IVTDSQYALG
CRF11_cpx_	AGYVTDKGRQ	KVITLTETTN	QKTELEAIHL	ALQDSGLEVN	IVTDSQYALG
CRF11_cpx_	AGYVTNKGRQ	KVITPIETTN	QKTELEAIHL	ALKDSGLEVN	IVTDSQYALG
D_CD_84ZR0	AGYVTDGRGRQ	KVVPFTDTTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
D_CD_ELI_K	AGYVTDGRGRQ	KVVPFTDTTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
D_CD_NDK_M	AGYVTDGRGRQ	KVVPFTDTTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
D_UG_94UG1	AGYVTDGRGRQ	KVVS LTDTTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
F1_BE_VI85	AGYVTDKGKQ	KVVS LTETTN	QKAEHQAIYL	ALQDSGSEVN	IVTDSQYALG
F1_BR_93BR	AGYVTDGRGRQ	KAVSLTETTN	QKAEHQAIQL	ALQDSGSEVN	IVTDSQYALG
F1_FI_FIN9	AGYVTDGRGRQ	KVVS LTETTN	QKAEHQAIHL	ALQDSGSEVN	IVTDSQYALG
F1_FR_MP41	AGYVTDGRGRQ	KAVILTETTN	QKAEHQAIHL	ALQDSGSEVN	IVTDSQYVLG
F2_CM_MP25	AGYITDRGRQ	KVVS LTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
F2KU_BE_VI	AGYVTDKGRQ	KVVS LTETTN	QKTELQTIYL	ALQDSGSEVN	IVTDSQYAIG
G_BE_DRCBL	AGYVTDKGRQ	IIITLTETTN	QKAEHQAIQL	ALQDSQSEVN	IVTDSQYALG
G_NG_92NG0	AGHVTDKGKQ	KIITLTETTN	QKAEHQAIQL	ALQDSRPEVN	IVTDSQYALG
G_SE_SE616	AGYVTDKGKQ	KIITLTETTN	QKAEHQAIQL	ALQDSRSEVN	IVTDSQYALG
H_BE_VI991	AGYVTDGRGKQ	KIVSLTETTN	QKTELQAIYL	ALQESGPEVN	IVTDSQYALG
H_BE_VI997	AGYVTDKGKQ	KVVALTETTN	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
H_CF_90CF0	AGYVTDGRGKQ	KVVS LTETTN	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
J_SE_SE702	AGYVTDKGRQ	KVITLTDTTN	QKTELQAIYL	ALQDSGIEVN	IVTDSQYALG
J_SE_SE788	AGYVTDKGRQ	KVVTLTDTTN	QKTELHAIYL	ALRDSGLEVN	IVTDSQYALG
K_CD_EQTB1	AGYVTDKGRQ	KVISITETTN	QKTELQAIHL	ALQDSGSEVN	IVTDSQYALG
K_CM_MP535	AGYVTDGRGRQ	KVVS ITETTN	QKAEHQAIQL	ALQDSGSEVN	IVTDSQYALG
N_CD_YBF30	AGFVTDGRGRQ	KVVS IADTTN	QKAEHQAILM	ALQESGRDVN	IVTDSQYAMG
O_CM_ANT70	AGYVTEQKQ	KIIKLDETTN	QKAEHMAILL	ALQDSKETVN	IVTDSQYALG
O_CM_MVP51	AGYVTEQKQ	NIIKLEETTN	QKAEHMAVLI	ALQDSKEQVN	IVTDSQYVLG
O_SN_99SE_	AGYVTEKGRQ	KIIKLEETTN	QRAELMAVLL	ALQDSKETVN	IVQDSQYVLG
O_SN_99SE_	AGYVTEKGRQ	KIVKLEETTN	QKAEHMAVLL	ALQDSKETVN	IVTDSQYVLG
U_CD_83C	AGYVTDGRGRQ	KVISLTETTN	QKAEHQALYL	ALQDSGLEAN	IVTDSQYALG

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00BW0762_1	IIQAQPDKSE	SELVNQIIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQIDKLVS
00BW0768_2	IIQAQPDKSE	SELVNQIIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVS
00BW0874_2	IIQAQPDKSE	SELVNQIIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVS
00BW1471_2	IIQAQPDSE	SELVNQIIIEQ	LIKDKVYLS	WVPAHKGIGG	NEQVDKLVS
00BW1616_2	IIQAQPDKSE	SELVNQIIIEQ	LINKERIYLS	WVPAHKGIGG	NEQVDKLVS
00BW1686_8	IIQAQPDKSE	SELVNQIIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVS
00BW1759_3	IIQAQPDKSE	SELVNQIIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVS
00BW1773_2	IIQAQPDKSE	SELVNQIIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVS
00BW1783_5	IIQAQPDKSE	SELVNQIIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVS
00BW1795_6	IIQAQPDKSE	SELVSQIIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVS
00BW1811_3	IIQAQPDKSE	SELVNQIIIEQ	LIKKERVYLS	WVPAHKGIGG	NERVDKLVS
00BW1859_5	IIQAQPDKSE	SELVNQIIIEQ	LIKKERVYLS	WVPAHKGIGE	NEQVDKLVS
00BW1880_2	ITQAQPDKSE	SELVNQIIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVS
00BW1921_1	IIQAQPDKSE	SELVNQIIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVS
00BW2036_1	IIQAQPDKSE	SELVNQIIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVS
00BW2063_6	IIQAQPDKSE	SELVNQIIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVS
00BW2087_2	IIQAQPDKSE	SELVNQIIIEQ	LINKKIYLS	WVPAHKGIGG	NEQVDKLVS
00BW2127_2	IIQAQPDKSE	SELVNQIIIEQ	LIKDRVYLS	WVPAHKGIGG	NEQVDKLVS
00BW2128_3	IIQAQPDKSE	SELVNQIIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVS
00BW2276_7	IIQAQPDKSE	SELVNQIIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVS
00BW3819_3	IIQAQPDKSE	SEIVNQIIIEQ	LIQKDRVYLS	WVPAHKGIGG	NEQVDKLVS

00BW3842_8	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW3871_3	IIQAQPDKSE	SELVNQIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW3876_9	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW3886_8	IIQAQPDKSE	SELVNQIIEQ	LIKKEGVYLS	WVPAHKGIGG	NEQVDKLVSK
00BW3891_6	IIQSQPGKSE	SELVNQKIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSK
00BW3970_2	IIQAQPDTSSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW5031_1	IIQAQPDKSE	SELVNQIIEQ	LIKKERIYLS	WVPAHKGIGG	NEQIDKLVSS
96BW01B21	IIQAQPDKSE	SELVNQMIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
96BW0407	IIQAQPDKSE	SELVTQIIEQ	LIKKERIYLS	WVPAHKGIGG	NEQVDKLVSS
96BW0502	IIQAQPDKSE	SELVNQIIEQ	LIQKEWVYLS	WVPAHKGIGG	NEQVDKLVSS
96BW06_J4	IIQAQPDKSE	SELVNQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSN
96BW11_06	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEKVDKLVSS
96BW1210	IIQAQPDKSE	SELVNQIIEQ	LICKERVYLS	WVPAHKGIGG	NEQVDKLVSS
96BW15B03	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQIDKLVSK
96BW16_26	IIQAQPDKSE	SELVNQIIEQ	LINKERIYLS	WVPAHKGIGG	HEQVDKLVSS
96BW17A09	IIQAQPDSESE	SELVNQIIEQ	LIQKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
96BWM01_5	IIQAQPDKSE	SELVNQIIEQ	LIKKDRVYLS	WVPAHKGIGG	NEQVDKLVSS
96BWM03_2	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
98BWMC12_2	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
98BWMC13_4	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
98BWMC14_a	IIQAQPDKSE	SELVNQIIEQ	LIQKERVYLS	WVPAHKGIGG	NEQVDKLVSS
98BWM014_1	IIQAQPDKSE	SELVNQIIEQ	LINKKIYLS	WVPAHKGIGG	NEQVDKLVSS
98BWM018_d	IIQAQPDKSE	SEIVNQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSR
98BWM036_a	IIQAQPDKSE	SELVNQIIEQ	LINKEKIYLS	WVPAHKGIGG	NEQVDKLVSS
98BWM037_d	IIQAQPDNSE	SELVNQIIEQ	LIQKERVYLS	WVPAHKGIGG	NEQVDKLVSK
99BW3932_1	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
99BW4642_4	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSN
99BW4745_8	IIQAQPDKSE	AELVNQIIEQ	LIQKERVYLS	WVPAHKGIGG	NEQVDKLVSK
99BW4754_7	IIQAQPDKSE	SELVNQIIEQ	LIKKKKVYLS	WVPAHKGIGG	NEQVDKLVSS
99BWMC16_8	IIQAQPDKSE	SELVNQIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSN
A2_CD_97CD	IIQAQPDSSSE	SELVNQIIEE	LIEKERVYLS	WVPAHKGIGG	NEQVDKLVSS
A2_CY_94CY	IIQAQPERSE	SEIVNQIIEE	LIEKERVYLS	WVPAHKGIGG	NEQVDKLVSS
A2D_97KR	IIQAQPDPRSE	SEIVNLIIEE	LIEKERVYLS	WVPAHKGIGE	NEQVDKLVSS
A2G_CD_97C	IIQAQPDSSSE	AEIVNQIIEQ	LIRKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_BY_97BL0	IISAQPDPRSE	SEIVNKIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSN
A_KE_Q23_A	IIQAQPDKSE	SEIVNQIIEE	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE659	IIQAQPDPRSE	SELVNQIIEE	LVGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE725	IIQAQPDSSSE	SEIVNQIIEE	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE753	IIQAQPDPRSE	SELVNQIIEE	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE853	IIQAQPDSSSE	SELVNQIIEE	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE889	IIQAQPDPRSE	SELVNQIIEE	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSA
A_SE_UGSE8	IIQAQPDKSE	SELVNQIIEE	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_UG_92UG0	IIQAQPDPRSE	SELVNQIIEE	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_UG_U455_	IIQAQPDPRSE	SEIVNQIIEE	LIEKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
AC_IN_2130	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSN
AC_RW_92RW	IIQAQPDSSSE	SEAVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
AC_SE_SE94	IIQAQPDPRSE	SEIVNQIIEE	LIQKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
ACD_SE_SE8	IIQAQPDPRSE	SELVNQIIEE	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
ACG_BE_VI1	IIQAQPDKSE	SELVNQIIEQ	LIRKDRVYLS	WVPAHKGIGG	NEQVDKLVSS
AD_SE_SE69	IIQAQPDKSE	SELVSQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSN
AD_SE_SE71	IIQAQPDPRSE	SELVNQIIEE	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
ADHK_NO_97	IIQAQPDKSE	SDLVNQIIEQ	LIQKDKVYLT	WVPAHKGIGG	NEQVDKLVSS
ADK_CD_MAL	IIQAQPDKSE	SEIVNQIIEQ	LIQKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
AG_BE_VI11	IIQAQPDPRSE	SELVNQIIEE	LIEKDKVYVS	WVPAHKGIGG	NEQVDKLVSS
AG_NG_92NG	IIQAQPDPRSE	SELVNQIIEQ	LIKKEKVYLT	WVPAHKGIGG	NEQVDKLVSS
AGHU_GA_VI	IIQAQPDKSE	SELVNQIIEE	LIQKNKVYLS	WVPAHKGIGG	NEKVDKLVSA
AGU_CD_Z32	IIQAQPDKSE	SELVSQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
AJ_BW_BW21	IIQAQPDKSE	SELVSQIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
B_AU_VH_AF	IIQAQPDKSE	SELVNQIIEQ	LIKKEKIYLA	WVPAHKGIGG	NDKVDKLVSA
B_CN_RL42	IIQAQPDKSE	SELVSQIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQIDKLVSA
B_DE_D31_U	IIQAQPDKSE	SELVSQIIEQ	LIKKEKVYLT	WVPAHKGIGG	NEQVDKLVSA

B_DE_HAN_U	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_FR_HXB2_	IIQAQPDQSE	SELVNQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_GA_OYI_	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_GB_CAM1_	IIQAQPDKSE	SELVSQIIEE	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_GB_GB8_A	IIQAQPDRSE	SEVVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSS
B_GB_MANC_	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_KR_WK_AF	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_NL_3202A	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_TW_TWCYS	IIQAQPDKSE	SELVSQIIEE	LIIKKEKVYLT	WVPAHKGIGG	NEQVDKLVSA
B_US_BC_L0	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_DH123	IIQAQPDKSE	SELVNQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVST
B_US_JRCFS	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_MNCG_	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_P896_	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_RF_M1	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDRLVST
B_US_SF2_K	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_WEAU1	IIQAQPDQSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSS
B_US_WR27_	IIQAQPDKSE	SELVSQIIEQ	LIXKXXVYLA	WVPAHKGIGG	NEQVDKLVSS
B_US_YU2_M	IIQAQPDRSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
BF1_BR_93B	IIQAQPDKSE	LEIVNQIIEQ	LIIKKEKIYLA	WVPAHKGIGG	NEQVDKLVSS
C_BR_92BR0	IIQAQPDKSE	SELVNQIIEQ	LIIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_BW_96BW0	IIQAQPDKSE	SELVTQIIEQ	LIIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_BW_96BW1	IIQAQPDKSE	SELVNQIIEQ	LIIKKEKVYLS	WVPAHKGIGG	NEKVDKLVSS
C_BW_96BW1	IIQAQPDKSE	SELVNQIIEQ	LICKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_BW_96BW1	IIQAQPDKSE	SELVNQIIEQ	LIIKKEKVYLS	WVPAHKGIGG	NEQIDKLVS
C_ET_ETH22	IIQAQPDKSE	SEIVNQIIEQ	LISKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_93IN1	IIQAQPDKSE	SELVNQIIEQ	LIIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_93IN9	IIQAQPDKSE	SELVNQIIEQ	LIIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_93IN9	IIQAQPDKSE	SELVNQIIEQ	LIIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_94IN1	IIQAQPDKSE	SELVNQIIEQ	LIIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_95IN2	IIQAQPNKSE	SELVNQIIEQ	LIIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF01_AE_C	IIQAQPDRSE	SEIVNQIIEK	LIEKERVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF01_AE_C	IIQAQPDRSE	SDIVNQIIEK	LIEKERVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF01_AE_C	IIQAQPDRSE	SEIVNQIIEK	LIEKERVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF01_AE_T	IIQAQPDRSE	SEVVNQIIEE	LIIKKEKVYLS	WVPAHKGIGG	DEQVDKLVSS
CRF01_AE_T	IIQAQPDRSE	SEVVSQMIEE	LIIKKEKDYLS	WVPAHKGIGG	NEQVDKLVSS
CRF01_AE_T	IIQAQPDRSE	SEVVSQIIEE	LIIKKEKVYLS	WVPAHKGIGG	NEQVDKLVIS
CRF01_AE_T	IIQAQPDRSE	SEVVNQLIBE	LIIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF01_AE_T	IIQAQPDRSE	SEVVNQIIEE	LIIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF01_AE_T	IIQAQPDRSE	SEVVNQIIEE	LIIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF02_AG_F	IIQAQPDRSE	SELVNQIIEK	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVS
CRF02_AG_F	IIQAQPDRSE	SELVNQIIEK	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVS
CRF02_AG_G	IIQAQPDRSE	SELVNQIIEK	LIGKDKVYLS	WVPAHKGIGG	NEQVDNLVSS
CRF02_AG_N	IIQAQPDRSE	SELVNQIIEK	LIIKDKVYLS	WVPAHKGIGG	NEQVDKLVS
CRF02_AG_S	IIQAQPDRSE	SELVTQIIEE	LIIKDRVYLS	WVPAHKGIGG	NEQVDKLVS
CRF02_AG_S	IIQAQPDRSE	SELVNQIIEK	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVS
CRF03_AB_R	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLA	WVPAHKGIGG	NEQVDKLVS
CRF03_AB_R	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKFYLA	WVPAHKGIGG	NEQVDKLVS
CRF04_cpx_	IIQAQPDRSE	SDLVNQIIEQ	LIRKDKVYLS	WVPAHKGIGG	NEQVDKLVS
CRF04_cpx_	IIQAQPDRSE	SDLVNQIIEE	LIIQDKVYLS	WVPAHKGIGG	NEQVDKLVS
CRF04_cpx_	IIQAQPDKSE	SDLVNQIIEQ	LIIQDKVYLS	WVPAHKGIGG	NEQVDKLVS
CRF05_DF_B	IIQAQPDKSE	SELVNQIIEQ	LIEKKKVYLS	WVPAHKGIGG	NEQVDKLVS
CRF05_DF_B	IIQAQPDKSE	SELVNKIIIEQ	LVQKERVYLS	WVPAHKGIGG	NEQVDKLVS
CRF06_cpx_	IIQAQPDKSE	SELVNQIIEQ	LIIKKEKIYLS	WVPAHKGIGG	NEQVDKLVS
CRF06_cpx_	IIQAQPDKSE	SELVNQIIEQ	LIIKKEKVYLS	WVPAHKGIGG	NEQVDKLVS
CRF06_cpx_	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLS	WVPAHKGIGG	NEQVDKLVS
CRF06_cpx_	IIQAQPDRSE	SELVNQIIEQ	LIIKKEKVYLS	WVPAHKGIGG	NEQVDKLVS
CRF11_cpx_	IIQAQPDKSE	SELVSQIIEQ	LIIKKEKVYLT	WVPAHKGIGG	NEQVDKLVS
CRF11_cpx_</					

D_CD_NDK_M	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSQ
D_UG_94UG1	IIQAQPDKSE	SEVVSQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSN
F1_BE_VI85	IIQAQPDKSE	SEIVNQIIEQ	LIQKERVYLS	WVPAHKGIGG	NEQVDKLVSA
F1_BR_93BR	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSA
F1_FI_FIN9	IIQAQPDKSE	SELVNQIIEQ	LIQKEKIYLS	WVPAHKGIGG	NEQVDKLVSA
F1_FR_MP41	IIQAQPDKSE	SEIVNKIIEK	LIQKERVYLS	WVPAHKGIGG	NEQVDRLVSA
F2_CM_MP25	IIQAHPDKSE	SEIVNQIIEQ	LIQKERVYLS	WVPAHKGIGG	NEQVDKLVST
F2KU_BE_VI	IIQAQPDKSE	SELVNQIIEQ	LIQKDQIYLS	WVPAHKGIGG	NEQVDKLVSS
G_BE_DRCBL	IIQAQPDPRSE	SEIVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
G_NG_92NG0	IIQAQPDPRSG	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
G_SE_SE616	IIQAQPDPRSE	AELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
H_BE_VI991	IIQAQPDKSE	SELVNQIIEE	LIKKEKFYLS	WVPAHKGIGG	NEQVDKLVSS
H_BE_VI997	IIQAQPDKSE	SELVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
H_CF_90CF0	IIQAQPDKSE	SELVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
J_SE_SE702	IIQAQPDKSE	SELVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
J_SE_SE788	IIQAQPDKSE	SELVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
K_CD_EQTB1	IIQAQPDKSE	SELVNQIIEQ	LIKKDRVYLS	WVPAHKGIGG	NEQVDKLVSS
K_CM_MP535	IIQAQPDKSE	SDLVNQIIEQ	LIKKERYLS	WVPAHKGIGG	NEQVDKLVSA
N_CM_YBF30	IIHSQPDKSE	SELVSIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
O_CM_ANT70	VISSQPTQSE	SPIVQIIEE	LTKKEQVYLT	WVPAHKGIGG	NEKIDKLVSK
O_CM_MVP51	IISSQPTQSD	SPIVQIIEE	LTKKERVYLT	WVPAHKGIGG	NEKIDKLVSK
O_SN_99SE_	IISSQPTQSE	SSLVQIIEE	LTKKEQVYLT	WVPAHKGIGG	NEKIDKLVSK
O_SN_99SE_	IISSQPTQSE	SPLVQIIEE	LTKKEQVFLT	WVPAHKGIGG	NEKIDKLVSK
U_CD___83C	IIQAQPDSSSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQADKLVSA

751

800

00BW0762_1	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKQC
00BW0768_2	GIRRVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKQC
00BW0874_2	GIRKALFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKQC
00BW1471_2	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKQC
00BW1616_2	GIRKVLFLDG	IDKAQEEHEK	YHSSWRAMAN	EFNLPPIVAK	EIVASCDKQC
00BW1686_8	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPVVA	EIVASCDKQC
00BW1759_3	GIRKVLFLDG	IDKAQGGSEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKQC
00BW1773_2	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVA	EIVASCDKQC
00BW1783_5	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKQC
00BW1795_6	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKQC
00BW1811_3	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPVVA	EIVASCDKQC
00BW1859_5	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKQC
00BW1880_2	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPVVA	EIVASCDKQC
00BW1921_1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPVVA	EIVASCDKQC
00BW2036_1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKQC
00BW2063_6	GIRKVLFLDG	IDKAQEDHER	YHSNWRMTAS	EFNLPPIVAK	EIVASCDKQC
00BW2087_2	GVRRVLFLDG	IDKAQEDHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKQC
00BW2127_2	GIRKVLFLNG	IDKAQEEHEK	YHSNWRAMAN	EFNLPPVVA	EIVASCDKQC
00BW2128_3	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKQC
00BW2276_7	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKQC
00BW3819_3	GIRKVLFLDG	IDKAQEDHEK	YHNNWRAMVS	EFNLPPIVAK	EIVASCDKQC
00BW3842_8	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKQC
00BW3871_3	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKQC
00BW3876_9	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKQC
00BW3886_8	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKQC
00BW3891_6	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPVVA	EIVASCDKQC
00BW3970_2	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKQC
00BW5031_1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRSMAS	DFNLPPIVAK	EIVASCDKQC
96BW01B21	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	EFNLPPIVAK	EIVASCDKQC
96BW0407	GIRKVLFLDG	IDKAQEEHEK	YHCNWRAMAS	DFNLPPVVA	EIVASCDKQC
96BW0502	GIRKMLFLDG	IDKAQEEHEK	YHNNWRAMAD	EFNLPPIVAK	EIVASCDKQC
96BW06_J4	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKQC
96BW11_06	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKQC
96BW1210	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKQC
96BW15B03	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKQC

96BW16_26	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
96BW17A09	GIRKVLFLDG	IDKAQEDHEK	YHGNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
96BWM01_5	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
96BWM03_2	GIRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWMC12_2	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWMC13_4	GIRKVLFLDG	IDKAQDDHER	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
98BWMC14_a	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWM014_1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRARAS	EFNLPPIVAK	EIVASCDKCQ
98BWM018_d	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWM036_a	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWM037_d	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
99BW3932_1	GIRKVLFLDG	IDKAREEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
99BW4642_4	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
99BW4745_8	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPVVAK	EIVASCDKCQ
99BW4754_7	GIRKILFLDE	IDKAQDEHEK	YHSNWRAMAS	EFNLPPVVAK	EIVACCDKCQ
99BWMC16_8	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
A2_CD_97CD	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAH	DFNLPPIVAK	EIVASCDKGQ
A2_CY_94CY	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAH	DFNLPPVVAK	EIVASCDKCQ
A2D_97KR	GIRKVLFLDG	IDKAQDEHEK	YRSNWRAMAH	DFNLPPVVAK	EIVACCDKCQ
A2G_CD_97C	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKGQ
A_BY_97BL0	XIRXVLFLEX	IDKAQEXHEK	YHSN.KAMAS	DFNLPPIVAK	EIVASXDKCQ
A_KE_Q23_A	GIRKVLFLDG	IDKAQEEHER	YHSNWRMTAS	DFNLPPIVAK	EIVASCDKCQ
A_SE_SE659	GIRKVLFLDG	IDKAQEEHER	YHSNWRMTAS	DFNLPPVIAK	EIVASCDKCQ
A_SE_SE725	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
A_SE_SE753	GIRKVLFLDG	IDKAQEEHER	YHSNWRMTAS	DFNLPPIVAK	EIVASCDKCQ
A_SE_SE853	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPVIAK	EIVASCNKCQ
A_SE_SE889	GVRRIFLDG	IDKAQEEHER	YHSNWRMTAS	DFNLPPIVAK	EIVASCDKCQ
A_SE_UGSE8	GIRKVLFLDG	IDKAQEEHER	YHSNWRMTAS	DFNLPPIVAK	EIVASCDKCQ
A_UG_92UG0	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
A_UG_U455_	GIRKVLFLDG	IDKAQEDHEK	YHCNWRAMAS	DFNLPPVVAK	EIVASCNKCQ
AC_IN_2130	GIRRVFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPIIAK	EIVASCNQCQ
AC_RW_92RW	GIRRVFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
AC_SE_SE94	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
ACD_SE_SE8	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
ACG_BE_VI1	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
AD_SE_SE69	GIRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
AD_SE_SE71	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
ADHK_NO_97	GIRKVLFLDG	IDKAQEAHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
ADK_CD_MAL	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
AG_BE_VI11	GIRKVLFLDG	IDKAQADHER	YHXNWGAMAS	DFNLPPIVAK	EIVASCDKCQ
AG_NG_92NG	GIRKVLFLDG	IDKAQEDHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
AGHU_GA_VI	GIRKVLFLDG	IDKAQEDHER	YHSNWKAMAS	DFNLPPIVAK	EIVASCDKCQ
AGU_CD_Z32	GIRKVLFLDG	IDKAQEEHER	YHCNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
AJ_BW_BW21	GIRKVLFLDG	IDKAQEEHEK	YHSKWRAMAS	DFNLPPIVAK	EIVASCDKCQ
B_AU_VH_AF	GIRKVLFLDG	IDKAQDDHEI	YHSNWRAMAN	DFYLPPIVAK	DIVASCDKCQ
B_CN_RL42_	GIRKVLFLDG	IDKAQEEHEK	YHCNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
B_DE_D31_U	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
B_DE_HAN_U	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAN	DFNLPPVVAK	EIVASCDKCQ
B_FR_HXB2_	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
B_GA_OYI_	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
B_GB_CAM1_	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
B_GB_GB8_A	GIRKILFLDG	IDKAQEDHEK	YHSNWRAMAN	DFNLPPVVAK	EIVASCDKCQ
B_GB_MANC_	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
B_KR_WK_AF	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAG	DFNLPPVVAK	EIVACCDKCQ
B_NL_3202A	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
B_TW_TWCYS	GIRKVLFLDG	IDRAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
B_US_BC_L0	GVRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
B_US_DH123	GIRRVFLFLDG	IEKAQEEHEK	YHSNWRAMAS	EFNLPAVVAK	EIVACCDKCQ
B_US_JRCSF	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
B_US_MNCG_	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
B_US_P896_	GIRKVLFLDG	IDKAQEEHEK	YHTNWRAMAS	DFNLPPVVAK	EIVASCNKCQ

B_US_RF_M1	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
B_US_SF2_K	GIRKVLFLNG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
B_US_WEAU1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
B_US_WR27_	GIRKVLFXDG	IDXAQEDHEK	YHSNWRAMAG	EFNLPPVXAK	EIVACCDKCQ
B_US_YU2_M	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
BF1_BR_93B	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNIPPVVAK	EIVASCDKCQ
C_BR_92BR0	GIRKVLFLDG	INKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
C_BW_96BW0	GIRKVLFLDG	IDKAQEEHEK	YHCNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
C_BW_96BW1	GIREVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
C_BW_96BW1	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
C_BW_96BW1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
C_ET_ETH22	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAN	EFNIPPVVPK	EIVACCDKCQ
C_IN_93IN1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDQCQ
C_IN_93IN9	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDQCQ
C_IN_93IN9	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCGQCQ
C_IN_94IN1	GIRRVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDQCQ
C_IN_95IN2	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPVVAK	EIVASCDQCQ
CRF01_AE_C	GIRKVLFLDG	IDKAQEEHER	YHSNWRMTAS	DFNLPPIVAK	EIVANCDKCQ
CRF01_AE_C	GIRKVLFLDG	IDKAQEDHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
CRF01_AE_C	GIRKVLFLDG	IDKAQEEHER	YHSNWRMTAS	DFNLPPIVAK	EIVANCDKCQ
CRF01_AE_T	GIRKVLFLDG	IDKAQEEHER	YHSNWRMTAS	DFNLPPIVAK	EIVANCDKCQ
CRF01_AE_T	GIRKVLFLDG	IDKAQEEHER	YHSNWRMTAS	DFNLPPIVAK	EIVANCDKCQ
CRF01_AE_T	GIRKVLFLDG	INKAQEEHER	YHSNWRMTAS	DFNLPPIVAK	EIVANCDKCQ
CRF01_AE_T	GIRKVLFLDG	IDKAQEEHER	YHSNWRMTAS	DFNLPPVVAK	EIVANCDKCQ
CRF01_AE_T	GIRKVLFLDG	IDKAQEEHER	YHSNWRMTAS	DFNLPPIVAK	EIVTNCDCQ
CRF01_AE_T	GIRKVLFLDG	IDKAQEEHER	YHSNWRMTAS	DFNLPPIVAK	EIVANCDKCQ
CRF02_AG_F	GIRKVLFLDG	IDKAQEEHGR	YHSNWRAMAS	DFNLPPIIAK	EIVACCDQCQ
CRF02_AG_F	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPIVAK	EIVACCDKCQ
CRF02_AG_G	GFRKILFLDG	LDKAQEEHEK	FHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
CRF02_AG_N	GIRKVLFLDG	IDKAQEEHER	YHSNWKAMAS	DFNLPPIVAK	EIVASCDKCQ
CRF02_AG_S	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
CRF02_AG_S	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
CRF03_AB_R	GIREVLFLDG	IDKAQEEHEK	YHGNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
CRF03_AB_R	GIRKVLFLDG	IDKAQEAHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
CRF04_cpx_	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPSVVAK	EIVASCNKCQ
CRF04_cpx_	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCNKCQ
CRF04_cpx_	GIRKVLFLDG	IDKAQEEHEK	YHNNWKAMAS	DFNLPPVVAK	EIVASCNKCQ
CRF05_DF_B	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
CRF05_DF_B	GIRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
CRF06_cpx_	GIRKVLFLDG	IDKAQEDHER	YHSNWRAMAN	DFNLPPIVAK	EIVASCDKCQ
CRF06_cpx_	GIRKVLFLDG	IDKAQEDHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
CRF06_cpx_	GIRKVLFLDG	IDKAQEDHER	YHSNWRAMAS	DFNLPPILAK	EIVACCDKCQ
CRF06_cpx_	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAN	DFNLPPIVAK	EIVASCDKCQ
CRF11_cpx_	GIRKVLFLDG	IDKAQEDHDR	YHSNWRMTAS	DFNLPPIVAK	EIVASCDKCQ
CRF11_cpx_	GIRKVLFLDG	IDKAPEGHER	YHSNWRAMAS	DFNLPPVIAK	EIVANCDKCQ
D_CD_84ZR0	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
D_CD_ELI_K	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
D_CD_NDK_M	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
D_UG_94UG1	GIRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	EFNLPPVVAK	EIVASCDKCQ
F1_BE_VI85	GVRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
F1_BR_93BR	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNIPAVVAK	EIVASCDKCQ
F1_FI_FIN9	GIRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
F1_FR_MP41	GIRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
F2_CM_MP25	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
F2KU_BE_VI	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
G_BE_DRCBL	GIRKVLFLDG	IDKAQEEHER	YHSNWKAMAS	DFNLPPIVAK	EIVASCDKCQ
G_NG_92NG0	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCQ
G_SE_SE616	GIRKVLFLDG	IDKAQEEHER	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
H_BE_VI991	GIRKVLFLDG	IDKAQVQHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
H_BE_VI997	GIRKVLFLDG	IDKAQEAHER	YHNNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
H_CF_90CF0	GVRKVLFLDG	IDKAQEEHER	YHNNWRAVAS	DFNLPPIVAK	EIVASCDKCQ

J_SE_SE702	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVAK	EIVASCDKCQ
J_SE_SE788	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAS	DFNLPPVAK	EIVASCDKCQ
K_CD_EQTB1	GIRKVLFLDG	IDKAEHEHEK	YHNNWRAMAS	DFNLPPVAK	EIVASCDKCQ
K_CM_MP535	GIRKVLFLDG	IDKAEHEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
N_CM_YBF30	GIRKILFLDG	IEKAQEDHDR	YHSNWKAMAS	DFNLPPIVAK	EIVASCDKCQ
O_CM_ANT70	DIRRVLFLEG	IDQAQEDHEK	YHSNWKALAS	DFGLPPVAK	EIIASCPKCH
O_CM_MVP51	DIRRVLFLEG	IDQAQEDHEK	YHSNWRALAS	DFGLPPIVAK	EIIASCPKCH
O_SN_99SE_	DIRRVLFLEG	IDQAQEDHEK	YHSNWRALAS	DFGLPPVAK	EIIANCPQCH
O_SN_99SE_	DIRRVLFLEG	IDQAQEDHEK	YHSNWRALAS	DFGLPPVAK	EIIANCPKCH
U_CD___83C	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ

	801			850	
00BW0762_1	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKTIL	VAVHVASGYM	EAEVIPAETG
00BW0768_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
00BW0874_2	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW1471_2	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW1616_2	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW1686_8	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW1759_3	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPTETG
00BW1773_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVII	VAVHVASGYI	EAEVIPAETG
00BW1783_5	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW1795_6	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIVL	VAVHVASGYL	EAEVIPTETG
00BW1811_3	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW1859_5	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
00BW1880_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVTPEETG
00BW1921_1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW2036_1	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIII	VAAHVASGYI	EAEVIPAETG
00BW2063_6	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYV	EAEVIPAETG
00BW2087_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW2127_2	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW2128_3	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW2276_7	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYM	EAEVIPAETG
00BW3819_3	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAIHVASGYM	EAEVTPAETG
00BW3842_8	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW3871_3	LKGEATHRQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW3876_9	QKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW3886_8	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKTIL	VAVHVASGYI	EAEVIPAETG
00BW3891_6	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW3970_2	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW5031_1	LKGEAMHGQV	DCSPGVWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
96BW01B21	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYM	EAEVIPAETG
96BW0407	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
96BW0502	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYM	EAEVIPAETG
96BW06_J4	SKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
96BW11_06	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
96BW1210	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVRVASGYI	EAEVIPAETG
96BW15B03	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
96BW16_26	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
96BW17A09	LKGEAMHGQV	DCSPGMWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
96BWM01_5	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
96BWM03_2	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYM	EAEVIPAETG
98BWMC12_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVITAETG
98BWMC13_4	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
98BWMC14_a	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVISAETG
98BWM014_1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
98BWM018_d	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
98BWM036_a	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
98BWM037_d	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIII	VAVHVASGYV	EAEVIPAETG
99BW3932_1	LKGEATHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
99BW4642_4	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
99BW4745_8	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG

99BW4754_7	QKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
99BWMC16_8	LKGEAIHGQV	DCSPGVWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A2_CD_97CD	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIV	VAVHVASGYI	EAEVIPAETG
A2_CY_94CY	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPTETG
A2D_97KR	VKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
A2G_CD_97C	LKGEAMHGQV	DCSPGVWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
A_BY_97BL0	LKXEXMHXQV	DCSPXIWQLD	CTHLXXXKVII	XAVXVASGYI	EAEVIPAETG
A_KE_Q23_A	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIV	VAVHVASGYI	EAEVIPAETG
A_SE_SE659	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_SE725	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_SE753	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_SE853	LKGEAMHGQV	DCSPGMWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_SE889	LKGEAMHGQV	DCSPGMWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_UGSE8	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_UG_92UG0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYV	EAEVIPAETG
A_UG_U455_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
AC_IN_2130	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
AC_RW_92RW	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHAASGYI	EAEVIPAETG
AC_SE_SE94	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
ACD_SE_SE8	IKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
ACG_BE_VI1	LKGEAMHGQV	DCSPGIWQID	CTHLEGKVII	VAVHVASGYM	EAEVIPAETG
AD_SE_SE69	LKGEALHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
AD_SE_SE71	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
ADHK_NO_97	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
ADK_CD_MAL	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIII	VAVHVASGYI	EAEVIPAETG
AG_BE_VI11	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIII	VAVHVASGYI	EAEVIPAETG
AG_NG_92NG	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVII	VAVHVASGYI	EAEVIPAETG
AGHU_GA_VI	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
AGU_CD_Z32	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
AJ_BW_BW21	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVII	VAVHVASGYM	EAEVIPAETG
B_AU_VH_AF	QKGEAMHGQV	DCSPGLWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_CN_RL42_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_DE_D31_U	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_DE_HAN_U	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPVETG
B_FR_HXB2_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_GA_OYI_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_GB_CAM1_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_GB_GB8_A	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_GB_MANC_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_KR_WK_AF	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_NL_3202A	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_TW_TWCYS	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_BC_L0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_DH123	VKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_US_JRCSF	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_MNCG_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_US_P896_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_US_RF_M1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_SF2_K	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_WEAU1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_WR27_	LKGEAMHGQV	DCSPGIWXL	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_YU2_M	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
BF1_BR_93B	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVAGGYI	EAEVIPAETG
C_BR_92BR0	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_BW_96BW0	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_BW_96BW1	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
C_BW_96BW1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVRVASGYI	EAEVIPAETG
C_BW_96BW1	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_ET_ETH22	LKGEAIHGQV	NCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_IN_93IN1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_IN_93IN9	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG

C_IN_93IN9	QKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_IN_94IN1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
C_IN_95IN2	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
CRF01_AE_C	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_C	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_C	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_F	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_F	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_G	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_N	MKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_S	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_S	LKGEAMHGQV	DCSPGIWQID	CTHLEGKIII	VAVHVASGYI	EAEVIPAETG
CRF03_AB_R	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF03_AB_R	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF04_cpx_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIM	VAVHVASGYI	EAEVIPAETG
CRF04_cpx_	LKGEAMHGQX	DCSPGIWQLD	CTHLEGKIIL	VPVHVASGYI	EAEVIPAETG
CRF04_cpx_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF05_DF_B	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF05_DF_B	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF06_cpx_	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF06_cpx_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF06_cpx_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF06_cpx_	LKGEPMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF11_cpx_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIM	VAVHVASGYI	EAEVIPTETG
CRF11_cpx_	LKGEAMHGQV	DCSPRIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
D_CD_84ZR0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
D_CD_ELI_K	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
D_CD_NDK_M	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
D_UG_94UG1	VKGEALHGQV	DCSPGIWQLD	CTHLEGKGIL	VAVHVASGYI	EAEVIPAETG
F1_BE_VI85	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASEYI	EAEVIPAETG
F1_BR_93BR	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYL	EAEVIPAETG
F1_FI_FIN9	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
F1_FR_MP41	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
F2_CM_MP25	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
F2KU_BE_VI	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
G_BE_DRCBL	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
G_NG_92NG0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIII	VAVHVASGYI	EAEVIPAETG
G_SE_SE616	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIII	VAVHVASGYI	EAEVIPAETG
H_BE_VI991	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
H_BE_VI997	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	XPEVIPAETG
H_CF_90CF0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGQVIL	VAVHVASGYI	EAEVIPAETG
J_SE_SE702	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
J_SE_SE788	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
K_CD_EQTB1	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
K_CM_MP535	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
N_CM_YBF30	LKGEAMHGQV	DCSPGVWQLD	CTHLEGKIIL	VAVHVASGYL	EAEVIPAETG
O_CM_ANT70	IKGEATHGQV	DCSPEVWQID	CTHMEGKIII	VAVHVASGFI	EAEVIPAETG
O_CM_MVP51	IKGEATHGQV	DYSPEIWQMD	CTHLEGKIII	VAVHVASDFI	EAEVIPAETG
O_SN_99SE_	IKGEATHGQV	DCSPEVWQMD	CTHLEGKIII	VAVHVASGFI	EAEVIPAETG
O_SN_99SE_	IKGEATHGQV	DYSPEVWQID	CTHLEGKIII	VAVHVASGFI	EAEVIPAETG
U_CD___83C	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYL	EAEVIPAETG

851

900

00BW0762_1	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW0768_2	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN

00BW0874_2	QDTAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAD	IQQEFGIPYN
00BW1471_2	QEAAAYFILKL	AGRWPVQIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1616_2	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1686_8	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1759_3	QETAYLILKL	AGRWPVKIIH	TDNGSNFTST	TVKAACWWAG	IQQEFGIPYN
00BW1773_2	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	VQQEFGIPYN
00BW1783_5	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	TVKAACWWAG	IQQEFGIPYN
00BW1795_6	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1811_3	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSN	AMKAACWWAG	IQQEFGIPYN
00BW1859_5	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1880_2	QETAYYILKL	AGRWPVKIIH	TDNGRNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1921_1	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
00BW2036_1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW2063_6	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW2087_2	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW2127_2	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW2128_3	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYS
00BW2276_7	QETAYFILKL	AGRWPVKVIH	TDNGSNFTST	TVKAACWWAG	IQQEFGIPYN
00BW3819_3	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	IQQEFGIPYN
00BW3842_8	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW3871_3	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	VVKAACWWAG	IQQEFGIPYN
00BW3876_9	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSS	AVKAACWWAG	TQQGFGIPYN
00BW3886_8	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW3891_6	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	IQQEFGIPYN
00BW3970_2	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IKQEFGIPYN
00BW5031_1	QETVYFILKL	AGRWPVKAIH	TDNGSNFTSA	AVKAACWWAG	INQEFGIPYN
96BW01B21	QETAYYILKL	AGRWPVKVIH	TDNGTNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW0407	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
96BW0502	QETAYFILKL	AGRWPVRVIH	TDNGTNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW06_J4	QDTAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW11_06	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW1210	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	TQQEFGIPYN
96BW15B03	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW16_26	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	TVKAACWWAG	IQQEFGIPYN
96BW17A09	QETADFILKL	AGRWPVQIIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
96BWM01_5	QETAYFLLKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
96BWM03_2	QDTAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AMKAACWWAG	IQQEFGIPYN
98BWMC12_2	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSG	AVKAACWWAG	IQQEFGIPYN
98BWMC13_4	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWMC14_a	QETAYYILKL	AARWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWM014_1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWM018_d	QETAYYILKL	AGRWSVKTIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWM036_a	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWM037_d	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
99BW3932_1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
99BW4642_4	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
99BW4745_8	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
99BW4754_7	QETAYYILKL	AGRWPVKTIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
99BWMC16_8	QDTAYYMLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	VQQEFGIPYN
A2_CD_97CD	QETAYFLLKL	AGRWPVKVIH	TDNGPNFTSA	AVKAACWWAD	VKQEFGIPYN
A2_CY_94CY	QDTAYFILKL	AGRWPVKVIH	TDNGPNFISA	TVKAACWWAG	IQQEFGIPYN
A2D_97KR	QETAYFILKL	AGRWPVKVIH	TDNGPNFISA	PVKAACWWAG	VQQEFGIPYN
A2G_CD_97C	QETAYFILKL	AGGWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
A_BY_97BL0	QETAYFLLKL	AGRWPVKVVH	TDNGPNFTSS	AVKAACWAN.	IQQEFXIPYN
A_KE_Q23_A	QETAYFLLKL	AGRWPVKIVH	TDNGSNFTSA	AVKAACWWAN	IQQEFGIPYN
A_SE_SE659	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	IQQEFGIPYN
A_SE_SE725	QETAYFLLKL	AGRWPVKIVH	TDNGSNFTSA	AFKAACWWAS	IQQEFGIPYN
A_SE_SE753	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VKQEFGIPYN
A_SE_SE853	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AFKAACWWAN	VQQEYGIPYN
A_SE_SE889	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AFKAACWWAN	VQQEFGIPYN
A_SE_UGSE8	QEAAAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AFKAACWWAN	VQQEFGIPYN

A_UG_92UG0	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	VKQEFGIPYN
A_UG_U455_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAVCWWAN	IQQEFGIPYN
AC_IN_2130	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
AC_RW_92RW	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	TVKAACWWAG	IQQEFGIPYN
AC_SE_SE94	QETAYFLLKL	AGRWPVRRVH	TDNGSNFTSA	AVKAACWWAN	IQQEFGIPYN
ACD_SE_SE8	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AFKAACWWAS	VQQEFGIPYN
ACG_BE_VI1	QETAYFLLKL	AGRWPVRVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
AD_SE_SE69	QETAYFLLKL	AGRWPVRVVH	TDNGSNFTST	AVKAACWWAG	IKQEFGIPYN
AD_SE_SE71	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
ADHK_NO_97	QETAYFILKL	AGRWPVKVIH	TDNGSNFISA	AVKAACWWAD	IKQEFGIPYN
ADK_CD_MAL	QETAYFILKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	IKQEFGIPYN
AG_BE_VI11	QETAYFILKL	AGRWPVKILH	TDNGSNFISA	AVKAACWWAD	IKQEFGIPYN
AG_NG_92NG	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AMKAACWWAN	IQQEFGIPYN
AGHU_GA_VI	QETAYFILKL	AGRWPVKVIH	TDNGTNFTSA	AVKAACWWAN	VTQEFGIPYN
AGU_CD_Z32	QETAYFILKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	ITQEFGIPYN
AJ_BW_BW21	QETAYFLLKL	AGRWPVTVIH	TDNGSNFTSA	AVKAACWWAG	VRQEFGIPYN
B_AU_VH_AF	QETAYFLLKL	AGRWPVKTVH	TDNGPIFIST	AVKAACWWAG	IKQEFGIPYN
B_CN_RL42_	QETAYFLLKL	AGRWPVKTIH	TDNGRNFTSN	SVKAACWWAG	IKQEFGIPYN
B_DE_D31_U	QETAYFILKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	VKQEFGIPYN
B_DE_HAN_U	QETAYFLLKL	AGRWPVKTVH	TDNGPNFTST	TVKAACWWAG	IKQEFGIPYN
B_FR_HXB2_	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTGA	TVRAACWWAG	IKQEFGIPYN
B_GA_OYI_	QETAYFILKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_GB_CAM1_	QETAYFLLKL	AGRWPVKTIH	TDNGGNFIST	TVKAACWWAG	IKQEFGIPYN
B_GB_GB8_A	QDTAYFILKL	AGRWPVKTIH	TDNGRNFTST	TVKAACWWAG	IKQEFGIPYN
B_GB_MANC_	QETAYFLLKL	AGRWPVTTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_KR_WK_AF	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTSN	TVKAACWAR.	IKQEFGIPYN
B_NL_3202A	QETAYFILKL	AGRWPVTTIH	TDNGSNFTSA	TVKAACWWAG	IKQEFGIPYN
B_TW_TWCYS	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTSA	AVKAACWWAG	IKQKFGIPYN
B_US_BC_L0	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_DH123	QETAYFILKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_JRCSF	QETAYFLLKL	AGRWPVTTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_MNCG_	QETAYFLLKL	AGRWPVKTIH	TDNGPNFTST	TVKAACWWTG	IKQEFGIPYN
B_US_P896_	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_RF_M1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_SF2_K	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_WEAU1	QETAYFILKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_WR27_	QETAYFILKL	AXRWPVXTIH	TDNGSNFIST	TVXAAXWWAG	IXQEFGIPYN
B_US_YU2_M	QETAYFLLKL	AGRWPVTTIH	TDNGSNFTSA	TVKAACWWAG	IKQEFGIPYN
BF1_BR_93B	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
C_BR_92BR0	QETAYFILKL	AGRWPVKVIH	TDNGSNFISN	TVKAACWWAG	IQQEFGIPYN
C_BW_96BW0	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
C_BW_96BW1	QETAYYILKL	AGRWPVKI IH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_BW_96BW1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	TQQEFGIPYN
C_BW_96BW1	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_ET_ETH22	QETAYFLLKL	AGRWPVRVIH	TDNGSNFTSN	AVKAACWWAG	IQQEFGIPYN
C_IN_93IN1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_IN_93IN9	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAS	IQQEFGIPYN
C_IN_93IN9	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_IN_94IN1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_IN_95IN2	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
CRF01_AE_C	QETAYFLLKL	AG.RPVKVIH	TDNGSNFTSA	AMKAACWWAN	VQQEFGIPYN
CRF01_AE_C	QETAYFLLKL	AGRWPVRVIH	TDNGSNFTSA	AVKAACWWAN	VQQEFGIPYN
CRF01_AE_C	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	TVKAACWWAN	VQQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF02_AG_F	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF02_AG_F	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN

CRF02_AG_G	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	AVRAACWWAN	VTQEFGIPYN
CRF02_AG_N	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF02_AG_S	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF02_AG_S	QETAYFILKL	AGRWP.KVVH	TDNGSNFTSA	AVKAACWWPK	LHQELGIYN.
CRF03_AB_R	QETAYFVLKL	AGRWPVKIIH	TDNGSNFTST	AVKAACWWAG	IKQEFGIPYN
CRF03_AB_R	QETAYFVLKL	AGRWPVKVIH	TDNGSNFIST	AVKAACWWAG	IKQEFGIPYN
CRF04_cpx_	QETAYFILKL	AGRWPVKMIH	ADNGPNFTSA	AVKAACWWAD	INQEFGIPYN
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CRF04_cpx_	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAN	IQQEFGVYPYN
CRF05_DF_B	QDTAYFILKL	AGRWPVKMIH	TDNGPNFTSG	AVKAACWWAG	IQQEFGIPYN
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CRF06_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	ITQEFGIPYN
CRF06_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	ITQEFGIPYN
CRF06_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAN	VTQEFGIPYN
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CRF11_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	IQQEFGIPYN
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D_CD_ELI_K	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAG	IKQEFGIPYN
D_CD_NDK_M	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	TVKAACWWAG	IKQEFGIPYN
D_UG_94UG1	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAG	IKQEFGIPYN
F1_BE_VI85	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	AVKASCWWAG	IQQEFGIPYN
F1_BR_93BR	QETAYFLLKL	AGRWPVKTIH	TDNGTNFTSA	TVKAACWWAG	IQQEFGIPYN
F1_FI_FIN9	QDTAYFILKL	AGRWPVKMIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
F1_FR_MP41	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSS	AVKAACWWAG	IQQEFGIPYN
F2_CM_MP25	QEAAAYFILKL	AGRWPVKIIH	TDNGSNFTSA	VVKAACWWAG	IQQEFGIPYN
F2KU_BE_VI	QETAFFILKL	AGRWPVKIIH	TDNGSNFISA	TVKAACWWAG	IQQEFGISYN
G_BE_DRCBL	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAS	ITQEFGIPYN
G_NG_92NG0	QETAYFILKL	AGRWPVKVIH	TDNGPNFISA	AVKAACWWAN	ITQEFGIPYN
G_SE_SE616	QETAYFILKL	AGRWPVTVIH	TDNGSNFTSA	AVKAACWWAN	ITQEFGIPYN
H_BE_VI991	QETAYFILKL	AGRWPVKMIH	TDNGSNFTSA	AVKAACWWAD	IHQEFGIPYN
H_BE_VI997	QETAYFILKL	AGRWPVKMIH	TDNGTNFTST	AVKAACWWAD	IQQDFGIPYN
H_CF_90CF0	KETAYFLLKL	ASRWPVKVIH	TDNGSNFTSA	AVKAACWWAD	IQQEFGIPYN
J_SE_SE702	QEAAFFILKL	AGGWPKVAIH	TDNGSNFTSG	AVKAACWWAD	IKQEFGIPYN
J_SE_SE788	QEAAFFILKL	AGRWPVKVIH	TDNGSNFTSG	AVKAACWWAD	IKQEFGIPYN
K_CD_EQTB1	QETAYFILKL	AGRWPVRVIH	TDNGSNFTSA	VVKAACWWAD	IKQEFGIPYN
K_CM_MP535	QETAYFILKL	AGRWPVKVIH	TDNGTNFTST	VVKAACWWAG	VKQEFGIPYN
N_CM_YBF30	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	TVKAACWWAN	IKQEFGIPYN
O_CM_ANT70	QETAYFLLKL	AARWPVKVIH	TDNGPNFTST	TMKAACWWAN	IQHEFGIPYN
O_CM_MVP51	QETAYFLLKL	AARWPVKVIH	TDNGPNFTSA	AMKAACWWTG	IQHEFGIPYN
O_SN_99SE_	QETAYFLLKL	AARWPVKVIH	TDNGPNFTSA	AMKAACWWAN	IKHEFGIPYN
O_SN_99SE_	QETAYFLLKL	AARWPVKIIH	TDNGPNFTSA	TMKAACWWTG	IKHEFGIPYN
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901

950

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96BWM01_5	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
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A2_CD_97CD	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A2_CY_94CY	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A2D_97KR	PQSQGVVESH	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	SKRKGIGGY
A2G_CD_97C	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A_BY_97BL0	XQSQGVVESH	NXELKKIIRQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_KE_Q23_A	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE659	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE725	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE753	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE853	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE889	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_UGSE8	PQSQGVVESH	NKELKKIIGQ	VREQAHLRT	AVQMAVFIHN	FKRKGIGGY
A_UG_92UG0	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_UG_U455_	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
AC_IN_2130	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AC_RW_92RW	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLRT	AVQMAVFIHN	FKRKGIGGY
AC_SE_SE94	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
ACD_SE_SE8	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
ACG_BE_VI1	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AD_SE_SE69	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLRT	AVQMAVFIHN	FKRKGIGGY
AD_SE_SE71	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
ADHK_NO_97	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AXQMAVFIHN	FKRKGIGGY
ADK_CD_MAL	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
AG_BE_VI11	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AG_NG_92NG	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AGHU_GA_VI	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY

AGU_CD_Z32	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AJ_BW_BW21	PQSQGVVESM	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_AU_VH_AF	PQRQGVVDSM	NNDLTTIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_CN_RL42	PQSQGVVESM	DKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
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B_DE_HAN_U	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
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B_GB_CAM1	PQSQGVVESM	NNELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
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B_US_YU2_M	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
BF1_BR_93B	PQSQGVIESM	NKELKKIIGQ	VRDQAEHLKT	AVQTAVFIHN	FKRKGIGGY
C_BR_92BR0	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
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C_ET_ETH22	PQSQGVVESM	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
C_IN_93IN1	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
C_IN_93IN9	PQSQGVVEAM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
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C_IN_95IN2	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
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CRF11_cpx_	PQSQGVVESM	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
CRF11_cpx_	PQSQGVVESM	NKGLKEIIGQ	VREQAEHLKT	AVQMAVFIHN	FKGKGIGGY
D_CD_84ZR0	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
D_CD_ELI_K	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRRRGIGGY
D_CD_NDK_M	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
D_UG_94UG1	PQSQGVVESM	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
F1_BE_VI85	PQSQGVVESI	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
F1_BR_93BR	PQSQGVVESM	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
F1_FI_FIN9	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
F1_FR_MP41	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
F2_CM_MP25	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
F2KU_BE_VI	PQSQGVVESM	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
G_BE_DRCBL	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
G_NG_92NG0	PQSQGVVESM	NKELKKIIGQ	VGDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
G_SE_SE616	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
H_BE_VI991	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLRT	AVQMAVFIHN	FKRKGIGGY
H_BE_VI997	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLRT	AVQMAVFIHN	FKRKGIGGY
H_CF_90CF0	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
J_SE_SE702	PQSQGVVESM	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
J_SE_SE788	PQSQGVVESM	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
K_CD_EQTB1	PQSQGVVESM	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
K_CM_MP535	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
N_CM_YBF30	PQSQGVVESM	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
O_CM_ANT70	PQSQGVVEAM	NKELKSIIQ	VRDQAEHLRT	AVQMAVFIHN	FKRKGIGGY
O_CM_MVP51	PQSQGVVEAM	NKELKSIIQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
O_SN_99SE_	PQSQGVVEAM	NKELKSIIQ	VRDQAEHLKT	AVQMAVFIHN	YKRKGIGGY
O_SN_99SE_	PQSQGVVEAM	NKELKSIIQ	VRDQAEHLKT	AVQMAVFIHN	YKRKGIGGY
U_CD_83C	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY

	951				1000
00BW0762_1	SAGERIIDII	ATDIQTRELQ	KRIIQIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW0768_2	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW0874_2	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1471_2	SAGERIVDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSREP	WKGPAKLLWK
00BW1616_2	SAGERIVDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1686_8	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1759_3	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1773_2	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1783_5	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYGDSRDPI	WKGPAKLLWK
00BW1795_6	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDNRPDI	WKGPAKLLWK
00BW1811_3	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1859_5	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1880_2	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1921_1	SAGERIIDII	ATDIQTKELQ	KQITNIQKFR	VYYRDSRDPI	WKGPAKLLWK
00BW2036_1	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW2063_6	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW2087_2	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW2127_2	SAGERIIDII	ATDIQTKELQ	KRIIQIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW2128_3	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW2276_7	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW3819_3	SAGERIIDII	ATDIQTRELQ	KQIIQIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW3842_8	SAGERIIDII	ATDIQTKELQ	NQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW3871_3	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW3876_9	SAGERIIDII	ATDIQTKELQ	NQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW3886_8	SAGERIIDII	ATDIQTKELQ	NQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW3891_6	SAGGRIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW3970_2	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW5031_1	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
96BW01B21	SAGERIIDII	ATDIRTKELQ	KQIMKIRNFR	VYYRDSRDPI	WKGPAKLLWK
96BW0407	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK

96BW0502	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
96BW06_J4	SAGERIIDII	ATDIQTKELQ	KQITNIQKFR	VYYRDSRDPI	WKGPAKLLWK
96BW11_06	SAGERIIDMI	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
96BW1210	SAGERIIDII	ATDIQTTELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
96BW15B03	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLIWK
96BW16_26	TAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
96BW17A09	SAGERIVDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSREPV	WKGPAKLLWK
96BWM01_5	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDNRDPI	WKGPAKLLWK
96BWM03_2	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
98BWMC12_2	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPV	WKGPAKLLWK
98BWMC13_4	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDNRDPI	WKGPAKLLWK
98BWMC14_a	SAGERIIDII	ATDIQTQELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWR
98BWM014_1	SAGERIIDII	ATDIQTKELQ	KQILNIQKFR	VYYRDSRDPI	WKGPAKLLWK
98BWM018_d	SAGERIIDII	ATDIQTRELQ	RQIIKIQIFR	VYYRDSRDPI	WKGPAKLLWK
98BWM036_a	SAGERIIDII	ATDIQTKELQ	RQILKIQNFR	VYYRDSRDPI	WKGPAKLLWK
98BWM037_d	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSGDPI	WKGPAKLLWK
99BW3932_1	SAGERIIDII	ATDIQTRELQ	KQIIQIQNFR	VYYRDSRDPI	WKGPAKLLWK
99BW4642_4	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
99BW4745_8	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
99BW4754_7	SAGERIIDII	ASDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
99BWMC16_8	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A2_CD_97CD	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A2_CY_94CY	SAGERIIDII	ATDIQTKELQ	RQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A2D_97KR	SAGERIIDII	ATDIQTKELQ	RQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A2G_CD_97C	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_BY_97BL0	SAXERIIDII	ATDIQTKELQ	KXITKIQNFX	VYYRDSRDPI	WKGPAKLLXK
A_KE_Q23_A	SAGERIIDII	ATDIQTKELQ	KHITKIQNFR	VYYRDSRDPL	WKGPAKLFWK
A_SE_SE659	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_SE_SE725	SAGERIIDII	ATDIQTKELQ	KQITKIQKFR	VYYRDSRDPI	WKGPAKLLWK
A_SE_SE753	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_SE_SE853	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_SE_SE889	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
A_SE_UGSE8	SAGERIIDII	ATDIQTKELQ	KQIT_ IQNFR	VYYRDSRDPI	WKGPAKLLWK
A_UG_92UG0	SAGERIIDII	ASDLQTKELQ	KQITKIQKFR	VCYRDSRDPI	WKGPAKLLWK
A_UG_U455_	SAGERIIDII	ATDIQTKELQ	KQISKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AC_IN_2130	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AC_RW_92RW	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AC_SE_SE94	SPGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
ACD_SE_SE8	SVGERIIDII	ATDIQTKELQ	KQITKIQKFR	VYYRDSRNPI	WKGPAKLLWK
ACG_BE_VI1	SARERIIDII	ASDIQTKELQ	KPITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AD_SE_SE69	SAGERIIDII	ATDIQTKELQ	RQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AD_SE_SE71	SAGERIIDII	ATDIQTKELQ	KHITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
ADHK_NO_97	SAGERIIDXI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
ADK_CD_MAL	SAGERIIDMI	ATDIQTKELQ	KQITKIQNFR	VYYRDNRDPI	WKGPAKLLWK
AG_BE_VI11	SAGERIIDII	ASDIQTKELQ	KXITKIXNFR	VYYRDSRDPI	WKGPAKLLWK
AG_NG_92NG	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AGHU_GA_VI	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AGU_CD_Z32	SAGERIVDII	ASDIQTKELQ	NQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AJ_BW_BW21	SAGERIIDMI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
B_AU_VH_AF	SAGERIIDII	ASDIQTKELQ	KQITKVQNFR	VYYRDSRDPL	WKGPAKLLWK
B_CN_RL42_	SAGERIVDII	ATDIQTRELQ	KQITKIQNFR	VYYRGSRDPL	WKGPAKLLWK
B_DE_D31_U	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_DE_HAN_U	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSREPF	WKGPAKLLWK
B_FR_HXB2_	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRNPL	WKGPAKLLWK
B_GA_OYI_	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSREPL	WKGPAKLLWK
B_GB_CAM1_	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_GB_GB8_A	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_GB_MANC_	SAGGRIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRNPL	WKGPAKLLWK
B_KR_WK_AF	SAGERIIDII	ATDIQTKELQ	KQVTKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_NL_3202A	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_TW_TWCYS	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDNRDPL	WKGPAKLLWK

B_US_BC_L0	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDNKDPL	WKGPAKLLWK
B_US_DH123	SAGERIVDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_US_JRCSE	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDNRPDI	WKGPAKLLWK
B_US_MNCG	SAGERIVGII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_US_P896	SAGERIVDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_US_RF_M1	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_US_SF2_K	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDNKDPL	WKGPAKLLWK
B_US_WEAU1	SAGERIIDII	ATDIQTQQLQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_US_WR27	SAGERIIDII	ATDIQXKXLQ	XQXTIXQNXR	VYYRDSRDPL	WKGPAKLLWK
B_US_YU2_M	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
BF1_BR_93B	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
C_BR_92BR0	SAGERIIDII	ATDIQTKELQ	KQIMKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_BW_96BW0	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPV	WKGPAKLLWK
C_BW_96BW1	SAGERIDMI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_BW_96BW1	SAGERIIDII	ATDIQTTELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_BW_96BW1	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_ET_ETH22	SAGERIIDII	ASDIQTKELQ	NQILKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_IN_93IN1	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_IN_93IN9	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_IN_93IN9	SAGERIIDII	ATDIQTKELQ	KQIIKIHNFR	VYYRDSRDPI	WKGPAKLLWK
C_IN_94IN1	SAGERIIDII	STDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_IN_95IN2	SAGERIIDII	ATDIQTKELQ	KQITKVQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_C	SAGERIIDII	ATEIQTKEQX	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_C	SAGERIIDII	ATDIQTKALQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_C	SAGERIIDII	ATDIQTKELQ	KHITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_T	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_T	SVGERIIDII	AADIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_T	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_T	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_T	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_T	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF02_AG_F	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF02_AG_F	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF02_AG_G	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF02_AG_N	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF02_AG_S	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF02_AG_S	SAGERIIDII	ASDIQTKELQ	KQITNIQKFR	VYYRDSRDPI	WKGPAKLLWK
CRF03_AB_R	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF03_AB_R	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF04_cpx	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSREPI	WKGPAKLLWK
CRF04_cpx	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF04_cpx	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSKDP	WKGPAKLLWK
CRF05_DF_B	GAGERIIDII	TTDIQTKELQ	KQIIKIQNFR	VYYRDSRDPV	WKGPAKLLWK
CRF05_DF_B	SAGEGIIDII	STDIQTKELQ	KQITKIQNFR	VYYRDSRDPV	WKGPAKLLWK
CRF06_cpx	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF06_cpx	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF06_cpx	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF06_cpx	SAGERIIDII	ASDIQTKELQ	KQITKIRNFR	VYYRDSRDPI	WKGPAKLLWK
CRF11_cpx	SAGERIVDII	ATDLQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF11_cpx	SAGERIIDII	ATDLQTKELQ	KQITKIQKFR	VYYRDSRDPI	WKGPAKLLWK
D_CD_84ZR0	SAGERIIDII	ASDIQTRELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
D_CD_ELI_K	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
D_CD_NDK_M	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
D_UG_94UG1	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPV	WKGPAKLLWK
F1_BE_VI85	SAGERIIDII	STDIQTRELQ	KQITKIQNFR	VYYRDSRNPV	WKGPAKLLWK
F1_BR_93BR	SAGERTIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPV	WKGPAKLLWK
F1_FI_FIN9	SAGERIIDII	ATDIQTKELQ	KQVTKIQNFR	VYYRDSRDPV	WKGPAKLLWK
F1_FR_MP41	SAGERIIDII	STDIQTRELQ	KQIIKIQNFR	VYYRDSRDPV	WKGPAKLLWK
F2_CM_MP25	SAGERIIDII	ATDIQTKELQ	KQISKIQNFR	VYFRDSRDPV	WKGPAKLLWK
F2KU_BE_VI	SAGERIVDII	ASDIQTRALQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
G_BE_DRCBL	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK

G_NG_92NG0	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
G_SE_SE616	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPV	WKGPAKLLWK
H_BE_VI991	SARERIIDII	ATDIPTKELQ	KQISQIQKFR	VYYRDSRDPI	WKGPAKLLWK
H_BE_VI997	SAGERIIDII	ATDIQTKELQ	KQISNIQKFR	VYYRDSRDPI	WKGPAKLLWK
H_CF_90CF0	SAGERIIDII	ATDIQTKELQ	KQISNIQKFR	VYYRDSRDPI	WKGPAKLLWK
J_SE_SE702	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
J_SE_SE788	SAGERIIDII	ATDIQTRELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLPWK
K_CD_EQTB1	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSREPI	WKGPAKLLWK
K_CM_MP535	SAGERIVDII	ATDIQTKELQ	KQILNIQKFR	VYYRDSREPI	WKGPAKLLWK
N_CM_YBF30	TAGERIIDII	ATDIQTTNLQ	TQILKVQNFR	VYYRDSRDPI	WKGPAKLLWK
O_CM_ANT70	TAGERIIDIL	ASQIQTTTELQ	KQILKXHKFR	VYYRDSRDPI	WKGPAQLLWK
O_CM_MVP51	TAGERLIDIL	ASQIQTTTELQ	KQILKINNFR	VYYRDSRDPI	WKGPAQLLWK
O_SN_99SE_	TAGERIIDIL	ASQIQTTTELQ	KQIFKIQKFQ	VYYRDSRDPI	WKGPAQLLWK
O_SN_99SE_	TAGERIIDIL	ASQIQTTTELQ	KQIFKIQKFQ	VYYRDSRDPI	WKGPAQLLWK
U_CD___83C	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK

	1001			1046
00BW0762_1	GE.GAVVIQD	NSDIKVIPRR	KAKI IKDYGK	QMAGADCVAG RQDED.
00BW0768_2	GE.GAVVIQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCVAG RQDED.
00BW0874_2	GE.GAVVIQD	NGDIKVPPRR	KVKI IKDYGK	QMAGADCVAG RQDED.
00BW1471_2	GE.GAVVIQD	NSDIKVPPRR	KAKI IRDYGK	QMAGADCVAG RQDED.
00BW1616_2	GE.GAVVIQD	NSDIKVPPRR	KVKI IRDYGK	QMAGADCVAG RQDED.
00BW1686_8	GE.GAVVIQD	NSDIKVPPRR	KAKI IRDYGK	QMAGADCVAG RQDEDQ
00BW1759_3	GE.GAVVIQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCVAG RQDEDQ
00BW1773_2	GE.GAVVIQD	NNDIKVPPRR	KVKI IKGYGK	QMAGADCVAG GQDEN.
00BW1783_5	GE.GAVVIQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCMAG RQDEDQ
00BW1795_6	GE.GAVVLQD	NSEIKVPPRR	KVKI IRDYGK	QMAGADCVAG RQDEDQ
00BW1811_3	GE.GAVVIQD	NSDIKVPPRR	KVKI IRDYGK	QMAGADCVAG GQDEN.
00BW1859_5	GE.GAVVIQD	NSDIKVPPRR	KAKI IRDYGK	QMAGADCVAS RQDED.
00BW1880_2	GE.GAVVIQD	KSDIKVPPRR	KVKI IRDYGK	QMAGADCVAD RQDED.
00BW1921_1	GE.GAVVIQD	NSDVKVPPRR	KAKI IRDYGK	QMAGADCVAD RQDED.
00BW2036_1	GE.GAVVIQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCVAG RQDED.
00BW2063_6	GE.GAVVIQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCVAG RQDED.
00BW2087_2	GE.GAVVIQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCVAG RQDED.
00BW2127_2	GE.GAVVIQD	NSDIKVPPRR	KAKI IKDYGK	QMAGADCVAS RQDED.
00BW2128_3	GE.GAVVLQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCVAG GQDEN.
00BW2276_7	GE.GAVVIQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCVAG RQDED.
00BW3819_3	GE.GAVVIQD	NGDIKVPPRR	KAKI IKDYGK	QMAGADCVAS RQDEN.
00BW3842_8	GE.GAVVIQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCVAG RQDED.
00BW3871_3	GE.GAVVIQD	NSDIKVPPRR	KAKI IKDYGK	QMAGADCVAG RQDED.
00BW3876_9	GE.GAVVIQD	NSDIKVPPRR	KAKI IKNYGK	QMAGADCVAG RQDED.
00BW3886_8	GE.GAVVIQD	KGDIKVPPRR	KAKI IKDYGK	QMAGADCVAG RQDED.
00BW3891_6	GE.GAVVIQD	NSDIKVPPRR	KVKI IRDYGK	QMAGDDCVAG RQDED.
00BW3970_2	GE.GAVVIQD	NSDIKVPPRR	RAKI IRDYGK	QMAGADCVAD RQDED.
00BW5031_1	GE.GAVVIQD	NSDIKAVPRR	KAKI IKDYGQ	QMAGADCVAG RQDEN.
96BW01B21	GE.GAVVIQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCVAG RQDED.
96BW0407	GE.GAVVIQD	NSDIKVPPRR	KVKI IRDYGK	QMAGDDCVAG RQDED.
96BW0502	GE.GAVVIQD	NSDIKVPPRR	KAKI IKDYGK	QMAGADCVAG GQDEN.
96BW06_J4	GE.GAVVIQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCVAS RQDED.
96BW11_06	GE.GAVVIQD	NSDIKVPPRR	KVKI IRDYGK	QMAGADCVAG RQDED.
96BW1210	GE.GAVVIQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCVAG RQDED.
96BW15B03	GEGAVVVIQD	NSDIKVPPRR	KVKI IRDYGK	QMAGADCVAG RQDED.
96BW16_26	GE.GAVVLQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCVAG GQDEN.
96BW17A09	GE.GAVVIQD	NSDIKVPPRR	KAKI IRDYGK	QMAGADCVAG RQDED.
96BWM01_5	GE.GAVVIQD	NSEIKVPPRR	KAKI IRDYGK	QMAGADCVAG RQDEDQ
96BWM03_2	GE.GAVVIQD	NSDIKVPPRR	KAKI IRDYGK	QMAGADCVAG RQDEDQ
98BWMC12_2	GD.GAVVIQD	NSDIKVPPRR	KAKI IRDYGK	QMAGADCVAG RQDED.
98BWMC13_4	GE.GAVVIQD	NSEIKVPPRR	KVKI IRDYGK	QMAGADCVAG RQDEDQ
98BWMC14_a	GE.GAVVIQD	SSDIKVPPRR	KAKI IKDYGK	QMAGADCVAG RQDED.
98BWM014_1	GE.GAVVIQD	NSDIKVPPRR	KAKI IKDYGK	QMAGADCVAG RQDED.
98BWM018_d	GE.GAVVIQD	NSDIKVPPRR	KVKI IKDYGK	QMAGADCVAG RQDEDQ

98BWM036_a	GE.GAVVIQD	NSDIKVVPRR	KAKIIKDYGK	QMAGADCVAG	GQDED.
98BWM037_d	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDEDQ
99BW3932_1	GE.GAVVIQD	NSDIKVVPRR	KAKIIKDYGK	QMAGADCVAS	RQDED.
99BW4642_4	GE.GAVVIQD	NSDIKVVPRR	KAKIIKDYGK	QMAGADCVAD	RQDED.
99BW4745_8	GE.GAVVIQD	NSDIKVVPRR	KVKIIKDYGK	QMAGADCVAG	RQDED.
99BW4754_7	GE.GAVVIQD	KSDIKVVPRR	KAKIIKDYGK	QMAGDDCVAG	RQDED.
99BWMC16_8	GE.GAVVIQD	NSDIKVVPRR	KAKIIKDYGK	QMAGADCVAG	RQDED.
A2_CD_97CD	GE.GAVVIQD	NGDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
A2_CY_94CY	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
A2D__97KR	GE.GAVVIQD	NSDIKVVPRR	RAKIIIRDYGK	QMAGDDCVAG	RQDED.
A2G_CD_97C	GE.GAVVIQD	NNEIKVVPRR	KTKILRDYGK	QMAGDDCVAG	RQDED.
A_BY_97BL0	GE.GAVVIQD	NXDIKVVPRR	KAKIIXDXXK	QMAGXDCVAS	RQDED.
A_KE_Q23_A	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
A_SE_SE659	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
A_SE_SE725	GE.GAVVIQD	NNDIKVVPRR	KAKILRDYGK	QMAGDDCVAG	RQDED.
A_SE_SE753	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGDDCVAG	RQDED.
A_SE_SE853	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
A_SE_SE889	GE.GAVLIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDGCVAG	RQDED.
A_SE_UGSE8	GE.GAVVIQD	QSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
A_UG_92UG0	GE.GAVVIQD	NSDIKVVPRR	KVKIIKDYGK	QMAGDDCVAG	RQDED.
A_UG_U455_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCMAG	RQDED.
AC_IN_2130	GE.GAVVIQD	NSDIKVVPRR	KAKIIKDYGK	QMAGADCVAG	RQDED.
AC_RW_92RW	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
AC_SE_SE94	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGDDCVAG	RQDED.
ACD_SE_SE8	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDEDW
ACG_BE_VI1	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDGCVAG	RQDED.
AD_SE_SE69	GE.GAVVIQD	NSEIKVVPRR	KVKIIRDYGK	QMAGDDCVAS	RQDED.
AD_SE_SE71	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
ADHK_NO_97	GE.GAVVIQD	NGDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
ADK_CD_MAL	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	GQDED.
AG_BE_VI11	GE.GAVAIQD	NNEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
AG_NG_92NG	GE.GAVVIQD	NSEIKVVPRR	KVKIIKDYGK	QMAGGDCVAG	RQDED.
AGHU_GA_VI	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
AGU_CD_Z32	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
AJ_BW_BW21	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
B_AU_VH_AF	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_CN_RL42_	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGDDCVAS	RQDED.
B_DE_D31_U	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
B_DE_HAN_U	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMGSDDCVAS	RQDED.
B_FR_HXB2_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_GA_OYI_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_GB_CAM1_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_GB_GB8_A	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_GB_MANC_	GE.GAVVIQD	NSEIKVVPRR	KVKIIRDYGK	QMAGDDCVAG	RQDED.
B_KR_WK_AF	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_NL_3202A	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_TW_TWCYS	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
B_US_BC_L0	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_DH123	GE.GAVVIQD	KSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_JRCSF	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_MNCG_	GE.GAVVIQD	NNDIKVVPRR	KAKVIRDYGK	QTAGDDCVAS	RQDED.
B_US_P896_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_RF_M1	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_SF2_K	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_WEAU1	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_WR27_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_YU2_M	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
BF1_BR_93B	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGGDCVAG	RQDED.
C_BR_92BR0	GE.GAVVLQD	NSDIKVVPRR	KVKIIKDYGK	QMAGADCMAS	RQDED.
C_BW_96BW0	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGADCVAG	RQDED.
C_BW_96BW1	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGADCVAG	RQDED.

C_BW_96BW1	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	RQDED.
C_BW_96BW1	GEGAVVVIQD	NSDIKVVPRR	KVKI IRDYGK	QMAGADCVAG	RQDED.
C_ET_ETH22	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGADCVAG	RQDED.
C_IN_93IN1	GE.GAVVIQD	NSDIKVVPRR	KAKI IKDYGK	QMAGADCVAG	RQDED.
C_IN_93IN9	GE.GAVVLQD	NSDIKVVPRR	KAKI IKDYGK	QMAGADCVAG	RQDED.
C_IN_93IN9	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGADCVAG	RQDED.
C_IN_94IN1	GE.GAVVIQD	NSDIKVVPRR	KAKI IKDYGK	QMAGADCVAG	RQDED.
C_IN_95IN2	GE.GAVVIQD	NSDIKVVPRR	KAKI IKDYGK	QMAGADCVAG	RQDED.
CRF01_AE_C	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDEN.
CRF01_AE_C	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_C	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAS	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_F	GE.GAVVIQD	KSDIKVVPRR	KAKI IKDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_F	GE.GAVVIQD	KSDIKVVPRR	KAKI IKDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_G	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_N	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_S	GE.GAVVIQD	NSDIKVVPRR	KVKI IRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_S	GE.GAVVIQD	NSDIKVVPRR	KTKI LRDYGK	QMAGDDCVAG	GQDED.
CRF03_AB_R	GE.GAVVIQD	NNDIKVVPRR	KAKI IRDYGK	QMAGDDCVAS	RQDED.
CRF03_AB_R	GE.GAVVIQD	NNDIKVVPRR	KAKI IRDYGK	QMAGDDCVAS	RQDED.
CRF04_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGNDCVAG	RQDED.
CRF04_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF04_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF05_DF_B	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF05_DF_B	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF06_cpx_	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF06_cpx_	GE.GAVVIQD	NSEIKVVPRR	KAKI IKDYGK	QMAGDDCVAG	RQDED.
CRF06_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF06_cpx_	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF11_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
CRF11_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	SQDED.
D_CD_84ZR0	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAS	RQDED.
D_CD_ELI_K	GE.GAVVIQD	KSDIKVVPRR	KVKI IRDYGK	QMAGDDCVAS	RQDED.
D_CD_NDK_M	GE.GAVVIQD	NSDIKVVPRR	KVKI IRDYGK	QMAGDDCVAS	RQDED.
D_UG_94UG1	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAS	RQDED.
F1_BE_VI85	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAVDDCVAG	RQDED.
F1_BR_93BR	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
F1_FI_FIN9	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
F1_FR_MP41	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
F2_CM_MP25	GE.GAVVIQD	NNEIKVIPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
F2KU_BE_VI	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
G_BE_DRCBL	GE.GAVVIQD	NNEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
G_NG_92NG0	GE.GAVVIQD	NNEIKVVPRR	KAKI LRDYGK	QMAGDDCVAG	RQDED.
G_SE_SE616	GE.GAVVIQD	NNEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
H_BE_VI991	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
H_BE_VI997	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
H_CF_90CF0	GE.GAVVIQD	NSEIKVVPRR	EAKI IRDYGK	QMAGDDCVAS	RQDED.
J_SE_SE702	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
J_SE_SE788	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
K_CD_EQTB1	GE.GAVVIN.	.SEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
K_CM_MP535	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
N_CM_YBF30	GE.GAVVIQD	NGDIKVVPRR	KAKI IRDYGK	QMAGDGCVAS	GQDENQ
O_CM_ANT70	GE.GAVVIQD	KGDIKVVPRR	KAKI IREYK	QMAGTDSMAS	GQTESE
O_CM_MVP51	GE.GAVVIQD	KGDIKVVPRR	KAKI IRDYGK	QMAGTDSMAN	RQTESE
O_SN_99SE_	GE.GAVVIQD	KGDIKVVPRR	KAKI IRHYGK	QMAGTDSMAS	GQTESE
O_SN_99SE_	GE.GAVVIQD	KGDIKVVPRR	KAKI IRHYGK	QMAGTDSMAS	GQTESE

U_CD__83C GE.GAVVIQD NSEIKVPPRR KAKIIRDYGK QMAGDDCVAS RQDEN.

Table 15. HIV Rev Sequence Alignment

GCG Multiple Sequence File.

Written by Omiga 1.1

Name: 00BW0762_1	SEQ	ID NO: 970	Len: 129	Check: 4903	Weight: 1.00
Name: 00BW0768_2	SEQ	ID NO: 971	Len: 129	Check: 5102	Weight: 1.00
Name: 00BW0874_2	SEQ	ID NO: 972	Len: 129	Check: 5815	Weight: 1.00
Name: 00BW1471_2	SEQ	ID NO: 973	Len: 129	Check: 4144	Weight: 1.00
Name: 00BW1616_2	SEQ	ID NO: 974	Len: 129	Check: 5298	Weight: 1.00
Name: 00BW1686_8	SEQ	ID NO: 975	Len: 129	Check: 3871	Weight: 1.00
Name: 00BW1759_3	SEQ	ID NO: 976	Len: 129	Check: 4976	Weight: 1.00
Name: 00BW1773_2	SEQ	ID NO: 977	Len: 129	Check: 5775	Weight: 1.00
Name: 00BW1783_5	SEQ	ID NO: 978	Len: 129	Check: 6142	Weight: 1.00
Name: 00BW1795_6	SEQ	ID NO: 979	Len: 129	Check: 5055	Weight: 1.00
Name: 00BW1811_3	SEQ	ID NO: 980	Len: 129	Check: 5804	Weight: 1.00
Name: 00BW1859_5	SEQ	ID NO: 981	Len: 129	Check: 5252	Weight: 1.00
Name: 00BW1880_2	SEQ	ID NO: 982	Len: 129	Check: 4995	Weight: 1.00
Name: 00BW1921_1	SEQ	ID NO: 983	Len: 129	Check: 6482	Weight: 1.00
Name: 00BW2036_1	SEQ	ID NO: 984	Len: 129	Check: 4770	Weight: 1.00
Name: 00BW2063_6	SEQ	ID NO: 985	Len: 129	Check: 5384	Weight: 1.00
Name: 00BW2087_2	SEQ	ID NO: 986	Len: 129	Check: 4848	Weight: 1.00
Name: 00BW2127_2	SEQ	ID NO: 987	Len: 129	Check: 5783	Weight: 1.00
Name: 00BW2276_7	SEQ	ID NO: 988	Len: 129	Check: 5364	Weight: 1.00
Name: 00BW3819_3	SEQ	ID NO: 989	Len: 129	Check: 5712	Weight: 1.00
Name: 00BW3842_8	SEQ	ID NO: 990	Len: 129	Check: 5586	Weight: 1.00
Name: 00BW3871_3	SEQ	ID NO: 991	Len: 129	Check: 5299	Weight: 1.00
Name: 00BW3876_9	SEQ	ID NO: 992	Len: 129	Check: 4423	Weight: 1.00
Name: 00BW3886_8	SEQ	ID NO: 993	Len: 129	Check: 5415	Weight: 1.00
Name: 00BW3891_6	SEQ	ID NO: 994	Len: 129	Check: 5426	Weight: 1.00
Name: 00BW3970_2	SEQ	ID NO: 995	Len: 129	Check: 2613	Weight: 1.00
Name: 00BW5031_1	SEQ	ID NO: 996	Len: 129	Check: 4597	Weight: 1.00
Name: 96BW01B21	SEQ	ID NO: 997	Len: 129	Check: 5653	Weight: 1.00
Name: 96BW0407	SEQ	ID NO: 998	Len: 129	Check: 4310	Weight: 1.00
Name: 96BW0502	SEQ	ID NO: 999	Len: 129	Check: 4675	Weight: 1.00
Name: 96BW06_J4	SEQ	ID NO: 1000	Len: 129	Check: 5079	Weight: 1.00
Name: 96BW11_06	SEQ	ID NO: 1001	Len: 129	Check: 5939	Weight: 1.00
Name: 96BW1210	SEQ	ID NO: 1002	Len: 129	Check: 5666	Weight: 1.00
Name: 96BW15B03	SEQ	ID NO: 1003	Len: 129	Check: 5102	Weight: 1.00
Name: 96BW16_26	SEQ	ID NO: 1004	Len: 129	Check: 5675	Weight: 1.00
Name: 96BW17A09	SEQ	ID NO: 1005	Len: 129	Check: 2825	Weight: 1.00
Name: 96BWM01_5	SEQ	ID NO: 1006	Len: 129	Check: 5636	Weight: 1.00
Name: 96BWM03_2	SEQ	ID NO: 1007	Len: 129	Check: 6552	Weight: 1.00
Name: 98BWMC12_2	SEQ	ID NO: 1008	Len: 129	Check: 3043	Weight: 1.00
Name: 98BWMC13_4	SEQ	ID NO: 1009	Len: 129	Check: 5518	Weight: 1.00
Name: 98BWMC14_a	SEQ	ID NO: 1010	Len: 129	Check: 4358	Weight: 1.00
Name: 98BWM014_1	SEQ	ID NO: 1011	Len: 129	Check: 7531	Weight: 1.00
Name: 98BWM018_d	SEQ	ID NO: 1012	Len: 129	Check: 5291	Weight: 1.00
Name: 98BWM036_a	SEQ	ID NO: 1013	Len: 129	Check: 6801	Weight: 1.00
Name: 98BWM037_d	SEQ	ID NO: 1014	Len: 129	Check: 4790	Weight: 1.00
Name: 99BW3932_1	SEQ	ID NO: 1015	Len: 129	Check: 5736	Weight: 1.00
Name: 99BW4642_4	SEQ	ID NO: 1016	Len: 129	Check: 6464	Weight: 1.00
Name: 99BW4745_8	SEQ	ID NO: 1017	Len: 129	Check: 6181	Weight: 1.00
Name: 99BW4754_7	SEQ	ID NO: 1018	Len: 129	Check: 5182	Weight: 1.00
Name: 99BWMC16_8	SEQ	ID NO: 1019	Len: 129	Check: 4245	Weight: 1.00
Name: A2_CD_97CD	SEQ	ID NO: 1020	Len: 129	Check: 2625	Weight: 1.00
Name: A2_CY_94CY	SEQ	ID NO: 1021	Len: 129	Check: 4125	Weight: 1.00
Name: A2D_97KR	SEQ	ID NO: 1022	Len: 129	Check: 4114	Weight: 1.00
Name: A2G_CD_97C	SEQ	ID NO: 1023	Len: 129	Check: 1115	Weight: 1.00
Name: A_BY_97BL0	SEQ	ID NO: 1024	Len: 129	Check: 9470	Weight: 1.00
Name: A_KE_Q23_A	SEQ	ID NO: 1025	Len: 129	Check: 2684	Weight: 1.00
Name: A_SE_SE659	SEQ	ID NO: 1026	Len: 129	Check: 4659	Weight: 1.00

Name: A_SE_SE725	SEQ	ID NO: 1027	Len:129	Check: 4491	Weight: 1.00
Name: A_SE_SE753	SEQ	ID NO: 1028	Len:129	Check: 3636	Weight: 1.00
Name: A_SE_SE853	SEQ	ID NO: 1029	Len:129	Check: 1862	Weight: 1.00
Name: A_SE_SE889	SEQ	ID NO: 1030	Len:129	Check: 2798	Weight: 1.00
Name: A_SE_UGSE8	SEQ	ID NO: 1031	Len:129	Check: 6865	Weight: 1.00
Name: A_UG_92UG0	SEQ	ID NO: 1032	Len:129	Check: 4427	Weight: 1.00
Name: A_UG_U455_	SEQ	ID NO: 1033	Len:129	Check: 3229	Weight: 1.00
Name: AC_IN_2130	SEQ	ID NO: 1034	Len:129	Check: 5110	Weight: 1.00
Name: AC_RW_92RW	SEQ	ID NO: 1035	Len:129	Check: 5015	Weight: 1.00
Name: AC_SE_SE94	SEQ	ID NO: 1036	Len:129	Check: 7976	Weight: 1.00
Name: ACD_SE_SE8	SEQ	ID NO: 1037	Len:129	Check: 2296	Weight: 1.00
Name: ACG_BE_VI1	SEQ	ID NO: 1038	Len:129	Check: 3968	Weight: 1.00
Name: AD_SE_SE69	SEQ	ID NO: 1039	Len:129	Check: 4558	Weight: 1.00
Name: AD_SE_SE71	SEQ	ID NO: 1040	Len:129	Check: 2678	Weight: 1.00
Name: ADHK_NO_97	SEQ	ID NO: 1041	Len:129	Check: 1890	Weight: 1.00
Name: ADK_CD_MAL	SEQ	ID NO: 1042	Len:129	Check: 5260	Weight: 1.00
Name: AG_BE_VI11	SEQ	ID NO: 1043	Len:129	Check: 4003	Weight: 1.00
Name: AG_NG_92NG	SEQ	ID NO: 1044	Len:129	Check: 5027	Weight: 1.00
Name: AGHU_GA_VI	SEQ	ID NO: 1045	Len:129	Check: 1978	Weight: 1.00
Name: AGU_CD_Z32	SEQ	ID NO: 1046	Len:129	Check: 1958	Weight: 1.00
Name: AJ_BW_BW21	SEQ	ID NO: 1047	Len:129	Check: 2263	Weight: 1.00
Name: B_AU_VH_AF	SEQ	ID NO: 1048	Len:129	Check: 4074	Weight: 1.00
Name: B_CN_RL42_	SEQ	ID NO: 1049	Len:129	Check: 4483	Weight: 1.00
Name: B_DE_D31_U	SEQ	ID NO: 1050	Len:129	Check: 5079	Weight: 1.00
Name: B_DE_HAN_U	SEQ	ID NO: 1051	Len:129	Check: 4550	Weight: 1.00
Name: B_FR_HXB2_	SEQ	ID NO: 1052	Len:129	Check: 3649	Weight: 1.00
Name: B_GA_OYI_M	SEQ	ID NO: 1053	Len:129	Check: 3334	Weight: 1.00
Name: B_GB_CAM1_	SEQ	ID NO: 1054	Len:129	Check: 3865	Weight: 1.00
Name: B_GB_GB8_A	SEQ	ID NO: 1055	Len:129	Check: 3083	Weight: 1.00
Name: B_GB_MANC_	SEQ	ID NO: 1056	Len:129	Check: 5502	Weight: 1.00
Name: B_KR_WK_AF	SEQ	ID NO: 1057	Len:129	Check: 4156	Weight: 1.00
Name: B_NL_3202A	SEQ	ID NO: 1058	Len:129	Check: 3826	Weight: 1.00
Name: B_TW_TWCYS	SEQ	ID NO: 1059	Len:129	Check: 3546	Weight: 1.00
Name: B_US_BC_L0	SEQ	ID NO: 1060	Len:129	Check: 4674	Weight: 1.00
Name: B_US_DH123	SEQ	ID NO: 1061	Len:129	Check: 4202	Weight: 1.00
Name: B_US_JRCSF	SEQ	ID NO: 1062	Len:129	Check: 3217	Weight: 1.00
Name: B_US_MNCG_	SEQ	ID NO: 1063	Len:129	Check: 3512	Weight: 1.00
Name: B_US_P896_	SEQ	ID NO: 1064	Len:129	Check: 3297	Weight: 1.00
Name: B_US_RF_M1	SEQ	ID NO: 1065	Len:129	Check: 5527	Weight: 1.00
Name: B_US_SF2_K	SEQ	ID NO: 1066	Len:129	Check: 3616	Weight: 1.00
Name: B_US_WEAU1	SEQ	ID NO: 1067	Len:129	Check: 4435	Weight: 1.00
Name: B_US_WR27_	SEQ	ID NO: 1068	Len:129	Check: 812	Weight: 1.00
Name: B_US_YU2_M	SEQ	ID NO: 1069	Len:129	Check: 4948	Weight: 1.00
Name: BF1_BR_93B	SEQ	ID NO: 1070	Len:129	Check: 3645	Weight: 1.00
Name: C_BR_92BR0	SEQ	ID NO: 1071	Len:129	Check: 4262	Weight: 1.00
Name: C_BW_96BW0	SEQ	ID NO: 1072	Len:129	Check: 4323	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 1073	Len:129	Check: 3054	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 1074	Len:129	Check: 3900	Weight: 1.00
Name: C_BW_96BW1	SEQ	ID NO: 1075	Len:129	Check: 4051	Weight: 1.00
Name: C_ET_ETH22	SEQ	ID NO: 1076	Len:129	Check: 3843	Weight: 1.00
Name: C_IN_93IN1	SEQ	ID NO: 1077	Len:129	Check: 2878	Weight: 1.00
Name: C_IN_93IN9	SEQ	ID NO: 1078	Len:129	Check: 4499	Weight: 1.00
Name: C_IN_93IN9	SEQ	ID NO: 1079	Len:129	Check: 3994	Weight: 1.00
Name: C_IN_94IN1	SEQ	ID NO: 1080	Len:129	Check: 4362	Weight: 1.00
Name: C_IN_95IN2	SEQ	ID NO: 1081	Len:129	Check: 3765	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 1082	Len:129	Check: 4444	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 1083	Len:129	Check: 3760	Weight: 1.00
Name: CRF01_AE_C	SEQ	ID NO: 1084	Len:129	Check: 3562	Weight: 1.00
Name: CRF01_AE_T	SEQ	ID NO: 1085	Len:129	Check: 5676	Weight: 1.00
Name: CRF01_AE_T	SEQ	ID NO: 1086	Len:129	Check: 6090	Weight: 1.00
Name: CRF01_AE_T	SEQ	ID NO: 1087	Len:129	Check: 6846	Weight: 1.00

Name:	CRF01_AE_T	SEQ	ID NO:	1088	Len:	129	Check:	5393	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	1089	Len:	129	Check:	6189	Weight:	1.00
Name:	CRF01_AE_T	SEQ	ID NO:	1090	Len:	129	Check:	5202	Weight:	1.00
Name:	CRF02_AG_F	SEQ	ID NO:	1091	Len:	129	Check:	5063	Weight:	1.00
Name:	CRF02_AG_F	SEQ	ID NO:	1092	Len:	129	Check:	3731	Weight:	1.00
Name:	CRF02_AG_G	SEQ	ID NO:	1093	Len:	129	Check:	2202	Weight:	1.00
Name:	CRF02_AG_N	SEQ	ID NO:	1094	Len:	129	Check:	4873	Weight:	1.00
Name:	CRF02_AG_S	SEQ	ID NO:	1095	Len:	129	Check:	3995	Weight:	1.00
Name:	CRF02_AG_S	SEQ	ID NO:	1096	Len:	129	Check:	6502	Weight:	1.00
Name:	CRF03_AB_R	SEQ	ID NO:	1097	Len:	129	Check:	2858	Weight:	1.00
Name:	CRF03_AB_R	SEQ	ID NO:	1098	Len:	129	Check:	2808	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	1099	Len:	129	Check:	3912	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	1100	Len:	129	Check:	3700	Weight:	1.00
Name:	CRF04_cpx	SEQ	ID NO:	1101	Len:	129	Check:	3297	Weight:	1.00
Name:	CRF05_DF_B	SEQ	ID NO:	1102	Len:	129	Check:	3974	Weight:	1.00
Name:	CRF05_DF_B	SEQ	ID NO:	1103	Len:	129	Check:	4062	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	1104	Len:	129	Check:	2954	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	1105	Len:	129	Check:	1655	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	1106	Len:	129	Check:	2327	Weight:	1.00
Name:	CRF06_cpx	SEQ	ID NO:	1107	Len:	129	Check:	2706	Weight:	1.00
Name:	CRF11_cpx	SEQ	ID NO:	1108	Len:	129	Check:	2064	Weight:	1.00
Name:	CRF11_cpx	SEQ	ID NO:	1109	Len:	129	Check:	1685	Weight:	1.00
Name:	D_CD_84ZR0	SEQ	ID NO:	1110	Len:	129	Check:	4305	Weight:	1.00
Name:	D_CD_ELI_K	SEQ	ID NO:	1111	Len:	129	Check:	4483	Weight:	1.00
Name:	D_CD_NDK_M	SEQ	ID NO:	1112	Len:	129	Check:	3024	Weight:	1.00
Name:	D_UG_94UG1	SEQ	ID NO:	1113	Len:	129	Check:	3298	Weight:	1.00
Name:	F1_BE_VI85	SEQ	ID NO:	1114	Len:	129	Check:	2602	Weight:	1.00
Name:	F1_BR_93BR	SEQ	ID NO:	1115	Len:	129	Check:	2572	Weight:	1.00
Name:	F1_FI_FIN9	SEQ	ID NO:	1116	Len:	129	Check:	3253	Weight:	1.00
Name:	F1_FR_MP41	SEQ	ID NO:	1117	Len:	129	Check:	2465	Weight:	1.00
Name:	F2_CM_MP25	SEQ	ID NO:	1118	Len:	129	Check:	2231	Weight:	1.00
Name:	F2KU_BE_VI	SEQ	ID NO:	1119	Len:	129	Check:	461	Weight:	1.00
Name:	G_BE_DRCBL	SEQ	ID NO:	1120	Len:	129	Check:	3194	Weight:	1.00
Name:	G_NG_92NG0	SEQ	ID NO:	1121	Len:	129	Check:	4325	Weight:	1.00
Name:	G_SE_SE616	SEQ	ID NO:	1122	Len:	129	Check:	2614	Weight:	1.00
Name:	H_BE_VI991	SEQ	ID NO:	1123	Len:	129	Check:	2347	Weight:	1.00
Name:	H_BE_VI997	SEQ	ID NO:	1124	Len:	129	Check:	1680	Weight:	1.00
Name:	H_CF_90CF0	SEQ	ID NO:	1125	Len:	129	Check:	2751	Weight:	1.00
Name:	J_SE_SE702	SEQ	ID NO:	1126	Len:	129	Check:	2099	Weight:	1.00
Name:	J_SE_SE788	SEQ	ID NO:	1127	Len:	129	Check:	2149	Weight:	1.00
Name:	K_CD_EQTB1	SEQ	ID NO:	1128	Len:	129	Check:	3510	Weight:	1.00
Name:	K_CM_MP535	SEQ	ID NO:	1129	Len:	129	Check:	2798	Weight:	1.00
Name:	N_CM_YBF30	SEQ	ID NO:	1130	Len:	129	Check:	3973	Weight:	1.00
Name:	O_CM_ANT70	SEQ	ID NO:	1131	Len:	129	Check:	9677	Weight:	1.00
Name:	O_CM_MVP51	SEQ	ID NO:	1132	Len:	129	Check:	8852	Weight:	1.00
Name:	O_SN_MP129	SEQ	ID NO:	1133	Len:	129	Check:	1678	Weight:	1.00
Name:	O_SN_MP130	SEQ	ID NO:	1134	Len:	129	Check:	2242	Weight:	1.00
Name:	U_CD__83C	SEQ	ID NO:	1135	Len:	129	Check:	9312	Weight:	1.00

SEQ	ID	NO	1						50
970	00BW0762_1	MAGRSGD...	NDDTLLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRWR			
971	00BW0768_2	MAGRSEDS..	.DATLLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRRR			
972	00BW0874_2	MAGRSGD...	SDEALLQAVR	IIKVLYQSNP	YPK.PEGTRQ	ARKNRRRRWR			
973	00BW1471_2	MAGRSGD...	SDEALLQAVR	IIRILYQSNP	YPKPEG.TRQ	ARKNRRRRWR			
974	00BW1616_2	MAGRSGDS..	.DEALLQAVR	TIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR			
975	00BW1686_8	MAGRSGDS..	.DEALLQAIK	SIKILYQSNP	YPE.PQGTRO	AQRNRRRRWR			
976	00BW1759_3	MAGRSGD...	NDEAVLQAIR	IIKILYQSNP	YPK.PRGTRQ	AQKNRRRRWR			
977	00BW1773_2	MAGRSGDS..	.DEALLQAVK	IIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR			
978	00BW1783_5	MAGRSGD...	SDEAVLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR			
979	00BW1795_6	MAGRSGD...	GDAALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR			
980	00BW1811_3	MAGRSGD...	SDEELLQVAR	IIKILYQSNP	YPE.PRGTRQ	ARKNRRRRWR			

981	00BW1859_5	MAGRSEDS..	.DAALLQAAK	IIKIIYQSNP	YPE.PKGTRQ	ARRNRRRRWR
982	00BW1880_2	MAGRSGD...	NDEALLQAVR	IIKILYQSNP	FPK.PEGTRQ	ARKNRRRRWR
983	00BW1921_1	MAGRSGD...	NDEALLQAVR	IIKILYQSNP	YPE.PQGTRQ	ARKNRRRRWR
984	00BW2036_1	MAGRSEDS..	.DEALLQAIR	LIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
985	00BW2063_6	MAGRSGDN.D	ADAALLQAVK	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
986	00BW2087_2	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
987	00BW2127_2	MAGRSGD...	NDEARLQVVK	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
988	00BW2276_7	MAGRSGD...	SDEALLQAVR	IIKIIYQSNP	YPK.PEGTRQ	ARRNRRRRWK
989	00BW3819_3	MAGRSGD...	SDEDLLKAVR	LIKILYQSNP	YPK.PEGTRR	AQRNRRRRWR
990	00BW3842_8	MAGRSEDS..	.DEALLRVVR	IIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
991	00BW3871_3	MAGRSGDS..	.DEALLQAIR	TIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
992	00BW3876_9	MAGRSGDS..	.DEALLHAVR	TIKILYXSNP	YPE.PKGTRQ	ARKNRKRRWR
993	00BW3886_8	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	YPE.HQTRQ	ARKNRRRRWG
994	00BW3891_6	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
995	00BW3970_2	MAGRSGDS..	.DEALLQAVK	IIKILYQSDP	YPK.PEGTRQ	ARKNRRRRWR
996	00BW5031_1	MAGRSGDN..	.DEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
997	96BW01B21	MAGRSGD...	SDEALLQAVR	IIRILYQSNP	YPE.PRGTRR	ARKNRRRRWR
998	96BW0407	MAGRSGD...	SDEALLQAVK	IIKILYQSNP	YPK.PEEIRQ	ARKNRRRRWR
999	96BW0502	MAGRSGDS..	.DEALLQAVK	AIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
1000	96BW06_J4	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	SPE.PKGNRQ	ARKNRRRRWR
1001	96BW11_06	MAGRSGD...	NDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRGRWR
1002	96BW1210	MAGRSGD...	SDEALLQAVR	IIKILYQNNP	YPK.PEGTRQ	ARKNRRRRWR
1003	96BW15B03	MAGRSEDS..	.DEALLHAVR	IIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
1004	96BW16_26	MAGRSGDS..	.DAALLQAVR	IIKILYQSNP	YPK.PKGTRQ	ARKNRRRRWR
1005	96BW17A09	MAGRSGD...	NDEALLQAMG	IIKILYQSNP	YPKPEG.TRR	ARKNRRRRWR
1006	96BWM01_5	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRWR
1007	96BWM03_2	MAGRSGD...	SDEALLQAVR	TIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
1008	98BWMC12_2	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	QPK.PEGTRQ	ARKNRRRRWR
1009	98BWMC13_4	MAGRSGD...	SDEALLQAVR	IIKILYQSNS	YPK.PEGTRQ	ARKNRRRRWR
1010	98BWMC14_a	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	PPE.RRGIGQ	ARXNRRRRWR
1011	98BWM014_1	MAGRSGD...	DDERLLQAVR	IIKILYQSNP	YPS.PEGTRQ	ARRNRRRRWR
1012	98BWM018_d	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
1013	98BWM036_a	MAGRSGV...	SDEALLQAVK	IIKILYQSNP	YPNNPEGSQ	AQRNRRRRWR
1014	98BWM037_d	MAGRSGD...	SDEALLQAVR	IIKILYQSNR	YPK.PEGTRQ	AQRNRRRRWR
1015	99BW3932_1	MAGRSGD...	PDEALLQAIR	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRWR
1016	99BW4642_4	MAGRSEDSG.	.DAALLQAVR	IIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
1017	99BW4745_8	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	YPK.PKETRQ	ARRNRRRRWR
1018	99BW4754_7	MAGRSGD...	NDAALLLAVQ	TIKLLYQSNP	YPK.PEGTRQ	ARRNRRRRWR
1019	99BWMC16_8	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	CPE.PRGTRQ	ARKNRRRRWR
1020	A2_CD_97CD	MAGRSGD...	PDEDLIRAIR	IIKILYQSNP	YPKPRG.TRQ	ARKNRRRRWR
1021	A2_CY_94CY	TAGRSDD...	PDESLLQAIR	TIKILYQSNP	YPKPRG.SRQ	AQRNRRRRWR
1022	A2D_97KR	MAGRSGD...	PDEDLLRAVR	AIRILYQSNP	SPDPRG.SRQ	ARKNRRRRWR
1023	A2G_CD_97C	MAGRSGS...	TDEELLQAAR	IIKILYQSNP	YPPPEG.TRQ	ARKNRRRRWR
1024	A_BY_97BL0	MAGRSGG...	TDAELLTAVR	IIXFLYQSNP	YPTPRK.TRQ	AXKNQRRRXR
1025	A_KE_Q23_A	MAGRSGD...	SDEELLRAVR	IIKILYKSNP	YPKPKG.SRQ	ARKNRRRRWR
1026	A_SE_SE659	MAGRSGP...	GDEELLKAIR	IIKILYQSNP	YPKPRG.TRQ	ARKNRRRRWR
1027	A_SE_SE725	MAGRSGD...	SDEELLRAVR	IIKILYQSNP	YPRPKG.SRQ	AQKNRRRRWR
1028	A_SE_SE753	MAGRSGN...	SDEELLRAIR	IIKILYNSNP	YPKPKG.SRQ	ARKNRRRRWR
1029	A_SE_SE853	MAGRSGN...	SDEELLRAIR	IIKILYQSNP	HPKPRG.SRQ	ARKNRRRRWR
1030	A_SE_SE889	MAGRSGD...	SDEELLKAVR	IIKILYQSNP	YPKPRG.TRQ	ARKNRRRRWR
1031	A_SE_UGSE8	MAGRSGD...	SDEELLKAVR	TIKILYQSNP	YPPPKG.SRQ	ARKNRRRRWR
1032	A_UG_92UG0	MAGRSGN...	PDEELLRAIR	IIKILYQSNP	YPEPKG.TRQ	ARKNRRRRWR
1033	A_UG_U455_	MARRSGN...	PDEDLLKAVR	IIKLLYQSNP	CPNPRG.SRQ	ARKNRRRRWR
1034	AC_IN_2130	MAGRSGD...	SDEELLQVVR	IIKILYRSNP	YPKPRG.TRQ	ARKNRRRRWR
1035	AC_RW_92RW	MAGRSGD...	SDETLLQAVK	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRWR
1036	AC_SE_SE94	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPKPRG.TRQ	ARKNRRRRWR
1037	ACD_SE_SE8	MAGRSGD...	SDEDLLRAIR	IIKILYKSNP	YPKPRG.SRQ	ARKNRRRRWR
1038	ACG_BE_VI1	MAGRSGA...	SDEELLRAVR	IVKILYQSNP	YPKPEG.TRQ	ARRNRRRRWR
1039	AD_SE_SE69	MAGRSGD...	SDEXLLKAVR	LIKTLYQSNP	PPSEEG.TRQ	ARRNRRRRWR
1040	AD_SE_SE71	MAGRSGN...	SDEELLQAAR	IIKILYQSNP	YPKPKG.SRQ	ARKNRRRRWR
1041	ADHK_NO_97	MAGRSGD...	RDADLLKAVR	IIKILYQSNP	YPE.PTGSQ	ARRNRRRRWR

1042	ADK_CD_MAL	MAGRSGD...	SDEDLLRAIR	LIKILYQSNP	PPNTEGTRQ	ARRNRRRRWR
1043	AG_BE_VI11	MAGRTGS...	TDEELLKAVR	TIKILYQSNP	YPSSEG.SRQ	ARKNRRRRWR
1044	AG_NG_92NG	MAGRSGD...	ADEELLRVTR	IIKILYQSNP	YPPPEG.TRQ	ARKNRRRRWR
1045	AGHU_GA_VI	MAGRSGA...	SDEELLKAVR	IIKILYQSNP	FPE.PTGTRQ	ARRNRRRRWR
1046	AGU_CD_Z32	MAGRSGD...	SDEELLKIVR	IIKILYQGNP	YPPPEG.TRQ	ARRNRRRRWR
1047	AJ_BW_BW21	MAGRSGD...	NDEQLLLAIR	IIKILYKSNP	YPKPNG.SRQ	ARRNRRRRWR
1048	B_AU_VH_AF	MAGRSGD...	SDDELLKTVR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
1049	B_CN_RL42	MAGRSED...	SDEELLKTVR	LIKLLYQSNP	LPSPEG.TRQ	ARRNRRRRWR
1050	B_DE_D31_U	MAGRSGD...	SDEELLKTVR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
1051	B_DE_HAN_U	MAGRSGD...	SDEELLKTVR	LIKFLYQSNP	PPSNEG.TPT	ARRNRRRRWR
1052	B_FR_HXB2	MAGRSGD...	SDEELIRTVR	LIKLLYQSNP	PPNPEG.TRQ	ARRNRRRRWR
1053	B_GA_OYI_M	MAGRSGD...	SDEELLKTVR	LIKFLYQSNP	PPNPEG.TRQ	ARRNRRRRWR
1054	B_GB_CAM1	MAGRSGD...	SDEELLKAVR	LIKLLYQSNP	LPSSKG.TRQ	ARRNRRRRWR
1055	B_GB_GB8_A	MAGRSGD...	SDEDFLKTVR	FIKFLYQSNP	PPNPKG.TRQ	ARRNRRRRWR
1056	B_GB_MANC	MAGRSGD...	SDEELLQTVK	LVKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
1057	B_KR_WK_AF	MAGRSGD...	SDEELLRTIR	IIKFLYQSNP	LPEPEG.TRQ	ARRNRRRRWR
1058	B_NL_3202A	MAGRSGD...	SDEDLLKTVR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
1059	B_TW_TWCYS	MAGRSGD...	SDEELLRTVR	LIKLIYQSNP	PPNPEG.TRQ	ARRNRRRRWR
1060	B_US_BC_L0	MAGRSGD...	SDEELLKTVR	LIKLLYQSNP	PPNPEG.TRQ	ARRNRRRRWR
1061	B_US_DH123	MAGRSGE...	SDEDLLNTVR	LIKLLYQSNP	LPSLEG.TRQ	ARRNRRRRWR
1062	B_US_JRCSF	MAGRSGD...	SDEDLLKTVR	LIKFLYQSNP	PPSNEG.TRQ	ARRNRRRRWR
1063	B_US_MNCG	MAGRSGD...	SDEELLKTVR	LIKFLYQSNP	PPSSEG.TRQ	ARRNRRRRWR
1064	B_US_P896	MAGRSGD...	SDEDLLKTVR	LIKFLYQSNP	PPSLEG.TRQ	ARRNRRRRWR
1065	B_US_RF_M1	MAGRSGD...	SDEDLLKAVR	LIKSLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
1066	B_US_SF2_K	MAGRSGD...	SDEELLRTVR	LIKLLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
1067	B_US_WEAU1	MAGRSGD...	SDEDLLKTVR	LIKILYQSNP	PPSPEG.TRQ	ARRNRRRRWR
1068	B_US_WR27	MAGRSGD...	SDEELLQKV.	LIRFLYQSNP	PPSSEG.TRQ	ARRNRRRRWE
1069	B_US_YU2_M	MAGRSGD...	SDEDLLRTVR	LIKVLYQSNP	PPSSEG.TRQ	ARRNRRRRWR
1070	BF1_BR_93B	MAGRSGD...	SDTELLKAVS	YIKILYQSNP	LPKPKG.TRQ	ARRNRRRRWR
1071	C_BR_92BR0	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRWR
1072	C_BW_96BW0	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	AWNRRRRWR
1073	C_BW_96BW1	MAGRSGD...	NDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
1074	C_BW_96BW1	MAGRSGD...	SDEALLQAVR	IIKILYQNNP	YPK.PEGTRQ	ARKNRRRRWR
1075	C_BW_96BW1	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
1076	C_ET_ETH22	MAGRSGD...	SDEELLKAVR	IIKILYQSNP	YPT.PEGTRQ	ARRNRRRRWR
1077	C_IN_93IN1	MAGRSGDS...	.DEALLQAVR	IIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
1078	C_IN_93IN9	MAGRSGDS...	.DEELLKAVR	IIKILYQSNP	YPE.PRGTRQ	ARKNRRRRWR
1079	C_IN_93IN9	MAGRSGDS...	.DEALLRAVR	IIKILYQSNP	YPE.PRGTRQ	ARKNRRRRWR
1080	C_IN_94IN1	MAGRSGDS...	.DEALLKAVR	IIKILYQSNP	YPE.PRGTRQ	ARKNRRRRWR
1081	C_IN_95IN2	MAGRSGDS...	.DEALLKAVR	IIKILYQSNP	YPE.PRGTRQ	ARKNRRRRWR
1082	CRF01_AE_C	MAGRSGN...	TDEDLLQAVR	IIKILYQSNP	YPPPEG.TRQ	ARKNRRRRWR
1083	CRF01_AE_C	MAGRSGS...	TDEDLLRTVR	IIKILYQSNP	YPPAEG.TRQ	ARKNRRRKWR
1084	CRF01_AE_C	MAGRSGS...	TDEELLRAAR	AIKILFQSNP	YPSSEG.TRQ	ARKNRRRRWR
1085	CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IINILYQSNP	YPSSEG.TRQ	TRKNRRRRWR
1086	CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IIKVLQYQSNP	YPSSEG.TRQ	TRKNRRRRWR
1087	CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IINILYQSNP	YPSSEGTRQ	TRKNRRRRWR
1088	CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IIKLLYESNP	PPSSEG.TRQ	TRKNRRRRWR
1089	CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IIKILYQSNP	FPSSEG.TRQ	TRNRRRRWR
1090	CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IINILYQSNP	LPSSEG.SRQ	TRKNRRRRWR
1091	CRF02_AG_F	MAGRSGD...	ADEELLRVVR	IIKILYQSNP	YPPPEG.TRQ	TRKNRRRRWR
1092	CRF02_AG_F	MAGRSGD...	ADEELLRVVR	IVKILYQSNP	YPPPEG.TRQ	ARKNRRGRWR
1093	CRF02_AG_G	MAGRSGD...	ADEELLRVIR	IIKILYQSNP	YPKPEG.TRQ	ARRNRRRRWR
1094	CRF02_AG_N	MAGRSGD...	ADEELLRAVR	IIKILYQSNP	YPPPEG.TRQ	TRKNRRRRWR
1095	CRF02_AG_S	MAGRSGN...	ADEELLRAVR	TIKILYQSNP	YPPPEG.TRQ	ARKNRRRRWR
1096	CRF02_AG_S	MAGRSGD...	ADEGLLRAVR	IIRILYQSNP	YPPPEG.SRQ	ARRNRRRRWR
1097	CRF03_AB_R	MAGRSGD...	SDEELLKTIR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
1098	CRF03_AB_R	MAGRSGD...	SDEDLLKTIR	LIKFLYQSNP	PPNPEG.TRQ	ARRNRRRRWR
1099	CRF04_cpx	MAGRSGN...	IDEDLFKAAR	AIKILYQSNP	YPNNPTGTRQ	ARRNRRRRWR
1100	CRF04_cpx	MAGRSGS...	SNEDLLGSVG	IVKILYQSNP	YPN.PTGTRK	ARRNRRRRWR
1101	CRF04_cpx	MAGRSGS...	TDEDLLKAVG	IVKILYQSNP	YPNNTAGTRQ	ARRNRRRRWR
1102	CRF05_DF_B	MAGRSGD...	RDEDLLKAVR	LIKILYQSNP	LPSPEG.TRQ	ARRNRRRRWR

1103	CRF05_DF_B	MAGRSGD...	RDEDLLKAVR	LIKFLYQSNP	PPRPEG.TRQ	ARRNRRRRWR
1104	CRF06_cpx_	MAGRSGD...	SDDRLLLA VR	IIKILYQSNP	YPKPNG.SRQ	ARRNRRRRWR
1105	CRF06_cpx_	MAGRSGD...	NDEQLLLAVR	TIKILYQNNP	YPKPNG.GRQ	ARRNRRRRWR
1106	CRF06_cpx_	MAGRSGD...	NDEQLLLAVR	TIKILYQSNP	YPKPSG.SRQ	ARRNRRRRWR
1107	CRF06_cpx_	MAGRSGD...	SDEQLLWAVR	VIKILYQSNP	YPKLSG.SRQ	ARRNRRRRWR
1108	CRF11_cpx_	MAGRSGD...	NDEQLLTAVK	IIKILYQSNP	QPNPTG.SRQ	ARRNRRRRWR
1109	CRF11_cpx_	MAGRSGD...	SDAQLLAAAR	IIKILYQSSP	YPKPAG.TRQ	ARRNQRRRWR
1110	D_CD_84ZR0	MAGRSGD...	SDEDLLTAVR	LIKILYQSNP	PPSPEG.TRQ	ARRNRRRRWR
1111	D_CD_ELI_K	MAGRSGD...	SDEDLLKAVR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
1112	D_CD_NDK_M	MAGRSGD...	SDENLLKAIR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
1113	D_UG_94UG1	MAGRSGD...	RDEELLQAVR	LIKILYQSNP	PPSPEG.TRQ	ARRNRRRRWR
1114	F1_BE_VI85	MAGRSGD...	SDTELLKAVK	CIKILYQSNP	YPKPEG.TRQ	ARRNRRRRWR
1115	F1_BR_93BR	MAGRSGD...	SDQELLKAVR	YIKILYQSNP	YPKPEG.TRQ	ARRNRRRRWR
1116	F1_FI_FIN9	MAGRSGD...	SDTELLKAVK	YIKILYQSNP	YPSPDG.TRQ	ARRNRRRRWR
1117	F1_FR_MP41	MAGRSGD...	NDEELLRAVR	AIKILYQSNP	YPKPEG.TRQ	ARRNRRRRWR
1118	F2_CM_MP25	MAGRSGD...	RDEELLKAVR	YIKILYQSNP	YPKLEG.TRK	ARRNRRRRWR
1119	F2KU_BE_VI	MAGRSGD...	SDEELLKAVR	LIKILYQSNP	YPKPEG.TRQ	ARRNRKRWR
1120	G_BE_DRCBL	MAGRSGS...	TDEELLTAVR	IIKLLYQSNP	SPPPEG.TRQ	ARRNRRRRWR
1121	G_NG_92NG0	MAGRSGD...	PDEELLRAVR	IIKTLYQSNP	YPSPEG.TRQ	ARKNRRRRWR
1122	G_SE_SE616	MAGRSGS...	TDEELLRAVR	AIKILYQSNP	YPPPEG.TRQ	ARRNRRRRWR
1123	H_BE_VI991	MAGRSGD...	NDEGLLRACR	IIRLLYQSNP	YPE.PAGTRQ	AQRNRRRRWR
1124	H_BE_VI997	MAGRSGA...	GDEQLPQVCK	IIKIIYQSNP	YPE.PAGTRQ	ARRNRRRRWR
1125	H_CF_90CF0	MAGRSGA...	SDTELLQVCK	IIKILYQSNP	CPE.PGTTRQ	ARRNRRRRWR
1126	J_SE_SE702	MAGRSGD...	NDDQLLLAVR	IIKILYQSNP	YSKPNG.SRQ	ARRNRRRRWR
1127	J_SE_SE788	MAGRSGD...	SDDQLLLAVR	LIKILYQSNP	YPKPNG.SRQ	ARRNRRRRWR
1128	K_CD_EQTB1	MAGRSGD...	SEQQLLTPVR	IIKILYQSNP	YPKPEG.TRQ	ARRNRRRRWR
1129	K_CM_MP535	MAGRSGD...	PDEQLLTTVR	TIKILYESNP	YPNLEG.SRQ	TRRNRRRRWR
1130	N_CM_YBF30	MAGRSGVN...	.DEELLRAVR	VIKILYQSNP	YPSNKG.TRQ	ARRNRRRRWR
1131	O_CM_ANT70	MAGRSED...	.DQ.LLQAIQ	IIKILYQSNP	QPSPRG.SRN	ARKNRRRRWR
1132	O_CM_MVP51	MAGRSEE...	.DQQLLQAIQ	IIKILYQSNP	CPTPAG.SRN	ARKNRRRRWR
1133	O_SN_MP129	MAGRSDG...	.DQPLLRAIQ	IIKILYQSNP	HTSPTG.SRS	ARRNRRRRWR
1134	O_SN_MP130	MAGRSDG...	.DQPLLRAIQ	IIKILYQSNP	HPSPTTGSTS	ARRNRRRRWR
1135	U_CD___83C	MAGRSGE...	SDEELLRAVR	IIKILYQSNP	PPNPEG.TRQ	ARKNRRRRWR

51

100

00BW0762_1	ARQRQIHSIS	ERILSTVLGR	PAEPVPFQLP	PIERLHIGCS	ESGGTSGTQQ
00BW0768_2	ARQRQINSIS	ERILSTCLGR	PAEAVPLQLP	PIERLHIGCN	ESGGTSGTQQ
00BW0874_2	ARQRQINSIS	GRILSACLGR	PTEPVPFQLP	PIERLHINCS	ENGGTSGTQQ
00BW1471_2	ARQRQIRAI	ERILDTCLGR	LTEPVHLPLP	PLERLHLDCS	EDCEPTGTEQ
00BW1616_2	ARQRQIHSIS	ERILSACLGR	SAEPVPFQLP	PIERLHIDCS	ESSGNSG...
00BW1686_8	ARQRQIHSIS	ERILSTCLGR	SAEPVPLQLP	PIERLHIDCS	ESGGTFGTQQ
00BW1759_3	ARQRQIDSIS	ERVLSTVLGR	PTEPVPFQLP	PIERLDIGDS	ESGGTSGTQR
00BW1773_2	ARQRQIREIS	QRILSTYLGR	PAEPVPLLLP	PIERLHIDCS	ESGGTSGTQQ
00BW1783_5	ARQRQIHSIS	ERILSTCLGR	STEPVPFQLP	PIERLHIGDS	KSSGTSGTQQ
00BW1795_6	ARQRQIHSIS	ERILSTCLGR	PAEPVPFLLP	PLERLHIGDS	ESSGTSGTQQ
00BW1811_3	ARQRQIREIS	ERILCTCLGR	STEPVPFLLP	PIERLHIGDS	EGSGTSGTQQ
00BW1859_5	ARQRQIHTIS	ERILSTCLGR	PAEPVPLQLP	PIERLHIDCS	ESSGTSGTQQ
00BW1880_2	ARQRQIHSIS	ERILSTCLGR	STEPVPFQLP	PIERLHIGDS	ESSGTSGTQR
00BW1921_1	ARQRQINSIS	ERILTCLGR	SEEPVPLQLP	PIERLNIGGS	ESSGTSGTQQ
00BW2036_1	ARQRQIDSIS	ARILSTCLGR	PAEPVPFQLP	PIERLNIGDN	ESGGTSGTQQ
00BW2063_6	ARQKQIHSIS	ERILSTCLGR	SEEPVPLLLP	PIERLRIGDS	ESSGTSGTQQ
00BW2087_2	ARQREIHSIS	ERILTTVLGR	SAEPVPFQLP	PIERLNINCS	EGSGTSGTQQ
00BW2127_2	ARQRQIHSIS	ERILSTCLGR	STEPVPFQLP	PIERLNIGDS	EGSGTSGTQR
00BW2276_7	ARQRQIHTIS	ERILSTCLGR	PAEPVPLQLP	PIERLYIGDS	EGGGTSGTQQ
00BW3819_3	ARQRQIHSIS	ERILSACLGR	PAEPVPFQLP	PIERLNIGDS	EGDRTYGTQQ
00BW3842_8	ARQRQIDSIS	GRLLSTCLGR	SAEPVPLQLP	PIERLNIGDS	ESGGTSGTQQ
00BW3871_3	ARQRQINSIS	ERILSTCLGR	SAEPVPLQLP	PIERLHIDCS	ESGGTSGTQQ
00BW3876_9	ARQKQIHSIS	ERILSACLGR	SAEPVPLQLP	PIERLHIGGS	ESGGTSGTQQ
00BW3886_8	ARQRQINSIT	ERILSDCLGR	SAEPVPLQLP	PIERLHIVDS	ESGGTSGTQQ
00BW3891_6	ARQRQIHSLS	ERILSTCLGR	SAEPVPLQLP	PLERLHIGDS	ESGGTSGTQQ
00BW3970_2	ARQKEIHSLS	ERILSTCLGR	PAEPVPLQLP	PLERLHIDCS	ESGGTSGTQQ

00BW5031_1	ARQRQIHSIG	ERILSTCLGR	SAEPVPLQLP	PLERLHIDCS	ESSGTPGTQQ
96BW01B21	ARQRQIHSIS	ERILTTCLGR	FTEPVPFQLP	PIERLHIGDS	ESSGTSGTQQ
96BW0407	ARQRQIHSIS	ERILSTCLGR	PTEPVPFQLP	PIERLHIDCS	ESSGASGTQR
96BW0502	ARQRQIHSLS	ERILSACLGR	PAEPVPFQLP	PIERLHIDCS	KSVGTSG...
96BW06_J4	ARQRQINSIS	ERILSTCLGR	SAEPVPFQLP	PIERLHIGGS	ESSGTSGTQQ
96BW11_06	TRQKQINSIS	ERILSTCLGR	SAEPVPFLLP	PIERLHISDS	ESSGTSGTQQ
96BW1210	ARQRQIHSIS	ERILSTCLGR	PAEPVPLQLP	PIERLHIGGS	ENSGTTGTQQ
96BW15B03	ARQRQIDSIS	TRILSTCLGR	PEEPVPFQLP	PIERLNIGDS	ESSGTSGTQQ
96BW16_26	ARQRQIRAIS	ARIFSACLGR	PAEPVPLQLP	PIERLHIGSS	ESSGTSGTQ.
96BW17A09	ARQRQIHSIS	ERILSTCLGR	PTEPVHLPLP	PLERLHLDCS	EDCEPTGEQ
96BWM01_5	ARQRQINSIS	ERILSACLGR	PAEPVPFLLP	PIERLHIGDS	ESSGTSGTQQ
96BWM03_2	ARQRQIHSIS	ERILSACLGR	PTEPVPFQLP	PIERLSIGDS	ESSGTSGTQQ
98BWMC12_2	ARQKHIHSIS	ERILSDCLGR	SAEPVPLQLP	PIERLHIDCS	ESSGTSGTQQ
98BWMC13_4	ARQRQINSIS	ERILSTCLGR	STEPVPLLLP	PIERLHIGDS	ESSGTSGTQQ
98BWMC14_a	ARQTQINSLS	ERIVSTCLGR	PAERAPFQLP	PIEKLHIDCS	ESSGTPG...
98BWM014_1	ARQRQIRALS	ERILSTVLGR	PTEPVPFQLP	PIERLNINCS	ESSGTSGTQQ
98BWM018_d	ARQRQINSIS	ERILSTCLGR	PAEPVPFQLP	PIERLHIDCS	ESSGTSGTQH
98BWM036_a	ARQRQIHSIS	ERILSSCLGR	PTEPVPFQLP	PIERLHIGDS	ESSGTYGTQQ
98BWM037_d	ARQRQIHSIS	ERILSTCLGR	SAEPVPLQLP	PIERLHIADS	KGGGTSIGQQ
99BW3932_1	ARQRQIHSIS	ERILFTCLGR	STEPVPFQLP	PIERLNIGDS	ESSGTYGTLQ
99BW4642_4	ARQRQISSLS	ERILSTCLGR	SAEPVPLQLP	PIERLHIDCS	ESSGTSGTQQ
99BW4745_8	ARQNQIRAIS	KRILSTCLGR	PAEPVPLQLP	PIERLHIGDS	ESSGTSGTQQ
99BW4754_7	ARQRQIHSIS	ERILSNCLGR	PAEPVPFQLP	PIEGLHIDCN	ESSGTSGTQQ
99BWMC16_8	ARQRQIDSIS	QRILSDCLGG	PAEPVSFQLP	PIERLNIDCN	ESSGTSGTQQ
A2_CD_97CD	ARQRQIDSIS	ERILSTCLGR	PTEPVPLQLP	PLERLHLDCS	EDCGTCGTQQ
A2_CY_94CY	ARQRQIDSIS	ERVLRSTCLGR	PTEPVPLQLP	PLERLHIDCS	EDCGTSGTLQ
A2D_97KR	ARQRQIRAIS	ERILSACLGR	PTEPVPLQLP	PLERLHLDCS	EDCGTSGTQQ
A2G_CD_97C	ARQRQIREIS	ERILSTCLGR	PTEPVPLLLP	PLERLHLDCS	EDGGTAETQQ
A_BY_97BL0	ARQRQINSIS	KRIFSTCXGR	SXEPVSLQLP	PIERLHLDCS	EDCXTSETQQ
A_KE_Q23_A	ARQRQIDSIS	ERILSTCLGR	PTEPVPLQLP	PLERLHLDCC	EDCGTSGTQQ
A_SE_SE659	ARQRQIDSIS	ERILSACLGR	STEPVPLQLP	PLERLNLDRC	EDCGTSGTQQ
A_SE_SE725	ARQRQIDSIS	ERILSTCLGR	SEEPVPLQLP	SLETLHLDCH	DDCGTSGTQQ
A_SE_SE753	ARQRQIDSIS	ERILNACLGG	STEPVPLQLP	PLERLNLDRC	EDCGTSGTQQ
A_SE_SE853	ARQRQIDSIS	ERILSTCLGR	SAEPVPLQLP	PLEGLHLDCC	EDCGTSGTEG
A_SE_SE889	ARQKQIDSLS	ERILSTCLGR	PQEPVPLLLP	PIERLHLDCS	EDCGTSGTQQ
A_SE_UGSE8	ARQRQIDSLS	QRILSACLGR	SEEPVPLQLP	PIERLHLDCH	EDCGTSGTG.
A_UG_92UG0	ARQRQIDTSL	ERVLRSTCLGR	PAEPVPLQLP	PIERLHLDCS	EDCGTSGTQQ
A_UG_U455_	ARQRQIDSLS	ERILSDCLGR	PAEPVPLQLP	PIERLRLDCS	ESCGTSGTQQ
AC_IN_2130	ARQRQIDSIS	ERILSTFLGR	SAEPVPLQLP	PLERLHLDCC	EDCGTSGTQQ
AC_RW_92RW	ARQRQIHSIS	ERILSTCLGR	PTEPVPFQLP	PIERLTIDCS	EDGGTSGTQQ
AC_SE_SE94	ARQRQIDSIS	ERILSTCLGR	SAEPVPLQLP	PLERLHLD..SGTQQ
ACD_SE_SE8	ARQRQIDSIS	QRILSTCLGR	SEEPVPLQLP	PLERLNLDCC	EDCGTSGTQQ
ACG_BE_VI1	ARQRHIHSLS	ERILCTCLGR	SEEPVHLPLP	PLEGLTLDCN	ESSGTSGTEG
AD_SE_SE69	ARQRQINSIG	ERILSTYLGR	SQEPVPLQLP	PLERLTLNCI	EDCGTSGTQG
AD_SE_SE71	ARQNQIDSIS	KRILSNCLGR	PAEPVPLQLP	PLERLNLNCS	KDCGTSGTQG
ADHK_NO_97	ARQXQIHSIG	ERVLRATCMGR	PAEPVPLQLP	PLERLTLDCS	EDCDIAGKQG
ADK_CD_MAL	ARQRQINSIG	ERILSTYLGR	PEEPVPLQLP	PLERLTLNCN	EDCGTSGTQG
AG_BE_VI11	ARQRHIQAIS	RRILDACLGR	PAEPVPLQLP	PLERLSLDCS	KDIGTSGTQR
AG_NG_92NG	ARQRQISALS	ERILSTCLGR	PAEPVPLQLP	PIERLSLDCS	EDSRTPETQQ
AGHU_GA_VI	ARQKQIHSIG	ERVLRATYLGR	PAEPVPLQLP	PLERLTLDCS	EDCGTSGEKG
AGU_CD_Z32	ARQRQIHSIG	ERILTTCLGR	STEPVPFLLP	PIERLRIDCS	EDRGSDPQGG
AJ_BW_BW21	ARQNQIDSIS	ERILSTCLGR	PTEPVPFQLP	PIERLRLDCS	EDCGHSGTQG
B_AU_VH_AF	ARQRQIRQIS	GWILSTYLGR	PAEPVPLQLP	PLERLTLDCS	KDCGTSGTQG
B_CN_RL42_	ARQRQIREIS	DRILVTYLGG	STEPVPLQLP	PLERLTLDCS	KDCGTSGTQG
B_DE_D31_U	QRQRQIQSIS	ERILSTYLGR	PEQPVPLPLP	PLERLTLDCS	EDCGTSGTQG
B_DE_HAN_U	ERQRQIRSIS	ERILSTFLGR	PAEPVPLQLP	PLERLTLDCS	EDCGNSGTQG
B_FR_HXB2_	ERQRQIHSIS	ERILGTYLGR	SAEPVPLQLP	PLERLTLDCN	EDCGTSGTQG
B_GA_OYI_M	ERQRQIRKIS	GWILSTYLGR	SAEPVPLQLP	PLERLNLDCS	EDCGTSGTQG
B_GB_CAM1_	ERQRHIRAIS	NWILSTHLGR	PAEPVPLQLP	PLERLTLDCS	KDCGTSGTQG
B_GB_GB8_A	ARQRQIHQIG	EWILSAFLGR	PAEPVPLQLP	PIERLTLDCD	EDCGTSGTQG
B_GB_MANC_	GRQRQIQSLS	AWILSTRLGR	STQPVPLQLP	PLERLTLDCS	EDCGTSGTQG

B_NL_WK_AF	RRQWWIQSLS	GWILNTHLGR	PAEPVPLQLP	PLERLTLDGN	EECGTSGTQG
B_NL_3202A	ERQRQIRSIS	ERILSTYLGR	SAEPVPLQLP	PLERLTLDGD	EDCGTSGTQG
B_TW_TWCYS	ERQRQIRTIS	GWILSNYLGR	PAEPVPLQLP	PLERLTLDGD	EDCGTSGTQG
B_US_BC_L0	ERQRQIRSIS	ERILSTFLGR	SAEPVPLQLP	PLERLNLCGN	EDCGTSGTQG
B_US_DH123	QRQRQIQSIS	GWILSNHLGR	PADAVPLQLP	PLERLTLDGN	EDCGTSGTQG
B_US_JRCFS	ERQRQIRTIS	ERILSTYLGR	PAEPVPLQLP	PLERLTLDGN	EDCGTSGTQG
B_US_MNCG	ERQRHIRSIS	AWILSNFLGR	PAEPVPLQLP	P.QRLTLDGS	EDCGTSGTQG
B_US_P896	ERQRQIRSIS	ERILGTYLGR	FEEPVPPLPL	PLEKLTLDGN	EDCGTSGTQG
B_US_RF_M1	ERQRQIRRCs	EWILDTYLGR	SVDVPQLQLP	PLERLTLDSS	EDCGTSGTQG
B_US_SF2_K	ERQRQIRSIS	GWILSTYLGR	SAEPVPLQLP	PLERLTLDGS	EDCGNSGAQG
B_US_WEAU1	ERQRQIRKIS	GWILNTYLGR	PTepVPLPLP	PLDRLTLDCK	EDCGTSGTQQ
B_US_WR27_	.RQRQIQSLS	AWIISTHLGR	PAEPVPLQLP	PLERLTLDGS	EDCGTSGTQG
B_US_YU2_M	ERQRQIRSIS	GWLLSNYLGR	PTepVPFQLP	PLERLTLDGN	EDCGTSGTQG
BF1_BR_93B	ARQRQIREIS	ERILSSCLGR	PEEPVPLQLP	PLERLHINCS	EDCGQGTEEG
C_BR_92BR0	ARQRQIHSIS	ERILSTCVGR	PAEPVPFQLP	PIERLNINCS	ESGGTSGTQQ
C_BW_96BW0	ARQRQIHSIS	ERILSTCLGR	PTepVPLQLP	PIERLHIDCS	ESSGASGTQQ
C_BW_96BW1	ARQKQINSIS	ERILSTCLGR	SAEPVPFLPL	PIERLHISDS	ESGGTSGTQQ
C_BW_96BW1	ARQRQIHSIS	ERILSTCLGR	PAEPVPLQLP	PIERLHIGGS	ENSGTTGTQQ
C_BW_96BW1	ARQRQIDSIS	TRILSTCLGR	PEEPVPFQLP	PIERLNIGDS	ESGGTSGTQQ
C_ET_ETH22	ARQRQIHTLS	ERILSNFLGR	PAEPVPLQLP	PLERLNLDGS	EDSGTSGTQQ
C_IN_93IN1	ARQRQIHSIS	ERILSTCLGR	STEPVPLQLP	PIERLHIGGS	ESGGTSGTQQ
C_IN_93IN9	ARQRQIHSLS	ERILSACLGR	PAEPVPLQLP	PLERLHISGS	ESGGTSGTQQ
C_IN_93IN9	ARQKQIHSLS	ERILSTCLGR	SAEPVPLQLP	PLERLHISGS	ESGGTSGTQQ
C_IN_94IN1	ARQRQIHSIS	ERILSACLGR	PAEPVPLQLP	PIERLHISGS	ESGGTSGTQQ
C_IN_95IN2	ARQRQIHSIS	ERILSTFLGR	PAEPVPLQLP	PIERLHISGS	ESAGTSGTPQ
CRF01_AE_C	RRQRQIHSLS	ERILVACVGR	STEPVPLQLP	PLERLHIDCS	EDCGTSGTQQ
CRF01_AE_C	ARQRQIHKIG	ERILSTCLGR	SPEPVPLQLP	PLERLHLDGS	EDCGTSGTQQ
CRF01_AE_C	ARQRQIRALS	ERILSACLGR	SAEPVPLQLP	PLERLHLDGS	EDCGTSGTQQ
CRF01_AE_T	ARQRQIRAIS	ERILITCLGR	STEPVPLQLP	PLERLHLDGN	EDCGTSGTQQ
CRF01_AE_T	ARQRQIRAIS	ERILNACVGR	STEPVPLQLP	PLERLHLDGS	EDCGTSGTQQ
CRF01_AE_T	ARQRQIRAIS	ERILSTCLGR	STEPVPLQLP	PLERLHLDGS	EDCGTSGTQQ
CRF01_AE_T	ARQRQIREIS	ERILSSCVGR	STEPVPLPLP	PLERLHLDGS	EDCGTSGTQQ
CRF01_AE_T	ARQRQISAIS	ERILSTCLGR	STEPVPLQLP	PVERLNLDGS	EDGGTSGTQQ
CRF01_AE_T	ARQRQISAIS	ERILSACLGR	STEPVSLPLP	PLERLHLDGS	EDCGTSGTQQ
CRF02_AG_F	ARQRQIRAIS	ERFLSTCLGR	SAEPVPLQLP	PIERLCLDGS	EGCGTSGTQQ
CRF02_AG_F	ARQRQIRAIS	QRILSTCLGR	SAEPVPLQLP	PLERLCLDGS	EGCGTSGTQQ
CRF02_AG_G	ARQRQIHSLS	ERILSTCLGR	PEEPVSFQLP	PLERLNLDGS	EDCGNSGTQS
CRF02_AG_N	ARQRQIRAIS	ERILSTCLGR	SAEPVPLQLP	PIERLNLDGS	EDCGTSGTQL
CRF02_AG_S	ARQRQIRAIS	ERILSTCLGR	SAEPVPLQLP	PIERLRLDGS	EDCGTSGTQG
CRF02_AG_S	ARQRQVRAIS	ERILSTCLGR	PAEPVPLPLP	PIERLCLDGS	EDSGTSGTQQ
CRF03_AB_R	ERQRHIHSIS	EQILSTYLGR	PEEPVLLHLP	PLERLTLDGS	EDCGTSGTQG
CRF03_AB_R	ERQRHIHSIS	QRILSTYLGR	PEEPVPLHLP	PLERLTLDGS	EDCGTSGTQG
CRF04_cpx_	ARQKQIHSLS	ERILATYLGR	PAEPVPLQLP	PLEKLTLNCS	EDCGTSGDKG
CRF04_cpx_	ARQKQIHSIS	ERVLATYLGR	PAEPVPLQLP	PLEKLTLNCS	EDCGTSGEKG
CRF04_cpx_	ARQNRIHSIS	ERILAACLGR	PAEPVPLQLP	PIEKLTLDGS	EDCGTSGDKG
CRF05_DF_B	ARQRQINSIG	ERLLSTYLGR	SEEPVPLQLP	PLERLNLNCS	EDCGTSGTQG
CRF05_DF_B	ARQRQIRSI	DRIVDTYLGR	PEEPVPLQLP	PLERLNLNCS	EDCGTSGTQG
CRF06_cpx_	ARQNQIDSIS	ERVLSTCLGR	SAEPVPLQLP	PIERLRLDGS	EDCGNSGTQG
CRF06_cpx_	ARQNQIDSIS	ERILSTCLGR	PTepVPFQLP	PIERLRLDGS	EDCGNSGTQG
CRF06_cpx_	ARQKQIDSIS	ERILSTCLGR	SAEPVPLQLP	PIERLRLDGS	EDCGNSGTQG
CRF06_cpx_	ARQNQIDSIS	ERILSSCLGR	SEEPVPLQLP	PIERLRLDCT	EDCGNSGTQG
CRF11_cpx_	ARQNQIDSIS	QRILSDCLGR	SEEPVPLQLP	PIERLHLDGS	EDCGNPGTQG
CRF11_cpx_	ARQNQLHSIS	QRILSTCLGR	SEEPVPLPLP	PIERLHLDGS	EDCGNSGTQG
D_CD_84ZR0	ARQRYIHSIG	ERILSTYLGR	SEEPVPLQLP	PLERINLNCS	EDCGTSGTQG
D_CD_ELI_K	ARQRQIREIA	ERILGTYLGR	PAEPVPLQLP	PLERLNLNCS	EDCRTSGTQG
D_CD_NDK_M	ARQRQIHSIG	ERIICTFLGR	PEEPVPLQLP	PLERLNLNCS	EDCGTSGTQG
D_UG_94UG1	ARQRQIHSIG	ERIISTYLGR	FEEPVPLQLP	PLERLNLNCS	EDCGTSGTQG
F1_BE_VI85	ARQRQIRALS	DRILSSCLGR	SEEPVPLQLP	PLERLHINCS	EDCGQGPEEG
F1_BR_93BR	ARQRQIREIS	DRILSSCLGR	PAEPVPLQLP	PLERLHINCS	EDCGQGAEEG
F1_FI_FIN9	ARQRQIRAIS	ERILSSCLGR	LEEPVPLQLP	PLERLHINCS	EDCGQGTEEG
F1_FR_MP41	ARQKQIRSIS	ERILVACLGR	PEEPVPLQLP		

F2_CM_MP25	ARQRQIHQIS	ERILSTCLGR	LQEPVRLQLP	LLEKLHINCS	EDCGQGTEKG
F2KU_BE_VI	ARQRQIHSIS	QRILSTCLGR	PAEPVPLQLP	PLERLNLDCS	EDSREGAEGE
G_BE_DRCBL	ARQRQIHSIS	ERILSTCLGR	PEEPVPLQLP	PLERLHLDGS	EDGGTSGTQQ
G_NG_92NG0	ARQRQIHSIS	ERILSACLGR	PAEPVPLQLP	PLEGLSLDCS	KDGGTSGTQQ
G_SE_SE616	ARQRQISASIS	ERILTAYLGR	PAEPVPLQLP	PLERLHLDGS	EDSGTSGTQQ
H_BE_VI991	ARQRQIHSIG	ERVLATCLGG	PAEPVPLQLP	PLERLTLDCS	EDCGTSGEKG
H_BE_VI997	ARQRQIRASIS	ERILTDCLGR	PPEPVPLQLP	PLERLTLDCN	KDCGTSGEKG
H_CF_90CF0	ARQRQIREIS	ERILTSCLGR	PPEPVTLQLP	PLERLTLNCS	EDCGTSGEKG
J_SE_SE702	ARQNQIDSIS	ERILSSCLGR	PAEPVPLQLP	PIERLRLDCS	EDCGNSGTQG
J_SE_SE788	ARQNQIDSIS	ERIPSSCLGR	PAEPVPLQLP	PIERLRLDCS	EDCGNSGTQG
K_CD_EQTB1	ARQRQIREIS	QRLVSSCLGR	STEPVPLQLP	PLERLSLDCS	EDSGQGTEGE
K_CM_MP535	ARQKQISSIS	ERLLSACLGR	SAEPVPLQLP	PIEKLNLDCS	EDPGKGTEGG
N_CM_YBF30	ARQRQIRASIS	ERILSSCLGG	PPEPVPLQLP	PLDRLTLDTE	EDSGTSGTES
O_CM_ANT70	RRQAQVDTLA	ARVLATVVHG	PQNNNIVDLP	PLEQLSIRDP	EGDQLSEAWT
O_CM_MVP51	RRQAQVDSL	TRILATVVHG	SQDNNLVLDLP	PLEQLNIRDP	EADRLPGTGT
O_SN_MP129	TRHAHVDTLA	ARILATVVHG	PQDNNLVLELP	PLEQLSIRDP	DGDQPSGTWT
O_SN_MP130	KRQAQIDTLA	ARILATVVHG	PQDNNLVLELP	PLEQLSIRDP	DGDQPSGTWT
U_CD___83C	RRQQQIRASIS	ERILSTCLGR	PAEPVHLQLP	PLERLNLDCSKGTATG

	101		129
00BW0762_1	PQGTPEGMGVN	P.....
00BW0768_2	SQGTSEGVGS	P.....
00BW0874_2	SQGTTEGVGN	P.....
00BW1471_2	SQGTTEGVGS	P.....
00BW1616_2TQGVGS	P.....
00BW1686_8	SQGATEGVGN	P.....
00BW1759_3VGS	P.....
00BW1773_2	SQGTTEGVGS	P.....
00BW1783_5	SQGTTEGVGN	P.....
00BW1795_6	SQGTPEGVGN	P.....
00BW1811_3	SQGTPEGVGN	P.....
00BW1859_5	SQGTTEGVGS	P.....
00BW1880_2	SQGTPEGVGN	P.....
00BW1921_1	SQGTTEGVGN	P.....
00BW2036_1	SQGTTEGVGS	P.....
00BW2063_6	SQGTPEGVGN	P.....
00BW2087_2	PQGTTEGVGN	P.....
00BW2127_2VGS	P.....
00BW2276_7	SQGTTEGVGS	P.....
00BW3819_3	SQGTTEGVGS	P.....
00BW3842_8	PQGTTEGVGS	P.....
00BW3871_3	SQGTTEGVGN	P.....
00BW3876_9	SQGTKEGVGS	P.....
00BW3886_8	SQGTTEGVGS	P.....
00BW3891_6	SQGTTEGVGS	P.....
00BW3970_2GVGH	P.....
00BW5031_1	PQGDTEGVGR	P.....
96BW01B21	SQGTTEGVGN	P.....
96BW0407	SQGTTEGVGN	P.....
96BW0502TEGVGS	P.....
96BW06_J4	SQGPTEGVGS	P.....
96BW11_06	SQGTPEGVGN	P.....
96BW1210	SQGTTEGVGS	P.....
96BW15B03	SQGTTEGVGS	P.....
96BW16_26GVGS	P.....
96BW17A09	SQGATEGVGS	P.....
96BWM01_5	SQGTPEGVGN	P.....
96BWM03_2	SQGTTEGVGS	S.....
98BWMC12_2	SQGTAEGVGS	P.....
98BWMC13_4	SHGTPEGVGN	P.....
98BWMC14_aTQGVGN	P.....

98BWM014_1	SLGTTEGVGS	P.....
98BWM018_d	SQGTTEGVGN	P.....
98BWM036_a	PQGTTEGVGN	P.....
98BWM037_d	PQGTTEGVGS	P.....
99BW3932_1	SQGTTEGVGS	P.....
99BW4642_4	SQGTTEGVGS	P.....
99BW4745_8	SQGTTEGVGS	P.....
99BW4754_7	SQGTPEGVGN	S.....
99BWMC16_8	SQGTTEGVGS	P.....
A2_CD_97CD	SQGAETGVGR	PQTSVESSGI	LGSGIEDX.
A2_CY_94CY	SQGTETGVGR	SQESVESSVI	LGSGTEEX.
A2D_97KR	PQGTETGVGR	PQISVEPSVV	LGSGTEEX.
A2G_CD_97C	PQGTETGVGG	.TIFVESSVI	LGSRKEQX
A_BY_97BL0	SQXTETXVXX	PQISXESSXI	XXSGTKEX.
A_KE_Q23_A	SQGAETGVGR	HQVSVESPVI	LGSGTKNX.
A_SE_SE659	SQGVETGVGR	PQVSGESPVI	LGSGTKNX.
A_SE_SE725	SQGVETGVGR	PQVPGEPTV	LGSGTKTX.
A_SE_SE753	SQGIETGVGR	PQVSVESPVI	LGSGTKEX.
A_SE_SE853VGR	PQVSVESPGV	LDSGTKNX.
A_SE_SE889	SQGAETGVGG	PQVSEESSII	LGSGTKTX.
A_SE_UGSE8	TQVSGESSVV	LDSGTKDX.
A_UG_92UG0	SQGVETGVGR	TQVSGESPVV	LGSGTKNX.
A_UG_U455_	PQGTETGVGG	PQISVESSAV	LGSGTKNX.
AC_IN_2130	SQGVETGVGR	PQVSVESPGI	LGSGTKNX.
AC_RW_92RW	SQGTTEGVGN	PVSRKSCAVL	GS GTKKEX.
AC_SE_SE94	SQGTETGVGR	PQVSVESSAI	LPGTKNX.
ACD_SE_SE8VGS	NQISVESPAV	LDSGTKEX.
ACG_BE_VI1VGS	SQTSGEHPVI	LESGTKEX.
AD_SE_SE69VGS	PQIPVEPPAV	LDSGTKEX.
AD_SE_SE71VGS	PQIPVESPAI	LDSGTENX.
ADHK_NO_97VGD	PQIPGESSAV	LGTGTKEX.
ADK_CD_MALVGS	PQISVESPAI	LGSGTEEX.
AG_BE_VI11	SQGTETGVGR	PQIFVESSGV	LGSGTKEX.
AG_NG_92NG	SPGTETGVGG	PQISVESPVV	LGSGTKEX.
AGHU_GA_VIVGS	PQISVESPTV	LGTGAKEX.
AGU_CD_Z32VGD	SQIPGESCDL	LGSGTKEX.
AJ_BW_BW21VGD	PQVSGESCPV	LGEGTKEX.
B_AU_VH_AFVGG	PQVLVESPAV	LESGAAEX.
B_CN_RL42_VGS	PQILVESPAV	LDSGTKEX.
B_DE_D31_UVGS	PQILVESPAV	LESGTKEX.
B_DE_HAN_UVGS	PQVLVESPAV	LEPGTKEX.
B_FR_HXB2_VGS	PQILVESPTV	LESGTKEX.
B_GA_OYI_MVGS	PEILVESPAV	LEPGTKEX.
B_GB_CAM1_VGS	PQILVESPAV	LESGTKEX.
B_GB_GB8_AVGS	PQVLVESPAV	LDPGTKEX.
B_GB_MANC_VGN	PQVLVESPAV	LESGSKEX.
B_KR_WK_AFVGN	PQILVESPAV	LESGTKEX.
B_NL_3202AVGS	PQILVESPAV	LESGTKEX.
B_TW_TWCYSVGS	PQIFVESPTV	LDSGTKEX.
B_US_BC_L0VGS	PQVLVESPTV	LEPGTKEX.
B_US_DH123VGT	PQILVESPAV	LESGTKEX.
B_US_JRCFSVGN	PEILVESPTV	LESGTKEX.
B_US_MNCG_VGS	PQILVESPTV	LESGTKEX.
B_US_P896_VGS	PQILVESPAI	LEPGTKEX.
B_US_RF_M1VGS	PQVLVESPAV	LESGAKEX.
B_US_SF2_KVGS	PQILVESPAV	LDSGTKEX.
B_US_WEAU1VGS	SQILLES PAV	LEPGTKEX.
B_US_WR27_VGD	PQILGESPTV	LGSGAKEX.
B_US_YU2_MVGS	PQILVESPPV	LDSGTKEX.
BF1_BR_93BVGS	PQTSGESRAV	LESGTKEX.
C_BR_92BR0	PQGNTERVGN	PVFGRPCAVL	ESRVKKEX.

HPCUNKCD	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNLRTG	VRTITTGAPI
MKC1A	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
NDM59	VAYAAQGYKV	LVLNPSVAAT	LGFGAYLSKA	HGINPNIRTG	VRTVTTGESI
NZLI	AAYVAQGYNV	LVLNPSVAAT	LGFGSFMRA	YGIDPNIRTG	NRTVTTGAKL
SA13	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSRA	YGVDPNIRTG	VRTVTTGAAI
Th580	AAAYATQGYKV	LVLNPSVAAT	LSFGAYMSKA	HGIDPNIRTG	VRTITTGGPV
Type_3a_CB	AAAYVAQGYTV	LVLNPSVAAT	LGFGSFMRA	YGIDPNIRTG	NRTVTTGAKL
TypeV_D	AAAYVAQGYNV	LVLNPSVAAT	LGFGSFMRA	YGTDPNIRTG	NRTVTTGAKL
VN004	AAAYAAQGYKV	LVLNPSVAAT	LGFGSYMSTA	HGIDPNIRTG	VRTITTGGAI
VN235	AAAYASQGYKV	LVLNPSVAAT	LGFGSYMSTA	HGIDPNIRTG	VRTITTGGPI
VN405	AAAYAAQGYKV	LVLNPSVAAT	LGFGSYMSTA	HGIDPNIRTG	VRTITTGGAI

	1301			1350	
BEBE1	TYSTYKFLA	DGGCSGGAYD	VIICDECHSV	DSTTILGIGT	VLDQAETAGV
D89815	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETVGA
ED43type_4	TYSTYKFLA	DGGCSGGAYD	IIICDECYST	DSTTILGIGT	VLDQAETAGV
HC_C2	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HC_G9	THSTYKFLA	DGGCSGGAYD	IIICDECHSV	DATSILGIGT	VLDQAETAGV
HCU16326	TYSTYKFLA	DGGSGGGAYD	IIMCDECHST	DSTTIYGIGT	VLDQAETAGA
HCV_H_CMV	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DATSILGIGT	VLDQAETAGA
HCV_J1	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DATSVLGIGT	VLDQAETAGA
HCV_J483	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HCV_J8	TYSTYKFLA	DGGCAAGAYD	IIICDECHSV	DATTILGIGT	VLDQAETAGV
HCV_JK1	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_JS	TYSTYKFLA	DGGCSGGAYD	IIMCDECHST	DSTTILGIGT	ALDQAETAGA
HCV_K1_R1	TYSTYKFLA	DGGCSGGAYD	IIMCDECHSI	DSTSILGIGT	VLDQAETAGA
HCV_K1_R2	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_K1_R3	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_K1_S1	TYSTYKFLA	DGGCSGGAYD	IIMCDECHSI	DSTSILGIGT	VLDQAETAGA
HCV_K1_S2	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_K1_S3	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_L2	TYSTYKFFA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HCV_N	TYSTYKFLA	DGGCSGGAYD	IIMCDECHST	DSTTILGIGT	VLDQAETAGA
HCV12083	TYSTYGEFLA	DGGCSGGAYD	IIICDECHST	DPTTVLGIGT	VLDQAETAGV
HCV1480	TYSTYKFFA	DGGCSGGAYD	VIICDECHSQ	DATTILGIGT	VLDQAETAGA
HCVPOLYP	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HD_1	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HPCCGAA	TYSTYKFLA	DAGCSGGAYD	IIICDECHST	DATSISGIGT	VLDQAETAGA
HPCFG	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGV
HPCGENANTI	TYSTYKFLA	DGGCSGGAYD	IIMCDECHST	DSTTILGIGT	VLDQAETAGA
HPCGENOM	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCUMR	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCJ	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCJCG	TYSTYCKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCJK046	TYSTYKFLA	DGGCSGGAYD	VIICDECHST	DPTTVLGIGT	VLDQAETAGC
HPCJK049	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGA
HPCJTA	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCJTB	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCK3A	TYSTYKFLA	GGGCSGGAYD	VIICDDCHAQ	DATSILGIGT	VLDQAETAGV
HPCPLYPRE	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DATSILGIGT	VLDQAETAGA
HPCPOLP	TYSTYKFLA	DGGCAGGAYD	IIICDECHAV	DSTTILGIGT	VLDQAETAGV
HPCPP	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HPCUNKCD	TYSTYKFLA	DGGSGGGAYD	IIMCDECHST	DSTTIYGIGT	VLDQAETAGA
MKC1A	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
NDM59	TYSTYKFLA	DGGCAGGAYD	IIICDECHAV	DATTILGVGT	VLDQAETAGV
NZLI	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGV
SA13	TYSTYKFLA	DGGCSGGAYD	VIICDECHSQ	DATTILGIGT	VLDQAETAGA
Th580	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DPTTVLGIGT	VLDQAETAGV
Type_3a_CB	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGV
TypeV_D	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGV
VN004	TYSTYKFLA	DGGCSGGAYD	VIICDECHST	DPTTVSGIGT	VLDQAETSGV

VN235	TYSTYGKFLA	DGGCSGGAYD	IIICDECHST	DPTTVLGIGT	VLDQAETAGV
VN405	TYSTYGKFLA	DGGCSGGAYD	IIICDECHST	DPTTVLGIGT	VLDQAETAGV
	1351				1400
BEBE1	RLTVLATATP	PGSVTTTPHPN	IEEVALGHEG	EIPFYGKAIP	LSAIKGGRHL
D89815	RFVVLATATP	PGSITFPHPN	IEEVPLANTG	EIPFYAKTIP	IEVIRGGRHL
ED43type_4	RLTVLATATP	PGSVTTTPHSN	IEEVALPTTG	EIPFYGKAIP	LELIKGRHL
HC_C2	RLVVLATATP	PGSVTVPHSN	IEEVALSTTG	EIPFYGKAIP	IETIKGRHL
HC_G9	RLTILATATP	PGSVTVPHSN	IEEVALSTEG	EIPFYGKAIP	LNYIKGRHL
HCU16326	RLVVLSTATP	PGSVTVPHLN	IEEVALSNTG	EIPFYGKAIP	IEAIKGGRHL
HCV_H_CMV	RLVVLATATP	PGSVTVSHPN	IEEVALSTTG	EIPFYGKAIP	LEVIKGGRHL
HCV_J1	RLVVLATATP	PGSITVPHAN	IEEVALSTTG	EIPFYGKAIP	LEAIKGGRHL
HCV_J483	RLVVLATATP	PGSVTVPHPN	IEEIGLSNNG	EIPFYGKAIP	IEAIKGGRHL
HCV_J8	RLVVLATATP	PGTVTTTPHSN	IEEVALGHEG	EIPFYGKAIP	LAFIKGRHL
HCV_JK1	RLVVLAAATP	PGSVTVPHPN	IEEVALPNTG	EIPFYGKAIP	LETIKGRHL
HCV_JS	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEVIKGGRHL
HCV_K1_R1	RLVVLATATP	PGSVTVPHPN	IEEIALSNTG	EIPFYGKAIP	IETIKGRHL
HCV_K1_R2	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IETIKGRHL
HCV_K1_R3	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LDTIKGRHL
HCV_K1_S1	RLVVLATATP	PGSVTVPHPN	IEEIALSNTG	EIPFYGKAIP	IETIKGRHL
HCV_K1_S2	RLVVLATATP	PGSVTVPHPN	IEEVALSNIG	EIPFYGKAIP	IETIKGRHL
HCV_K1_S3	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LDTIKGRHL
HCV_L2	RLVVLATATP	PGSTTVPHPN	IEEVALPNTG	EIPFYGRAIP	IEFIKGGRHL
HCV_N	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEAIMGGRHL
HCV12083	RLTVLPTATP	PGSVTVPHPN	ITETALPTTG	EIPFYGKAIP	LEYIKGRHL
HCV1480	RLVVLATAIP	PGSVTTTPHPN	IEEVALPSEG	EIPFYGRAIP	LVLIKGRHL
HCVPOLYP	RLVVLATATP	PGSVTVPHPN	IEEVALSNIG	EIPFYGKAIP	IETIKGRHL
HD_1	RLVVLATATP	PGSVTVPHSN	IEEVALSNIG	EIPFYGKAIP	LENIKGRHL
HPCCGAA	RLVVLATATP	PGSVTVSHPN	IEEVALSTTG	EIPFYGKAIP	LEVIKGGRHL
HPCFG	RLTVLATATP	PGSITVPHPN	IEEVGLTSDG	EIPFYGKALP	LAMIKGRHL
HPCGENANTI	RLVVLATATP	PGSVTVPHPN	IEEIALSNTG	EIPFYGKAIP	IETIKGRHL
HPCGENOM	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEAIRGGRHL
HPCHUMR	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEAIRGGRHL
HPCJ	RLVVLATATP	PGSVTVPHPN	IEEVGLSNTG	EIPFYGKAIP	IEVIKGGRHL
HPCJCG	RLVVLATATP	PGSITVPHPN	IEEVALSNTG	EIPFYGKAIP	IEAIKGGRHL
HPCJK046	RLTVLATATP	PGSVTVPHPN	IQETALPLTG	EVPFYGKAIP	LEYIKGRHL
HPCJK049	RLVVLATATP	PGSITVPHSN	IEEVALTGEG	EIPFYGRAIP	LGVIKGRHL
HPCJTA	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LEAIKGGRHL
HPCJTB	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEVIKGGRHL
HPCK3A	RLTVLATATP	PGSITVPHSN	IEEVALGSEG	EIPFYGKAIP	IACIKGRHL
HPCPLYPRE	RLVVLATATP	PGSVTVPHPN	IEEVALSTTG	EIPFYGKAIP	LEVIKGGRHL
HPCPOLP	RLTVLATATP	PGSVTTTPHPN	IEEVALGQEG	EIPFYGRAIP	LSYIKGRHL
HPCPP	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LEAIKGGRHL
HPCUNKCD	RLVVLSTATP	PGSVTVPHLN	IEEVALSNTG	EIPFYGKAIP	IEAIKGGRHL
MKC1A	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LEAIKGGRHL
NDM59	RLTVLATATP	PGSVTTTPHPN	IEEVALGQEG	EIPFYGRAIP	LSYIKGRHL
NZLI	RLTVLATATP	PGSITVPHSN	IEEVALGSEG	EIPFYGKAIP	IALIKGRHL
SA13	RLVVLATATP	PGSVTTTPHPN	IEEVALPSEG	EIPFYGRAIP	LALIKGRHL
Th580	RLTVLATATP	PGSVTVPHPN	ITETALPTTG	EIPFYGKCIP	LEFIKGGRHL
Type_3a_CB	RLTVLATRTP	PGSITVPHSN	IEEVALGSEG	EIPFYGKAIP	IALIKGRHL
TypeV_D	RLTVLATATP	PGSITVPHSN	IEEVALGSEG	EIPFYGKAIP	IALIKGRHL
VN004	RLTVLATATP	PGSVTVPHPN	ITESALPTTG	EIPFYGKAVP	LEYIKGRHL
VN235	RLTVLATATP	PGSVTVPHPN	ITETALPSTG	EVPFYGKAIP	LECIKGGRHL
VN405	RLTVLATATP	PGSVTVPHPN	ITEVALSSTG	EVPFYGKAIP	LEYIKGRHL
	1401				1450
BEBE1	IFCHSKKKCD	ELAVALLRGMG	LNAVAYYRGL	DVSIIPTQGD	VVVVATDALM
D89815	IFCHSKKKCD	ELPAKLSALG	LNAVAYYRGL	DVSVIPASGD	VVVVATDALM
ED43type_4	IFCHSKKKCD	ELARQLTSLG	LNAVAYYRGL	DVSVIPTSGD	VVVCATDALM
HC_C2	IFCHSKKKCD	ELAAKLSALG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HC_G9	IFCHSKKKCD	ELAAKLVLGL	VNAVAFYRGL	DVSVIPTTGD	VVVVATDALM

HCU16326	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_H_CMV	IFCHSKKKCD	ELAAKLVALG	INAVAYYRGL	DVSVIPTNGD	VVVVSTDALM
HCV_J1	IFCHSKKKCD	ELAAKLVALG	VNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_J483	IFCHSKKKCD	ELAAKLTLGLG	LNAVAYYRGL	DVSVIPPIGD	VAVVATDALM
HCV_J8	IFCHSKKKCD	ELAAALRGMG	VNAVAYYRGL	DVSVIPTQGD	VVVVATDALM
HCV_JK1	IFCHSKKKCD	ELAAKLSALG	VNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_JS	IFCHSKKKCD	ELAAKLSTLG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_K1_R1	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPASGD	VVVVATDALM
HCV_K1_R2	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPASGD	VVVVATDALM
HCV_K1_R3	IFWHSKKKCD	ELATKLSALG	VNAVAYYRGL	DVSVIPTSGN	VVVVATDALM
HCV_K1_S1	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPASGD	VVVVATDALM
HCV_K1_S2	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPASGD	VVVVATDALM
HCV_K1_S3	IFWHSKKKCD	ELATKLSALG	VNAVAYYRGL	DVSVIPTSGN	VVVVATDALM
HCV_L2	IFCPSKKKCD	ELAAKLSALG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_N	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV12083	IFCHSKKKCD	ELAGKLKSLG	LNAVAFYRGV	DVSVIPTSGD	VVVCATDALM
HCV1480	IFCHSKKKCD	ELAKQLTSLG	VNAVAYYRGL	DVAVIPATGD	VVVCSTDALM
HCVPOLYP	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HD_1	IFCHSRKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HPCCGAA	IFCHSKKKCD	ELAAKLVALG	INAVAYYRGL	DVSVIPTSGD	VVVVSTDALM
HPCFG	VFCHSKEKCD	ELASKLRGMG	VNAVAFYRGL	DVSVIPVSGD	VVVCATDALM
HPCGENANTI	IFCHSKKKCD	ELAAKLSALG	IHAVAYYRGL	DVSVIPASGN	VVVVATDALM
HPCGENOM	IFCHSKKKCD	ELAAKLSSLG	LNAVAYYRGL	DVSVIPSSGD	VVVVATDALM
HPCHUMR	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTIGD	VVVVATDALM
HPCJ	IFCHSKKKCD	ELAAKLSALG	INAVAYYRGL	DVSVIPASGD	VVVVATDALM
HPCJCG	IFCHSKKKCD	ELAAKLTLGLG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HPCJK046	IFCHSKKKCD	ELAAQLRTLGLG	LNAVAFYRGV	DVSVIPTSGD	VVVCATDALM
HPCJK049	IFCHSKKKCD	ELAKQLTSLG	VNAVAFYRGL	DVSVIPTQGD	VVVCATDALI
HPCJTA	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTSGD	VVIVATDALM
HPCJTB	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HPCK3A	IFCHSKKKCD	KMASKLRGMG	LNAVAYYRGL	DVSVIPTTGD	VVVCATDALM
HPCPLYPRE	IFCHSKKKCD	ELAAKLVALG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HPCPOLP	IFCHSKKKCD	ELAAALRGMG	LNAVAYYRGL	DVSVIPTQGD	VVVVATDALM
HPCPP	IFCHSKKKCD	ELAAKLSALG	VNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HPCUNKCD	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
MKC1A	IFCHSKKKCD	ELAAKLSALG	VNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
NDM59	IFCHSKKKCD	ELSAALRSMG	LNAVAYYRGL	DVSVIPTQGD	VVVVATDALM
NZLI	IFCHSKKKCD	EIASKLRGMG	LNAVAYYRGL	DVSVIPTTGD	VVVCATDALM
SA13	IFCHSKKKCD	ELAKQLTSQGD	VNAVAYYRGL	DVAVIPATGD	VVVCSTDALM
Th580	IFCHSKKKCD	ELSKQLTSLG	LNAVAFYRGV	DVAVIPTSGD	VVVCATDALM
Type_3a_CB	IFCHSKKKCD	EIASKLRGMG	LNAVAYYRGL	DVSVIPTTGD	VVVCATDALM
TypeV_D	IFCHSKKKCD	EIASKLRGMG	LNAVAYYRGL	DVSVIPTTGD	VVVCATDALM
VN004	IFCHPKKKCD	ELAKQLVSLG	LNAVAFYRGV	DVSVIPTSGD	VVVCATDALM
VN235	IFCHSKKKCD	ELAKQLRTLGLG	LNAVAFYRGV	DVSVIPTAGD	VVVCATDALM
VN405	IFCHSKKKCD	ELAKQLTSLG	LNAVAFYRGV	DVSVIPTSGD	VVVCATDALM

	1451		1500		
BEBE1	TGYTGDFDSV	IDCNVAVTQV	VDFS LDPTFT	ITTQTVPQDS	VSRSQRRGRT
D89815	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSRTQRRGRT
ED43type_4	TGFTGDFDSV	IDCNTSVIQT	VDFS LDPTFS	IEITTVPQDA	VSRSQRRGRT
HC_C2	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSRSQRRGRT
HC_G9	TGYTGDFDSV	IDCNTCVVQT	VDFS LDPTFS	IETSTVPQDA	VSRSQRRGRT
HCU16326	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSRSQRRGRT
HCV_H_CMV	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTLPQDA	VSRTQRRGRT
HCV_J1	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTLPQDA	VSRTQRRGRT
HCV_J483	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSRSQRRGRT
HCV_J8	TGYTGDFDSV	IDCNVAVSQI	VDFS LDPTFT	ITTQTVPQDA	VSRSQRRGRT
HCV_JK1	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTLPQDA	VSRSQRRGRT
HCV_JS	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSRSQRRGRT
HCV_K1_R1	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSRSQRRGRT
HCV_K1_R2	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSRSQRRGRT

HCV_K1_R3	TGYTGDFDSV	IDCNTCVIQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
HCV_K1_S1	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
HCV_K1_S2	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
HCV_K1_S3	TGYTGDFDSV	IDCNTCVIQT	DDFS LDPTFT	IETRTVPQDA	VSR SQRRGR T
HCV_L2	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSRTQRRGR T
HCV_N	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
HCV12083	TGYTGDFDSV	IDCNVAVTQV	VDFS LDPTFS	IETTTVPQDA	VSR SQRRGR T
HCV1480	TGFTGDFDSV	IDCN SAVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
HCVPOLYP	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
HD_1	TGYTGDFDSV	IDCNVCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
HPCCGAA	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTLPQDA	VSRTQRRGR T
HPCFG	TGYTGDFDTV	IDCNVAVEQY	VDFS LDPTFS	IETRTVPQDA	VSR SQRRGR T
HPCGENANTI	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTMPQDA	VSR SQRRGR T
HPCGENOM	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
HPCHUMR	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
HPCJ	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
HPCJCG	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTLPQDA	VSRAQRRGR T
HPCJK046	TGYTGDFDSV	IDCNVAVTQI	VDFS LDPTFS	IETTTVPQDA	VARSQRRGR T
HPCJK049	TGYTGDFDSV	IDCNVAVEQY	VDFS LDPTFS	IETHTVPQDA	VSR SQRRGR T
HPCJTA	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
HPCJTB	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
HPCK3A	TGFTGDFDSV	IDCNVAVEQY	VDFS LDPTFS	IETCTAPQDA	VSR SQRRGR T
HPCPLYPRE	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETITLPQDA	VSRTQRRGR T
HPCPOLP	TGFTGDFDSV	IDCNVAVTQV	VDFS LDPTFT	ITTQTVPQDA	VSR SQRRGR T
HPCPP	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
HPCUNKCD	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
MKC1A	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
NDM59	TGYTGDFDSV	IDCNVAVTQV	VDFS LDPTFT	ITTQTVPQDA	VSR SQRRGR T
NZLI	TGFTGDFDSV	IDCNVAVEQY	VDFS LDPTFS	IETRTAPQDA	VSR SQRRGR T
SA13	TGFTGDFDSV	IDCNTTVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
Th580	TGYTGDFDSV	IDCNVAVTQV	VDFS LDPTFS	IETTTVPQDA	VSR SQRRGR T
Type_3a_CB	TGYTGDFDSV	IDCNVAVEQY	VDFS LDPTFS	IETRTAPQDA	VSR SQRRGR T
TypeV_D	TGFTGDFDSV	IDCNVAVEQY	VDFS LDPTFS	IETRTAPQDA	VSR SQRRGR T
VN004	TGYTGDFDSV	IDCNVTVTQV	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGR T
VN235	TGYTGDFDSV	IDCNVAVTQI	VDFS LDPTFS	IETTTVPQDA	VARSQRRGR T
VN405	TGYTGDFDSV	IDCNVSVTQV	VDFS LDPTFT	IETTTMPQDA	VSR SQRRGR T

	1501			1550	
BEBE1	GRGRLGIYRY	VSSGERASGM	FDTVVLCECY	DAGAAWYELT	PAETTVRLRA
D89815	GRGRRGIYRF	VTPGERPSAM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
ED43type_4	GRGRLGTIYR	VTPGERPSGM	FDTAELCECY	DAGCAWYELT	PAETTTRLKA
HC_C2	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HC_G9	GRGKHGIYRY	VSPGERPSGM	FDSVVLCECY	DAGCAWYELT	PAETTVRLRA
HCU16326	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_H_CM	GRGKPGIYRF	VAPGERPSGM	FDSSVLCECY	DAGCAWYELM	PAETTVRLRA
HCV_J1	GRGKPGIYRF	VAPGERPSGM	FDSSILCECY	DTGCAWYELT	PAETTVRLRA
HCV_J483	GRGRSGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_J8	GRGRLGVYRY	VSSGERPSGM	FDSVVLCECY	DAGAAWYELT	PAETTVRLRA
HCV_JK1	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAVTSVRLRA
HCV_JS	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_R1	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_R2	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_R3	GRGRRGIYRF	VTPGERTSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_S1	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_S2	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_S3	GRGRRGIYRF	VTPGERTSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_L2	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HCV_N	GRGRGGIYRF	VTPGERPSGM	FDSVVLCECY	DAGCAWYELT	PAETSVRLRA
HCV12083	GRGKPGVYRF	VSQGERPSGM	FDTVVLCEAY	DTGCAWYELT	PSETTVRLRA
HCV1480	GRGRHGIYRY	VSSGERPSGI	FDSVVLCECY	DAGCAWYDLT	PAETTVRLRA
HCVPOLYP	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA

HD_1	GRGRMGIIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAEASVRLRA
HPCCGAA	GRGKPGIYRF	VAPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCFG	GRGRPGIYRF	VTPGERPSGM	FDSVVLCECY	DAGCSWYDLQ	PAETTVRLRA
HPCGENANTI	SRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HPCGENOM	GRGREGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCHUMR	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HPCJ	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DSGCAWYELT	PAETSVRLRA
HPCJCG	GRGRSGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HPCJK046	GRGKPGVYRY	VSQGERPSGM	FDTVVLCEAY	DTGAAWYELT	PAETTVRLRA
HPCJK049	GRGKSGTYRY	VSPGERPSGM	FDSVVLCECY	DAGCAWYELT	PSETTVRLRA
HPCJTA	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCJTB	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCK3A	GRGRLGTIYRY	VTPGERPSGM	FDSVVLCECY	DAGCSWYDLQ	PAETTVRLRA
HPCPLYPRE	GRGKPGIYRF	VAPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCPOLP	GRGRLGIYRY	VSTGERASGM	FDSVVLCECY	DAGAAWYELT	PAETTVRLRA
HPCPP	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HPCUNKCD	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
MKC1A	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
NDM59	GRGRLGIYRY	VSTGERASGM	FDSVVLCECY	DAGAAWYELT	PSETTVRLRA
NZLI	GRGRLGTIYRY	VASGERPSGM	FDSVVLCECY	DAGCSWYDLQ	PAETTVRLRA
SA13	GRGRHGIYRY	VSSGERPSGI	FDSVVLCECY	DAGCAWYDLT	PAETTVRLRA
Th580	GRGKPGVYRY	VSQGERPSGM	FDSVVLCEAY	DTGCAWYELT	PAETTVRLRA
Type_3a_CB	GRGRLGTIYRY	VAPGERPSGM	FDSVVLCECY	DAGCSWYDLQ	PAETTVRLRA
TypeV_D	GRGRLGTIYRY	VAPGERPSGM	FDSVVLCECY	DAGCSWYDLQ	PAETTVRLRA
VN004	GRGKHGVYRY	VSQGERPSGM	FDSVILCEAY	DTGCAWYELT	PAETTVRLRA
VN235	GRGKPGVYRY	VSQGERPSGM	FDTVVLCEAY	DVGCAWYELT	PSETTVRLRA
VN405	GRGKHGVYRY	VSQGERPSGI	FDTVVLCEAY	DTGCAWYELT	PSETTVRLRA

	1551			1600	
BEBE1	YFNTPGLPVC	QDHLEFWFWEAV	FTGLTHIDAH	FLSQTQKQAGE	GFPYLVAYQA
D89815	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
ED43type_4	YFDTPLPVC	QDHLEFWFWEV	FTGLTHIDGH	FLSQTQKQSGE	NFPYLVAYQA
HC_C2	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HC_G9	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQSGE	NFPYLVAYQA
HCU16326	YLNTPLPVC	QDHLEFWFSEGV	FTGLTHIDAH	FLSQTQKQAGE	NFPYLVAYQA
HCV_H_CMV	YMNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQSGE	NFPYLVAYQA
HCV_J1	YMNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQSGE	NFPYLVAYQA
HCV_J483	YLNTPLPVC	QDHLEFWFWEV	FTGLSHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HCV_J8	YFNTPGLPVC	QDHLEFWFWEAV	FTGLTHIDAH	FLSQTQKQSGE	NFAYLTAYQA
HCV_JK1	YLNTPLPVC	QVHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGE	NFPYLVAYQA
HCV_JS	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HCV_K1_R1	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGE	NFPYLVAYQA
HCV_K1_R2	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HCV_K1_R3	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HCV_K1_S1	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGE	NFPYLVAYQA
HCV_K1_S2	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HCV_K1_S3	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HCV_L2	YLNTPLPVC	QDHLEFWFWEV	FTGLNHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HCV_N	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HCV12083	YMNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSHTKQAGE	NFAYLVAYQA
HCV1480	YLNTPLPVC	QEHLEFWFWEV	FTGLTNIDAH	MLSQAKQSGE	NFPYLVAYQA
HCVPOLYP	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGE	NFPYLVAYQA
HD_1	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HPCCGAA	YMNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQSGE	NFPYLVAYQA
HPCFG	YLSTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HPCGENANTI	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HPCGENOM	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HPCHUMR	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HPCJ	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HPCJCG	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQAGD	NFPYLVAYQA
HPCJK046	YLNTPLPVC	QDHLEFWFWEV	FTGLTHIDAH	FLSQTQKQSGE	NFAYLVAYQA

HPCJK049	YLSTPGLPVC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQQGL	NFPYLTAYQA
HPCJTA	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCJTB	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVVYQA
HPCK3A	YLSTPGLPVC	QDHLDLWESV	FTGLTHIDAH	FLSQTQAGL	NFSYLTAYQA
HPCPLYPRE	YMNTPLPVC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQSGE	NLPYLVAYQA
HPCPOLP	YFNTPLPVC	QDHLEFWEAV	FTGLTHIDAH	FLSQTQSGE	NFAYLTAYQA
HPCPP	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCUNKCD	YLNTPLPVC	QDHLEFSEGV	FTGLTHIDAH	FLSQTQAGE	NFPYLVAYQA
MKC1A	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
NDM59	YFNTPLPVC	QDHLEFWEAV	FTGLTHIDAH	FLSQTQSGE	NFAYLVAYQA
NZLI	YLSTPGLPVC	QDHLDLWESV	FTGLTHIDAH	FLSQTQQGL	NFSYLTAYQA
SA13	YLNTPLPVC	QDHLEFWEGV	FTGLTNIDAH	MLSQTQGGG	NFPYLVAYQA
Th580	YLNTPLPVC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQGGG	NFAYLVAYQA
Type_3a_CB	YLSTPGLPVC	QDHLDLWESV	FTGLTHIDAH	FLSQTQQGL	NFSYLTAYQA
TypeV_D	YLSTPGLPVC	QDHLDLWESV	FTGLTHIDAH	FLSQTQQGL	NFSYLTAYQA
VN004	YLNTPLPVC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
VN235	YLNTPLPVC	QDHLEFWEGV	FTGMTHIDAH	FLSQTQGGG	NFAYLVAYQA
VN405	YLNTPLPVC	QDHLEFWEGV	FTGLTHIDAH	LLSQTQGGG	NFAYLVAYQA

	1601			1650	
	BEBE1	TVCARAKAPP	PSWDVMWKCL	IRLKPTLVGP	TPLLYRLGSV
	D89815	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV
ED43type_4	TVSAKVWLP	PSWDTMWKCL	IRLKPTLHGP	TPLLYRLGSV	QNEVTLTHPI
HC_C2	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HC_G9	TVCARAKAPP	PSWDQMWKCL	IRLKPTLTGA	TPLLYRLGGV	QNEITLTHPI
HCU16326	TVCARAKAPP	PSWDEMWRCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_H_CMR	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_J1	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QGEVTLTHPV
HCV_J483	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_J8	TVCARAKAPP	PSWDVMWKCL	IRLKPTLTGP	TPLLYRLGAV	TNEVTLTHPV
HCV_JK1	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_JS	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_K1_R1	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNDVTLTHPI
HCV_K1_R2	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_K1_R3	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_K1_S1	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNDVTLTHPI
HCV_K1_S2	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_K1_S3	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_L2	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEITLTHPI
HCV_N	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV12083	TVCARAKAPP	PSWDMWKCL	IRLKPTLTGP	TPLLYRLGAV	QNGVITTHPI
HCV1480	TVCARAKAPP	PSWDTMWKCL	IRLKPTLTGP	TPLLYRLGAV	QNEITLTHPI
HCVPOLYP	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HD_1	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCCGAA	TVCARAKAPP	PSWDQMRKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCFG	TVCARAKAPP	PCWDEMWKCL	IRLKPTLQGP	TPLLYRLGAI	QNDICMTHPI
HPCGENANTI	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCGENOM	TVCARAKAPP	PSWDQMWKCL	IRLKPTLQGP	TPLLYRLGAV	QNEVTLTHPI
HPCCHUMR	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCJ	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCJCG	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCJK046	TVCARAKAPP	PSWDTMWKCL	IRLKPTLTGP	TPLLYRLGAV	QNEVTPTHPV
HPCJK049	TVCARAKAPP	PSWDETWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEICTTHPV
HPCJTA	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEITLTHPI
HPCJTB	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEITLTHPI
HPCK3A	TVCARAKAPP	PSWDETWKCL	IRLKPTLHGP	TPLLYRLGPV	QNEICLTHPI
HPCPLYPRE	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEITLTHPV
HPCPOLP	TVCARAKAPP	PSWDVMWKCL	IRLKPTLVGP	TPLLYRLGSV	TNEVTLTHPV
HPCPP	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCUNKCD	TVCARAKAPP	PSWDEMWRCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
MKC1A	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI

NDM59	TVCARAKAPP	PSWDVMWKCL	TRLKPTLVGP	TPLLYRLGPV	TNEVTLTHPV
NZLI	TVCARAQAPP	PSWDEMWKCL	VRKPTLHGP	TPLLYRLGPV	QNETCLTHPI
SA13	TVCVRAKAPP	PSWDTMWKCL	LRLKPTLTGP	TPLLYRLGAV	QNEITLTHPI
Th580	TVCARAKAPP	PSWDVMWKCL	TRLKPTLTGP	TPLLYRLGAV	QNEIVTTHPI
Type_3a_CB	TVCARAQAPP	PSWDETWKCL	VRKPTLHGP	TPLLYRLGPV	QNEICLSHPI
TypeV_D	TVCARAQAPP	PSWDEMWKCL	VRKPTLHGP	TPLLYRLGPV	QNETCLTHPV
VN004	TVCARAKAPP	PSWDTMWKCL	IRLKPMLTGP	TPLLYRLGPV	QNEVVTTTHPI
VN235	TVCARAKAPP	PSWDTMWKCL	IRLKPMLTGP	TPLLYRLGAV	QNEIITTHPI
VN405	TVCARAKAPP	PSWDTMWKCL	IRLKPMLTGP	TPLLYRLGAV	QNEITTTTHPI

	1651			1700	
BEBE1	TKYIATCMQA	DLEIMTSTWV	LAGGVLAAVA	AYCLATGCVS	IIGRIHVNQK
D89815	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
ED43type_4	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSVGSVV	IVGRVVLSGQ
HC_C2	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIVLSGR
HC_G9	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSTGSVV	IVGRIILSGK
HCU16326	TKFIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_H_CMR	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSTGCVV	IVGRIVLSGK
HCV_J1	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSTGCVV	IVGRIVLSGR
HCV_J483	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_J8	TKYIATCMQA	DLEIMTSSWV	LAGGVLAAVA	AYCLATGCIS	IIGRLHLNDR
HCV_JK1	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HCV_JS	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_K1_R1	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALT	AYCLTTGSVV	IVGRIILSGK
HCV_K1_R2	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_K1_R3	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_K1_S1	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALT	AYCLTTGSVV	IVGRIILSGK
HCV_K1_S2	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_K1_S3	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_L2	TKLIMASMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HCV_N	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HCV12083	TKYIMTCMSA	DLEVITSTWV	LVGGVLAALA	AYCLSVGCVV	ICGRITLTGK
HCV1480	TKYIMACMSA	DLEVITSTWV	LVGGVLAALA	AYCLTVGSVA	IVGRIILSGR
HCVPOLYP	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HD_1	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGCVV	IVGRIILSGR
HPCCGAA	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSTGCVV	IVGRIVLSGK
HPCFG	TKYIMACMSA	DLEVTTSAWV	LVGGVLAALA	AYCLSVGCVV	IVGHIELGGK
HPCGENANTI	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HPCGENOM	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIVLSGS
HPCHUMR	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HPCJ	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HPCJCG	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HPCJK046	TKYIMACMSA	DLEVITSTWV	VAGGILAAIA	AYCLTVGSVV	ICGRITSSR
HPCJK049	TKYIATCMAA	DLEVATSAWV	LLGGVMAALT	AYCLSVGSVV	IVGHLVLGGK
HPCJTA	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HPCJTB	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HPCK3A	TKYVMACMSA	DLEVTTSTWV	LLGGVLAAVA	AYCLSVGCVV	IVGHIELGGK
HPCPLYPRE	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSTGCVV	IVGRVVLSGK
HPCPOLP	TKYIATCMQA	DLEVMTSTWV	LAGGVLAAVA	AYCLATGCVV	IIGRLHVNQR
HPCPP	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HPCUNKCD	TKFIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
MKC1A	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
NDM59	TKYIATCMQA	DLEVMTSTWV	LAGGVLAAVA	AYCLATGCVS	IIGRLHVNQR
NZLI	TKYLMACMSA	DLEVTTSTWV	LLGGVLAALA	AYCLSVGCVV	IVGHIELEGK
SA13	TKYIMACMSA	DLEVITSTWV	LVGGVLAALA	AYCLTVGSVA	IVGRIILSGR
Th580	TKYIMTCMSA	DLEVITSTWV	IVGGVLAALA	AYCLTVGCVV	ICGRIVTSGK
Type_3a_CB	TKYVMACMSA	DLEVTTSTWV	LLGGVLAALA	AYCLSVGCVV	IVGHIELGGK
TypeV_D	TKYIMACMSA	DLEVTTSTWV	LLGGVLAALA	AYCLSVGCVV	IVGHIELGGK
VN004	TKYIMTCMSA	DLEVITSTWV	LVGGVLAALA	AYCLSVGCVV	ICGRISTSGK
VN235	TKYIMTCMAA	DLEVITSTWV	LAGGIVAALA	AYCLTVGSVV	ICGRIVTSGK
VN405	TKYIMTCMSA	DLEVITSTWV	LVGGVLAALA	AYCLSVGCVV	VCGRISTTGK

	1701				1750	
BEBE1	TIIAPDKEVL	YEA	FDEMEEC	ASRTALIEEG	HRIAEMLKSK	IQGLMQQASK
D89815	PAVIPDREVL	YQEF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
ED43type_4	PAVIPDREVL	YQQF	DEMEEC	SKHLPVLEHG	LQLAEQFKQK	ALGLLNFAGK
HC_C2	PAVIPDREVL	YQEF	DEMEEC	GSHLPYIEQG	MQLAEQFKQK	ALGLLQIATK
HC_G9	PAVIPDREVL	YREF	DEMEEC	AAHIPYLEQG	MHLAEQFKQK	ALGLLQTASK
HCU16326	PAIIPDREVL	YQEF	DEMEEC	ASHLPYFEQG	MQLAEQFKQK	ALGLLQTATK
HCV_H_CM	PAIIPDREVL	YQEF	DEMEEC	SQHLPYIEQG	MMLAEQFKQK	ALGLLQTASR
HCV_J1	PAIIPDREVL	YREF	DEMEEC	SQHLPYIEQG	MMLAEQFKQK	ALGLLQTASR
HCV_J483	PAVVPDREVL	YQEF	DEMEEC	ASQLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV_J8	VVVPDKEIL	YEA	FDEMEEC	ASKAALIEEG	QRMAEMLKSK	IQGLLQQATR
HCV_JK1	PAIIPDREVL	YQEF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTASK
HCV_JS	PAVIPDREVL	YREF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV_K1_R1	PAVIPDREAL	YQEF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATN
HCV_K1_R2	PAIIPDREVL	YREF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV_K1_R3	PAVIPDREVL	YREF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV_K1_S1	PAVIPDREAL	YQEF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATN
HCV_K1_S2	PAIIPDREVL	YREF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV_K1_S3	PAVIPDREVL	YREF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV_L2	PAVIPDREVL	YREF	DEMEEC	ASHLPYIEQG	VQLAEQFKQK	ALGLLQTATK
HCV_N	PAVVPDREVL	YREF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV12083	PAVVPDREIL	YQQF	DEMEEC	SRHIPYLAEG	QQIAEQFRQK	VLGLLQASAK
HCV1480	PAITPDREVL	YQQF	DEMEEC	SASLPYVDEA	RAIAGQFKQK	VLGLIGTAGQ
HCVPOLYP	PAIIPDREVL	YQEF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HD_1	PAIVPDREVL	YQEF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCCGAA	PAIIPDREVL	YQEF	DEMEEC	SQHLPYIEQG	MMLAEQFKQK	ALGLLQTASR
HPCFG	PALVPDRQVL	YQQY	DEMEEC	SQSAPYIEQA	QAIAGQFKQK	VLGLLQASQ
HPCGENANTI	PAVVPDREVL	YQEF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCGENOM	PAIVPDREVL	YQDF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCCHUMR	PAIVPDRELL	YQEF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCJ	PAVIPDREVL	YREF	DEMEEC	ASHLPYIEQG	MLLAEQFKQK	ALGLLQMATK
HPCJCG	PAVIPDREVL	YQEF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCJK046	PAVIPDREVM	YQQY	DEMEEC	SRHLPYLV	QQLAEQFKQK	VLGLIQVTTK
HPCJK049	PALVPDKEVL	YQQY	DEMEEC	SRAAPYIEQA	QGIAGQFKQK	VIGLLQADQ
HPCJTA	PAVVPDREVL	YREF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCJTB	PAVVPDREVL	YREF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCK3A	PALVPDKEVL	YQQY	DEMEEC	SQARPYIEQA	QVIAHQFKQK	VLGLLQRATQ
HPCPLYPRE	PAIIPDREVL	YREF	DEMEEC	SQHLPYIEQG	MMLAEQFKQK	ALGLLQTASR
HPCPOLP	AVVAPDKEVL	YEA	FDEMEEC	ASRAALIEEG	QRIAEMLKSK	IQGLLQQASK
HPCPP	PAVIPDREVL	YQEF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCUNKCD	PAIIPDREVL	YQEF	DEMEEC	ASHLPYFEQG	MQLAEQFKQK	ALGLLQTATK
MKC1A	PAVIPDREVL	YQEF	DEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
NDM59	AVVAPDKEVL	YEA	FDEMEEC	ASRAALIEEG	QRIAEMLKSK	IQGLLQQASK
NZLI	PALVPDKEVL	YQQY	DEMEEC	SQAAPYIEQA	QVIAHQFKQK	ILGLLQRATQ
SA13	PAIIPDREVL	YQQF	DEMEEC	SASLPYMDEA	RAIAEQFKQK	VLGLIGTAGQ
Th580	PAVVPDREVL	YQQF	DEMEEC	SKHIPYLV	QQLAEQFKQK	VLGLLQAGTK
Type_3a_CB	PALVPDKEVL	YQQY	DEMEEC	SQAAPYIEQA	QAIAGQFKQK	VLGLLQRATQ
TypeV_D	PALVPDKEVL	YQQY	DEMEEC	SQAAPYIEQA	QAIAGQFKQK	VLGLLQRATQ
VN004	PVLIPDREVL	YQQF	DEMEEC	SRHIPYLAEG	HLIAEQFKQK	VLGLIQSTSK
VN235	PVPLPDREVL	YRQF	DEMEEC	SRHIPYLAEG	QQIAEQFKQK	ILGLLQNTAK
VN405	PVLIPDREVL	YQQF	DEMEEC	SRHIPYLV	QHLAEQFKQK	VLGLIQTTTR
	1751				1800	
BEBE1	QAQGVQPAVQ	ATWPKLEQFW	AKHMWNFISG	IQYLAGLSTL	PGNPAVASMM	
D89815	QAEAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM	
ED43type_4	QAQEATPVIQ	SNFAKLEQFW	ANDMWNFISG	IQYLAGLSTL	PGNPAIASLM	
HC_C2	QAEAAAPVVE	SKWRALETFW	AKHMWNFISG	VQYLAGLSTL	PGNPAIASLM	
HC_G9	QAETITPAVH	TNWQKLESFW	AKHMWNFVSG	IQYLAGLSTL	PGNPAIASLM	
HCU16326	QAEAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIRSPM	
HCV_H_CM	HAEVITPAVQ	TNWQKLEVFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM	

HCV_J1	QAEVIAPTVQ	TNWQKLEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_J483	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_J8	QAQDIQPAIQ	SSWPKLEQFW	AKHMWNFISG	IQYLAGLSTL	PGNPAVASMM
HCV_JK1	QAEAAAAPVVE	SKWQALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIVSLM
HCV_JS	QAEAAAAPVME	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_R1	QAEAAAAPVVE	SKWRALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_R2	QAEAAAAPVVE	SKWQALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_R3	QAEAAAAPVVE	SKWRTLEVFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_S1	QAEAAAAPVVE	SKWRALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_S2	QAEAAAAPVVE	SKWQALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_S3	QAEAAAAPVVE	SKWRTLEVFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_L2	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAALSTL	PGNPAIASLM
HCV_N	QAEAAAAPVVG	SKWRAFETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV12083	QAEELKPAVH	SAWPRVEDFW	RKHMWNFVSG	IQYLAGLSTL	PGNPAVASLM
HCV1480	KAETLKPAAT	SMWSKAEQFW	AKHMWNFVSG	IQYLAGLSTL	PGNPAVATLM
HCVPOLYP	QAEAAAPVVE	SKWQALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNLAIASLM
HD_1	QAEAAAAPVVE	SKWRALEAFW	AKHMRNFISG	IQYLAGLSTL	PGNPAIASLM
HPCCGAA	HAEVITPAVQ	TNWQKLEVFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCFG	QEAEIRPIVQ	SQWQKAEAFW	QQHMWNFVSG	IQYLAGLSTL	PGNPAVASLM
HPCGENANTI	QAEAAAAPVVE	SKWRTLEAFW	ANDMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCGENOM	QAEAAAAPVVE	SKWRALETFW	EKMWNFISG	IQYLAGLSTL	PGNPAMASLM
HPCHUMR	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCJ	QAEAAAAPVVE	TKWQALEVFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCJCG	QAEAAAAPVVE	SKWRALEVFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCJK046	QAEELKPAVH	SAWPKLEQFW	YKHMWNFISG	IQYLAGLSTL	PGNPAVAALM
HPCJK049	KAADIKPIAT	PYWQKLETFW	SKHMWNFVSG	IQYLAGLSTL	PGNPAIASLM
HPCJTA	QAEAAAAPVVE	SRWRALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCJTB	QAEAAAAPVVE	SRWRALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCK3A	QQAVIEPIV	SNWQKLEVLW	HKHMWNFVSG	IQYLAGLSTL	PGNPAVASLM
HPCPLYPRE	QAEVIAPAVQ	TNWQKLETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCPOLP	QAQDIQPAVQ	ASWPKVEQFW	AKHMWNFISG	IQYLAGLSTL	PGNPAVASMM
HPCPP	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCUNKCD	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIRSPM
MKC1A	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
NDM59	QAQDIQPAVQ	ASWPKVEQFW	AKHMWNFISG	IQYLAGLSTL	PGNPAVASMM
NZLI	QQAVIEPIVT	TNWQKLEAFW	HKHMWNFVSG	IQYLAGLSTL	PGNPAVASLM
SA13	KAETLKPAAT	SMWNRAEQFW	AKHMWNFVSG	IQYLAGLSTL	PGNPAVATLM
Th580	HAELKPAIH	STWPRVEEFW	RKHMWNFVSG	IQYLAGLSTL	PGSPAVASLM
Type_3a_CB	QQAVIEPIVA	TNWQKLEAFW	HKHMWNFVSG	IQYLAGLSTL	PGNPAVASLM
TypeV_D	QQAVIEPIVA	TNWQKLEAFW	HKHMWNFVSG	IQYLAGLPTL	PGNPAVASLM
VN004	QAEELKPAVH	AAWPKLEQFW	QKQLWNFVSG	IQYLAGLSTL	PGNPAIASLM
VN235	QAEDLKPAVQ	SAWPKLEQFW	QKHLWNFVSG	VQYLAGLSTL	PGNPAVASLM
VN405	QAEIEPVVH	SAWPKLEQFW	QKHLWNFVSG	IQYLAGLSTL	PGNPAVASLM

	1801			1850	
BEBE1	SFSAALTSP	STSTTILLNI	MGGWLASQIA	PPAGATGFVV	SGLVGAAVGS
D89815	AFTASITSP	ATQYTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGS
ED43type_4	SFTAAVTSP	TTQQTLLFNI	LGGWVASQIR	DSDASTAFVV	SGLAGAAVGS
HC_C2	AFTASVTSP	TTQSTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGS
HC_G9	SFTAAVTSP	TTQQTLLFNI	LGGWVAAQLA	APAAATAFVG	AGITGAVIGS
HCU16326	AFTASITSP	TTQHTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGT
HCV_H_CMR	AFTAAVTSP	TTGTLLFNI	LGGWVAAQLA	APGAATAFVG	AGLAGAAIGS
HCV_J1	AFTAAVTSP	TTSQTLLFNI	LGGWVAAQLA	APGAATAFVG	SGLAGAAVGS
HCV_J483	AFTASITSP	TTQNTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGS
HCV_J8	AFSAALTSP	PTSTTILLNI	MGGWLASQIA	PPAGATGFVV	SGLVGAAVGS
HCV_JK1	AFTASITSP	TTQHTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGS
HCV_JS	AFTASITSP	TTQSTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIVGAAVGS
HCV_K1_R1	AFTASITSP	TTQSTLLFNI	LGGWVAAQLA	PPRAVSFAVG	AGIAGAAVGS
HCV_K1_R2	AFTASITSP	TTQHTLLFNI	LGGWVAAQLA	PPRAASAFVG	AGIAGAAVGS
HCV_K1_R3	AFTASITSP	TTQHTLLFNI	LGGWVAAQLA	PPRAASAFVG	AGIAGAAVGS
HCV_K1_S1	AFTASITSP	TTQSTLLFNI	LGGWVAAQLA	PPRAVSFAVG	AGIAGAAVGS

HCV_K1_S2	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA	PPRAASAFVG	AGIAGAAVGS
HCV_K1_S3	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA	PPRAASAFVG	AGIAGAAVGS
HCV_L2	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA	PASAASAFVG	AGSAGAAIGT
HCV_N	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGS
HCV12083	SFTASLTSP	RTSQTLLLN	LGGWIAAQVA	PPPASTAFVV	SGLAGAAVGS
HCV1480	SFTAAVTSP	TTHQTLLFNI	LGGWVASQIA	PPTAATAFVV	SGMAGAAVGN
HCVPOLYP	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGS
HD_1	AFTASITSPL	TTQSTLLFDI	LGGWVAAQLA	PPSAASAFVG	AGIARAAGVS
HPCCGAA	AFTAAVTSP	TTGQTLLFNI	LGGWVAAQLA	APGAATAFVG	AGLAGAALDS
HPCFG	AFTASVTSP	TTNQTMTFFNI	LGGWVATHLA	GPAASSAFVV	SGLAGAAVGG
HPCGENANTI	AFTASITSPL	TTQSTLLFNI	LGGWVAAQLA	PPGAASAFVG	AGIAGAAVGS
HPCGENOM	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGS
HPCUMR	AFTASITSPL	TTQSTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGS
HPCJ	AFTSSITSPL	TTQSTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGS
HPCJCG	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGS
HPCJK046	SFSASLTSP	TTAQTLLLN	LGGWVASQIA	TPVPATAFVV	SGLAGAAIGS
HPCJK049	AFTASVTSP	TTNQTLLFNI	MGGWVASNLA	PPPASTAFVV	SGLAGAAVGS
HPCJTA	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAIGS
HPCJTB	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAIGS
HPCK3A	AFTASVTSP	TTNQTMTFFNI	LGGWVATHLA	GPQASSAFVV	SGLAGAAIGG
HPCPLYPRE	AFTAAVTSP	TTSQTLLFNI	LGGWVAAQLA	APGAATAFVG	AGLAGAAIGS
HPCPOLP	AFTAALTSPL	STSTTILLNI	LGGWLASQIA	PPAGATGFVV	SGLVGAAGVS
HPCPP	AFTASITSPL	TTQYTLFFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGS
HPCUNKCD	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGT
MKC1A	AFTASITSPL	TTQYTLFFNI	LGGWVAAQLA	PPSAASAFVG	AGIAGAAVGS
NDM59	AFTAALTSPL	STSTTILLNI	LGGWLASQIA	PPAGATGFVV	SGLVGAAGVS
NZLI	AFTASVTSP	TTNQTMTFFNI	LGGWVATHLA	GPQSSSAFVV	SGLAGAAIGG
SA13	SFTAAVTSP	TTQQTLLFNI	LGGWVASQIA	PPTAATAFVV	SGMAGAAVGS
Th580	SFTASLTSP	RTSQTLLLN	LGGWIASQVA	PPSASTAFVV	SGLAGATVAS
Type_3a_CB	AFTASVTSP	TTNQTMTFFNI	LGGWVATHLA	GPQSSSAFVV	SGLAGAAIGG
TypeV_D	AFTASVTSP	TTNQTMTFFNI	LGGWVATHLA	GPQSSSAFVV	SGLAGAAIGG
VN004	SFSASLTSP	STHQTLLLN	LGGWVASQIA	NPTASTAFVV	SGLAGAAVGS
VN235	SFTAALTSPL	STSTTLLLN	LGGWVASQIA	PPTASTAFVV	SGLAGAAVGS
VN405	SFSASLTSP	STSTTLLLN	LGGWVASQIA	NPTASTAFVV	SGLAGATVGS

	1851				1900
BEBE1	IGLGKILVDV	LAGEGAGISG	ALVAFKIMSG	EKPSVEDVNV	LLPAILSPGA
D89815	IGLGKVLVDI	LAGEGAGVAG	ALVAFKVMSG	DMPSTEDLVN	LLPAILSPGA
ED43type_4	VGLGKILVDI	LPGYGAGVRG	AVVTFKIMSG	EMPSTEDLVN	LLPAILSPGA
HC_C2	IGLGKVLVDI	LAGEGAGVAG	ALVAFKIMSG	ETPSAEDLVN	LLPAILSPGA
HC_G9	VGLGKVLVDI	LAGEGAGVAG	ALVAFKIMSG	EAPTAEDLVN	LLPAILSPGA
HCU16326	IGLGKVLVDI	LAGEGAGVAG	ALVAFKIMSG	EMPSAEDMVN	LLPAILSPGA
HCV_H_CMR	VGLGKVLVDI	LAGEGAGVAG	ALVAFKIMSG	EVPSTEDLVN	LLPAILSPGA
HCV_J1	VGLGRVLVDI	LAGEGAGVAG	ALVAFKIMSG	ELPSTEDLVN	LLPAILSPGA
HCV_J483	IGLGKVLVDI	LAGEGAGVAG	ALVAFKVMSG	EVPSTEDLVN	LLPAILSPGA
HCV_J8	IGLGKILVDV	LAGEGAGISG	ALVAFKIMSG	EKPTVEDVNV	LLPAILSPGA
HCV_JK1	IGLGKVLVDI	LAGEGAGVAG	ALVAFKIMSG	EMPSTEDLVN	LLPAILSPGA
HCV_JS	IGLGKVLVDI	LAGEGAGVAG	ALVAFKIMSG	EMPATEDLVN	LLPAILSPGA
HCV_K1_R1	IGLGKVLVDI	LAGEGAGVAG	ALVAFKVMSG	EMPSTEDLVN	LLPAILSPGA
HCV_K1_R2	IGLGKVLVDI	LAGEGAGVAG	ALVAFKVMSG	DMPSTEDLVN	LLPAILSPGA
HCV_K1_R3	IGLGKVLVDI	LAGEGAGVAG	ALVDFKVMSG	EMPSAEDIVN	LLPAILSPGA
HCV_K1_S1	IGLGKVLVDI	LAGEGAGVAG	ALVAFKVMSG	EMPSTEDLVN	LLPAILSPGA
HCV_K1_S2	IGLGKVLVDI	LAGEGAGVAG	ALVAFKVMSG	DMPSTEDLVN	LLPAILSPGA
HCV_K1_S3	IGLGKVLVDI	LAGEGAGVAG	ALVDFKVMSG	EMPSAEDIVN	LLPAILSPGA
HCV_L2	IGLGKVLVDI	LAGEGAGVAG	ALVAFKVMSG	EMPSTEDLVN	LLPAILSPGA
HCV_N	IGLGKVLVDI	LAGEGAGVAG	ALVAFKVMSG	EAPSAEDLIN	LLPAILSPGA
HCV12083	IRLGRVLVDV	LAGEGAGVSG	ALVAFKIMSG	ECPSTEDMVN	LLPALLSPGV
HCV1480	IGLGRVLIDI	LAGEGTGVAG	ALVAFKIMCG	ERPTAEELVN	LLPSILCPGA
HCVPOLYP	IGLGKVLVDI	LAGEGAGVAG	ALVAFKVMSG	EMPSTEDLVN	LLPAILSPGA
HD_1	IGLGKVLVDI	LAGEGAGVAG	ALVAFKVMSG	EVPSTEDLIN	LLPAILSPGA
HPCCGAA	VGLGKVLVDI	LAGEGAGVAG	ALVAFKIMSG	EVPSTEDLVN	LLPAILSPGA

HPCFG	IGIGRVLLDV	LAGEYAGVSG	ALVAFKIMGG	ELPTTEDMVN	LLPAILSPGA
HPCGENANTI	IGLGKVLVDM	VAGYAGVAG	ALVAFKVMSG	EMPSTEDLVN	LLPAILSPGA
HPCGENOM	IGLGKVLVDI	LAGEYAGVAG	ALVAFKVMSG	EMPSTEDLVN	LLPAILSPGA
HPCHUMR	IGLGKVLVDI	LAGEYAGVAG	ALVAFKVMSG	EMPSTEDLVN	LLPAILSPGA
HPCJ	IGLGKVLVDI	LAGEYAGVAG	ALVAFKVMSG	EVPSTEDLVN	LLPAILSPGA
HPCJCG	IGLGKVLVDI	LAGEYAGVAG	ALVAFKVMSG	EMPSTEDLVN	LLPAILSPGA
HPCJK046	IGLGKVLVDI	LAGEYAGVSG	ALVAFKIMSG	ETPSVEDMVN	LLPAILSPGA
HPCJK049	IGLGKVLVDI	LAGEYAGVAG	ALVAFKIMGG	EMPSTEDMVN	LLPAILSPGA
HPCJTA	IGLGKVLVDI	LAGEYAGVAG	ALVAFKVMSG	EAPSAEDLVN	LLPAILSPGA
HPCJTB	IGLGKVLVDI	LAGEYAGVAG	ALVAFKVMSG	EAPSAEDLVN	LLPAILSPGA
HPCK3A	IGLGRVLLDI	LAGEYAGVSG	ALVAFKIMGG	EPPTTEDMVN	LLPAILSPGA
HPCPLYPRE	VGLGKVLIDI	LAGEYAGVAG	ALVAFKIMSG	EVPSTEDLVN	LLPAILSPGA
HPCPOLP	IGLGKVLVDI	LAGEYAGISG	ALVAFKIMSG	EKPSMEDVNV	LLPGILSPGA
HPCPP	IGLGKVLVDI	LAGEYAGVAG	ALVAFKVMSG	DMPSTEDLVN	LLPAILSPGA
HPCUNKCD	IGLGKVLVDI	LAGEYAGVAG	ALVAFKIMSG	EMPSAEDMVN	LLPAILSPGA
MKC1A	IGLGKVLVDI	LAGEYAGVAG	ALVAFKVMSG	DMPSTEDLVN	LLPAILSPGA
NDM59	IGLGKVLVDI	LAGEYAGISG	ALVAFKIMSG	EKPSMEDVIN	LLPGILSPGA
NZLI	IGLGRVLLDI	LAGEYAGVSG	ALVAFKIMGG	ECPTAEDMVN	LLPAILSPGA
SA13	IGLGRVLIDI	LAGEYAGVAG	ALVAFKIMCG	EKPTAEDLVN	LLPSILCPGA
Th580	IGLGRVIVDI	LAGEYAGVAG	ALVAFKIMSG	ECPSTEDMVN	LLPAILSPGA
Type_3a_CB	IGLGRVLLDI	LAGEYAGVSG	ALVAFKIMGG	ELPTAEDMVN	LLPAILSPGA
TypeV_D	IGLGRVLLDI	LAGEYAGVSG	ALVAFKIMGG	ELPTTEDLVN	LLPAILSPGA
VN004	IGLGRVIVDV	LAGEYAGVSG	ALVAFKIMCG	ETPSAEDMVN	LLPAILSPGA
VN235	IGLGKVIIDI	LAGEYAGVSG	ALVAFKIMSG	EAPAVEDMVN	LLPAILSPGA
VN405	IGLGRVLVDI	LAGEYAGVSG	ALVAFKIMSG	ETPSAEDMVN	LLPAILSPGA

	1901			1950	
BEBE1	LVVGVICAAI	LRRHVGQEG	AVQWMNRLIA	FASRGNHVAP	THYVAESDAS
D89815	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
ED43type_4	LVVEVVCPI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HC_C2	LVVGVVCAAI	QRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HC_G9	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAS
HCU16326	LVVGIVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	RHYVPESEPA
HCV_H_CMV	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_J1	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_J483	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_J8	LVVGVICAAI	LRRHVGQEG	AVQWMNRLIA	FASRGNHVAP	THYVVEDSAS
HCV_JK1	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_JS	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_R1	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_R2	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_R3	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_S1	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_S2	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_S3	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_L2	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHDS	THYVPESDAA
HCV_N	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV12083	ALVGVVCAAI	LRRHVGPAEG	ANQWMNRLIA	FASRGNHVSP	THYVPETDAS
HCV1480	LVVGVICAAV	LRRHIGPGEG	AVQWMNRLIA	FASRGNHGSP	THYVPETDAS
HCVPOLYP	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HD_1	LVVGVVCAAI	LRGHVGPGEG	AVQWMNRLIA	FAFAGNHVSP	THYVPESDAA
HPCCGAA	LAVGVVFASI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCFG	LVVGVICAAV	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCGENANTI	LVVGVVCAAI	LRRHVDPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCGENOM	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCHUMR	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCJ	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCJCG	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCJK046	LVVGVVRAAI	LRRHVGPGEG	AAQWMNRLIA	FASRGNHVSP	THYVPETDAS
HPCJK049	LVVGVICAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVAP	THYVPESDAA
HPCJTA	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA

HPCJTB	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCK3A	LVVGVVCAAI	LRRHVGPGEG	PVQWMNRLIA	FASRGNHVSP	AHYVPESDAA
HPCPLYPRE	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCPOLP	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVAP	THYVTESDAS
HPCPP	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCUNKCD	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	RHYVPESEPA
MKC1A	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
NDM59	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVAP	THYVTESDAS
NZLI	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
SA13	LVVGVVCAAV	LRRHIGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPETDAS
Th580	LVVGVVCAAI	LRRHVGPGEG	ANQWMNRLIA	FASRGNHVSP	THYVPETDAS
Type_3a_CB	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
TypeV_D	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
VN004	LVVGVVCAAI	LRRHAGPSEG	ATQWMNRLIA	FASRGNHVSP	THYVPETDTS
VN235	LVVGVVCAAV	LRRHVGPGEG	ATQWMNRLIA	FASRGNHVSP	THYVPETDAS
VN405	LVVGVVCAAI	LRRHAGPAEG	ATQWMNRLIA	FASRGNHVSP	THYVPETDTS

	1951		2000		
BEBE1	QVVTQILGSL	TITSLRLRLH	QWITEDCPVP	CSGSWL RDVW	DWVCSILIDF
D89815	ARVTQILSNL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVLADF
ED43type_4	RRVTILSSL	TVTSLRLRLH	KWINE DCSTP	CAESWLWEVW	DWVLHVL SDF
HC_C2	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDIW	DWICSVLTDF
HC_G9	VRVTHILTS L	TVTQLLKR LH	VWISSDCTAP	CAGSWL KD V W	DWICEVLSDF
HCU16326	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSSSWLREIW	DWICTVL TDF
HCV_H_CM R	ARVTAI LSSL	TVTQLLKR LH	QWISSECTTP	CSGSWL RDIW	DWICEVLSDF
HCV_J1	ARVTAI LSSL	TVTQLLKR LH	QWLSSESTTP	CSGSWL RDIW	DWICEVLSDF
HCV_J483	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVL TDF
HCV_J8	QVVTQVLSSL	TITSLRLRLH	AWITE DC PVP	CSGSWL QDIW	DWVCSILTDF
HCV_JK1	ARVTKILSSL	TITQRLRLH	QWINE DCSTP	CSGSWL RDVW	DWICTVL TDF
HCV_JS	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDIW	DWICTVL TDF
HCV_K1_R1	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVL TDF
HCV_K1_R2	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVL SDF
HCV_K1_R3	VRVTQILSNL	TITQLLKR LH	QWISSECTTP	CSGSWL RDVW	DWICTVL TDF
HCV_K1_S1	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVL TDF
HCV_K1_S2	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVL TDF
HCV_K1_S3	VRVTQILSSL	TITQLLKR LH	QWISSECTTP	CSGSWL RDVW	DWICTVL TDF
HCV_L2	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVL TDF
HCV_N	ARVTQVLSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWVCTVLSDF
HCV12083	KNVTQILTS L	TITSLRLRLH	QWVNE DTATP	CATSWL RDVW	DWVCTVLSDF
HCV1480	AKVTQILSSL	TVTSLRLRLH	TWIGEDYSTP	CDGTWLRAIW	DWVCTALTDF
HCVPOLYP	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVL TDF
HD_1	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVL TDF
HPCCGAA	ARVTAI LSSL	TVTQLLKR LH	QWISSECTTP	CSGSWL RDIW	DWICEVLSDF
HPCFG	AKVTALLSSL	TVTRLLRLH	QWINE DY P SP	CNGDWLHDIW	DWVCIVLSDF
HPCGENANTI	ARVTQILSGL	TITQLLRLH	QWINE DCSTP	CSGSWL RDVW	DWICTVLADF
HPCGENOM	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVL TDF
HPCHUMR	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVL TDF
HPCJ	QVVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVL TDF
HPCJCG	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL KD V W	DWICTVLSDF
HPCJK046	RAVTNILSSL	TITSLRLKLH	HWITE DYATP	CGSTWL RDIW	DWVCTVLSDF
HPCJK049	AKVTALLSSL	TVTQLLRLH	QWINE DY P TP	CDGNWLYDIW	NWVCTVLADF
HPCJTA	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL KD V W	DWICTVL TDF
HPCJTB	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVL TDF
HPCK3A	ARVTALLSSL	TVTSLRLRLH	QWINE DY P SP	CSGDWLRIIW	DWVCSVVSDF
HPCPLYPRE	ARVTAI LSSL	TVTQLLRLH	QWISSECTTP	CSGSWL RDIW	DWICEVLSDF
HPCPOLP	QVVTQILGSL	TITSLRLRLH	NWITE DC P IP	CSGSWL RDVW	DWVCTILTDF
HPCPP	ARVTQILSNL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVLADF
HPCUNKCD	ARVTQILSSL	TITQLLKR LH	QWINE DCSTP	CSSSWLREIW	DWICTVL TDF
MKC1A	ARVTQILSNL	TITQLLKR LH	QWINE DCSTP	CSGSWL RDVW	DWICTVLADF
NDM59	QVVTQILGSL	TITSLRLRLH	NWITE DC P IP	CAGSWLREVW	DWVCTILTDF
NZLI	ARVTALLSSL	TVTSLRLRLH	QWINE DY P SP	CSDDWLRTIW	DWVCSVLADF

SA13	AKVTQLLSSL	TVTSLLRKLH	TWIGEDYSTP	CDGTWLRAIW	DWVCTALTDF
Th580	NKVTQILSSL	TITSLRRLH	QWIHEDTSTP	CASSWL RDVW	DWVCTVLSDF
Type_3a_CB	ARVTALLSSL	TVTSLRRLH	QWINEDYPSP	CSDDWLRIIW	DWVCSVL SDF
TypeV_D	AKVTALLSSL	TVTSLRRLH	QWINEDYPSP	CSDDWLRIIW	DWVCSVLADF
VN004	RQIMTILSSL	TVTSLLRKLH	EWINTDWSTP	CSSSWL RDIW	DWVCEVLSDF
VN235	RAVTTILSSL	TITSLRRLH	EWISGDWSAP	CSCSWL KD V W	DWVCTVLSDF
VN405	RQVMAILSSL	TVTSLLRKLH	EWINS DWSTP	CSGSWL RDIW	DWVCTVLSDF

	2001			2050	
BEBE1	KNWLSAKLFP	RLPGIPFISC	QKGYRG TWAG	TGIMTTRCPC	GANITGNVRL
D89815	KTWLQSKLLP	RLPGVPPFSC	QRGYKGVWRG	DGIMYTTCPC	GAQITGHVKN
ED43type_4	KTCLKAKFVP	LMPGIPLLSW	PRGYKGEWRG	DGVMHTTCPC	GADLAGHIKN
HC_C2	KTWLQSKLLP	RLPGVPPFSC	QRGYKGVWRG	DGIMQTTCPC	GAQITGHVKN
HC_G9	KSWLKAKLMP	QLPGIPFVSC	QRGYRGVWRG	EGIMHARCPC	GADITGHVKN
HCU16326	KTWLQSKLLP	RLPGVPPFSC	QRGYKGVWRG	DGIMHTTCPC	GAQITGHVKN
HCV_H_CM R	KTWLKAKLMP	QLPGIPFVSC	QRGYRGVWRG	DGIMHTRCHC	GAEITGHVKN
HCV_J1	KTWLKTKLMP	HLPGIPFVSC	QHGYKGVWRG	DGIMHTRCHC	GAEITGHVKN
HCV_J483	KTWLQSKLLP	RLPGVPFLSC	QRGYKGVWRG	DGIMQTTCPC	GAQIAGHVKN
HCV_J8	KNWLSKLLP	KMPGIPFISC	QKGYKGVWAG	TGVMTTRCPC	GANISGHVRM
HCV_JK1	KTWLQSKLLP	RLPGDPPFSC	QRGYRGVWRG	DGVMQTTCPC	GAQITGHVKN
HCV_JS	KTWLKSKLMP	RLPGVPPFSC	QRGYRGVWRG	DGIMHTTCPC	GAQITGHVKN
HCV_K1_R1	KTWLQSKLLP	RLPGVPPFSC	QRGYRGVWRG	DGIMQTTCPC	GAQITGHVKN
HCV_K1_R2	KTWLQSRVLP	RLPGVPFLSC	QRGYKGVWRG	DGIMQTTCPC	GAQITGHVKN
HCV_K1_R3	KTWLQSKLLP	RLPGIPFISC	QKGYKGVWRG	DGVMHTTCPC	GAQIAGHFKN
HCV_K1_S1	KTWLQSKLLP	RLPGVPPFSC	QRGYRGVWRG	DGIMQTTCPC	GAQITGHVKN
HCV_K1_S2	KTWLQSRVLP	RLPGVPFLSC	QRGYKGVWRG	DGIMQTTCPC	GAQITGHVKN
HCV_K1_S3	KTWLQSKLLP	RLPGIPFISC	QKGYKGVWRG	DGVMHTTCPC	GAQIAGHFKN
HCV_L2	KTWLQSKLLP	RLPGVPPFSC	QRGYKGVWRG	DGIMQTTCPC	GAQITGHVKN
HCV_N	KTWLQSKLLP	RLPGVPFLSC	QKGYKGVWRG	DGIMHTTCPC	GAQIAGHVKN
HCV12083	KVWLQAKLFP	RLPGIPFLSC	QAGYRGVWAG	DGVCHTTCTC	GAVIAGHVKN
HCV1480	KAWLQAKLLP	QLPGVPPFSC	QKGYKGVWRG	DGVNSTKCPC	GATISGHVKN
HCVPOLYP	KTWLQSKLLP	RLPGIPFYSC	QRGYKGVWRG	DGIMQTTCPC	GAQITGHVKN
HD_1	KTWLQSKLLP	RLPGVPFLSC	QRGYRGVWRG	DGIMHTTCPC	GAQMAGHVKN
HPCCGAA	KTWLKAKLMP	QLPGIPFVSC	QRGYRGVWRG	DGIMHTRCHC	GAEITGHVKN
HPCFG	KTWLSAKIMP	KVPGIPFLSC	QKGYKGVWRG	DGVMTTRCPC	GEDFTGHVRN
HPCGENANTI	KTWLQSKLLP	RLPGVPPFSC	QRGYKGVWRG	DGIMQTTCPC	GAQITGHVKN
HPCGENOM	KTWLQSKLLP	RLPGVPFLSC	QRGYKGVWRG	DGIMQTTCPC	GAQITGHVKN
HPCHUMR	KTWLQSKLLP	QLPGVPPFSC	QRGYKGVWRG	DGIMQTTCPC	GAQITGHVKN
HPCJ	KTWLQSKLLP	RLPGVPPFSC	QRGYKGVWRG	EGIMQTTCPC	GAQIAGHVKN
HPCJCG	KTWLQSKLLP	RLPGLPFLSC	QRGYKGVWRG	DGIMQTTCPC	GAQITGHVKN
HPCJK046	RVWLKSKLMP	SLPGVPPFSC	QRGYRG TWRG	DGICNTTCPC	GASIAGHVKN
HPCJK049	KLWLGA KILP	KMPGIPFLSC	QKGYRG TWRG	DGVVSTRCPC	GALLSGHVKN
HPCJTA	KTWLQSKLLP	KLPGVPPFSC	QRGYKGVWRG	DGIMQTTCPC	GAQITGHVKN
HPCJTB	KTWLQSKLLP	QLPGVPPFSC	QRGYKGVWRG	DGIMQTTCPC	GAQITGHVKN
HPCK3A	KTWLSAKIMP	ALPGLPFISC	QKGYKGVWRG	DGVMSTRCPC	GASIAGHVKN
HPCPLYPRE	KTWLKAKLMP	QLPGIPFVSC	QRGYKGVWRV	DGIMHTRCHC	GAEITGHVKN
HPCPOLP	KNWLTSKLFP	KMPGLPFISC	QKGYKGVWAG	TGIMTTRCPC	GANISGNVRL
HPCPP	KTWLQSKLLP	RLPGVPPFSC	QRGYKGVWRG	DGIMYTTCPC	GAQITGHVKN
HPCUNKCD	KTWLQSKLLP	RLPGVPPFSC	QRGYKGVWRG	DGIMHTTCPC	GAQITGHVKN
MKC1A	KTWLQSKLLP	RLPGVPPFSC	QRGYKGVWRG	DGIMYTTCPC	GAQITGHVKN
NDM59	KNWLTSKLFP	KMPGLPFISC	QKGYRGVWAG	TGIMTTRCPC	GANISGNVRL
NZLI	KAWLSAKIMP	ALPGLPFISC	QKGYKGVWRG	DGVMSTRCPC	GAAITGHVKN
SA13	KAWLQAKLLP	QLPGVPFLSC	QRGYRGVWRG	DGVNSTKCPC	GATISGHVKN
Th580	KTWLKAKITP	RIPGIPFISC	QAGYRGVWAG	DGVCHTT CSC	GAQIAGHVKN
Type_3a_CB	KSWLSAKIMP	ALPGLPFISC	QKGYKGVWRG	DGVMSTRCPC	GATITGHVKN
TypeV_D	KTWLSAKIMP	ALPGLPFISC	QKGYKGVWRG	DGVTTRCPC	GATITGHVKN
VN004	KTWLKAKLVP	ALPGVPFLSC	QRGFRGTWRG	DGICHTTCPC	GSEITGHVKN
VN235	KTWLRAKLVP	TLPGIPFISC	QRGFRGVWRG	DGVNYTTCSC	GANITGHVKN
VN405	KVWLKSKLVP	ALPGVPFLSC	QRGFRGVWRG	DGICRTTCPC	GADIVGHVKN

2051

2100

BEBE1	GTMRIISGPKT	CLNTWQGTFP	INCYTEGSCV	PKPAPNFKTA	IWRVAASEYA
D89815	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
ED43type_4	GSMRITGPKT	CSNTWHGTFP	INAYTTGPGV	PIPAPNYKFA	LWRVSAEDYV
HC_C2	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HC_G9	GSMRIVGPRT	CSNTWRGSFP	INAHTTGPCT	PSPAPNYTFA	LWRVSAEEYV
HCU16326	GSMRIVGPRT	CSNTWYGTFF	INAYTTGPCT	PSPAPNYSKA	LWRVAAEEYV
HCV_H_CM	GTMRIISGPKT	CRNMWSGTFF	INAYTTGPCT	PLPAPNYKFA	LWRVSAEEYV
HCV_J1	GTMRIISGPKT	CRNMWSGTFF	INAYTTGPCT	PLPAPNYTFA	LWRVSAEEYV
HCV_J483	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_J8	GTMKITGPKT	CLNLWQGTFP	INCYTEGPCV	PKPPPNYKTA	IWRVAASEYV
HCV_JK1	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_JS	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_R1	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_R2	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_R3	GSMKIVGPRT	CSNTWDGTFF	INGYTTGSST	PTPASNYSKA	LWRVVFEEYV
HCV_K1_S1	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_S2	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_S3	GSMKIVGPRT	CSNTWDGTFF	INGYTTGSST	PTPASNYSKA	LWRVVFEEYV
HCV_L2	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PAPTPNYSRA	LWRVAAEEYV
HCV_N	GSMRIISGPKT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSKA	LWRVAAEEYV
HCV12083	GTMKITGPKT	CSNTWHGTFP	INATTTGPST	PRPAPNYQRA	LWRVSAEDYV
HCV1480	GTMRIISGPKL	CSNTWQGTFP	INATTTGPSV	PAPAPNYKFA	LWRVGAADYA
HCVPOLYP	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HD_1	GSMRIVGPRT	CSNTWYGSFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCCGAA	GTMRIISGPKT	CKNMWSGTFF	INAYTTGPCT	PLPAPNYKFA	LWRVSAEEYV
HPCFG	GSMRIISGGL	CANMWHGTFP	INEYTTGPST	PVPAHNYTRA	LWRVTSDSYV
HPCGENANTI	GSMRIISGPKT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCGENOM	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAPPEYV
HPCHUMR	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCJ	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCS	PSPAPNYSRA	LWRVAAEEYV
HPCJCG	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCJK046	GTMRIISGPKT	CSNVWNGTFP	INATTTGPSI	PIPAPNYKKA	LWRVSATEYV
HPCJK049	GTMRLVGPRT	CANTWHGTFP	INGYTTGPST	PAPSYAYSRA	LWRVASDSYV
HPCJTA	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCJTB	GSMRIVGPRT	CSNMWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCK3A	GSMRLAGPRT	CANMCHGTFP	INEYTTGPST	PCPPPNYTRA	LWRVAANSYV
HPCPLYPRE	GTMRIISGPKT	CRNMWSGTFF	INAYTTGPCT	PLPAPNYTFA	LWRVSAEEYV
HPCPOLP	GSMRITGPKT	CMNIWQGTFP	INCYTEGQCV	PKPAPNFKIA	IWRVAASEYA
HPCPP	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCUNKCD	GSMRIVGPRT	CSNTWYGTFF	INAYTTGPCT	PSPAPNYSKA	LWRVAAEEYV
MKC1A	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
NDM59	GSMRITGPKT	CMNTWQGTFP	INCYTEGQCV	PKPAPNFKTA	IWRVAASEYA
NZLI	GSMRLAGPRT	CANMWHGTFP	INEYTTGPST	PCPSPNYTRA	LWRVAANSYV
SA13	GTMRIISGPKL	CSNTWHGTFP	INATTTGPSV	PAPAPNYKFA	LWRVGAADYA
Th580	GSMKITGPRM	CSNTWHGTFP	INATTTSPSV	PVPAPNYKRA	LWRVSAEEYV
Type_3a_CB	GSMRLAGPRT	CANMWHGTFP	INEYTTGPST	PCPSPNYTRA	LWRVAANSYV
TypeV_D	GSMRLAGPRT	CANMWYGTFF	INEYTTGPST	PCPSPNYTRA	LWRVAANSYV
VN004	GTMKISGPRW	CSNVSHRTFF	INATTTGPSV	PIPEPNYTRA	LWRVSAEEYV
VN235	GSMKIVGPKM	CSNVWNNRFP	INATTTGPSV	PVPEPNYHKA	LWRVSAEDYV
VN405	GSMRIISGSRW	CSNIWHGTFP	INATTTGPSV	PIPEPNYKRA	LWRVSAEEYV

	2101			2150	
BEBE1	EVTQHDASHY	VTGLTADNLK	VPCQLPCPEF	FSWVDGVQIH	RFAPTPKAFM
D89815	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTELDGVRLH	RYAPACKPLL
ED43type_4	EVRRVGDFHY	VTGVTQDNK	FPCQVPAPPEL	FTEVDGIRIH	RHAPCKKPLL
HC_C2	EVTRVGDFHY	ITGMTTDNIK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPVL
HC_G9	EVRRLGDFHY	ITGVTTDKIK	CPCQVPSPEF	FTEVDGVRLH	RYAPPCKPLL
HCU16326	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACRPLL
HCV_H_CM	EIRRVGDFHY	VSGMTTDNLK	CPCQIPSPEF	FTELDGVRLH	RFAPPCKPLL
HCV_J1	EIRRVGDFHY	VTGMTTDNLK	CPCQVPSPEF	FTELDGVRLH	RFAPPCKPLL
HCV_J483	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPLL

HCV_J8	EVTQHGSFSY	VTGLTSDNLK	VPCQVPAPPEF	FSWVDGVQIH	RFAPVPGPFF
HCV_JK1	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPACKPLL
HCV_JS	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVQLH	RYAPACKPLL
HCV_K1_R1	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRHLH	RNAPACGPLL
HCV_K1_R2	EVTRVGDFHY	VTGMTTDNLK	CPCQVPAPPEF	FKELDGVRHLH	RYAPASKPLL
HCV_K1_R3	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTELDGVRHLH	RYAPVSKPLL
HCV_K1_S1	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRHLH	RNAPACGPLL
HCV_K1_S2	EVTRVGDFHY	VTGMTTDNLK	CPCQVPAPPEF	FKELDGVRHLH	RYAPASKPLL
HCV_K1_S3	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTELDGVRHLH	RYAPVSKPLL
HCV_L2	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPACKTLL
HCV_N	EVTRVGDFHY	VTGITTDNVK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPVCKPLL
HCV12083	EVRRLGDCYH	VVGVTAEGLK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPPCKPLL
HCV1480	EVRRVGDYHY	ITGVTQDNLK	CPCQVPAPPEF	FTELDGVRHLH	RFAPPCNPLL
HCVPOLYP	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPACKPLL
HD_1	EVTRVGDFHY	VTGMTTDNIK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPACKPLL
HPCCGAA	EIRRVGDFHY	VSGMTTDNLK	CPCQIPSPPEF	FTELDGVRHLH	RFAPPCKPLL
HPCFG	EVRRVGDTHY	VVGATNDGLK	IPCQVPAPPEF	FTELDGVRHLH	RYAPPCKPLL
HPCGENANTI	EVRRVGDTHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPACKPLL
HPCGENOM	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPACKPLL
HPCCHUMR	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FSEVDGVRHLH	RYAPACRPLL
HPCJ	EVTRVGDFHY	VTGVTDDNVK	CPCQVPAPPEF	FTELDGVRHLH	RYAPACKPLL
HPCJCG	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPVCKPLL
HPCJK046	EVRRVGDYHY	ITGVTAEGLK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPECCKPIL
HPCJK049	EVRRVGDYHY	VTGTTDDGLK	CPCQVPAPPEF	FTELDGVRHLH	RYAPVCRPLL
HPCJTA	EITRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTELDGVRHLH	RYAPACRPLL
HPCJTB	EITRVGDFHY	VTGXTDDNVK	CPCQVPAPPEF	FTELDGVRHLH	RYAPACRPLL
HPCK3A	EVRRVGDYHY	ITGATEDGLK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPPCKPLL
HPCPLYPRE	EIRQVGDYHY	VTGMTTDNLK	CPCQVPAPPEF	FTELDGVRHLH	RFAPPCKPLL
HPCPOLP	EVTQHGSYHY	ITGLTTDNLK	VPCQLPSPEF	FSWVDGVQIH	RFAPIPKPPF
HPCPP	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTELDGVRHLH	RYAPACKPLL
HPCUNKCD	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPACRPLL
MKC1A	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTELDGVRHLH	RYAPACKPLL
NDM59	EVTQHGSYSY	ITGLTTDSLK	VPCQLPSPEF	FSWVDGVQIH	RFAPTPKPPF
NZLI	EVRRVGDYHY	ITGATEDGLK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPPCKPLL
SA13	EVRRVGDYHY	ITGVTQDNLK	CPCQVPAPPEF	FTELDGVRHLH	RYAPPCKPLL
Th580	EVERHGDRHY	VVGVTADGLK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPPCKPLL
Type_3a_CB	EVRRVGDYHY	ITGATEDGLK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPPCKPLL
TypeV_D	EVRRVGDYHY	ITGATEDGLK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPPCKPLL
VN004	EVRRVGDYHY	VVGATTDNLK	CPCQVPAPPEF	FTEVDGVRHLH	RYAPRCKPLL
VN235	EVRRVNDHHY	IVGATADNLK	CPCQVPAPPEF	FTEVDGVRHLH	RFAPPCKPLM
VN405	EVRRVGDYHY	VVGATNQLK	CPCQVPAPPEF	FTEVDGVRHLH	RFAPACKPLL

	2151		2200
BEBE1	RDEVFSFVGL	NSYVVGSQLP	CEPEPDTEVL ASMLTDPSHI TAEAAARRLA
D89815	RDEVTFFQVGL	NQYTVGSQPL	CEPEPDVTVV TSMLTDPSHI TAEAAARRLA
ED43type_4	RDEVFSFVGL	NSFVVGSQLP	CEPEPDVAVL TSMLTDPSHI TAESARRRLA
HC_C2	REEVDFQVGL	NQYPVGSQPL	CEPEPDVAVL TSMLTDPSHI TAEAAKRRLA
HC_G9	RDEVTFSIGL	NEYLVGSQPL	CEPEPDVAVL TSMLTDPSHI TAETAARRLN
HCU16326	REEVVFQVGL	HQYLVGSQPL	CEPEPDVAVL TSMLTDPSHI TAETAARRLA
HCV_H_CMV	REEVVFQVGL	HEYPVGSQPL	CEPEPDVAVL TSMLTDPSHI TAEAAARRLA
HCV_J1	REEVVFQVGL	HDYPVGSQPL	CEPEPDVAVL TSMLTDPSHI TAEAAARRLA
HCV_J483	REDVAFQVGL	NQYLVGSQPL	CEPEPDVTVL TSMLTDPSHI TAETAARRLA
HCV_J8	RDEVTFTVGL	NSFVVGSQLP	CDPEPDTEVL ASMLTDPSHI TAEAAARRLA
HCV_JK1	RDEVTFFQVGL	NQFPVGSQPL	CEPEPDVTVL TSMLTDPSHI TAETAARRLA
HCV_JS	RDEVTFFQVGL	NQYLVGSQPL	CEPEPDVAVL TSMLTDPSHI TAEAAKRRLA
HCV_K1_R1	REEVTFQVGL	NQYLVGSQPL	CEPEPDVTVL TSMLTDPSHI TGEAAKRRLA
HCV_K1_R2	RDEVTFFQVGL	NQYVVGSQLP	CEPEPDVAVL TSMLTDPSHI TAETAARRLA
HCV_K1_R3	RDEVTFFQVGL	NRYPVGSQPL	CEPEPDVAVL TSMLTDPSHI TAETAARRLA
HCV_K1_S1	REEVTFQVGL	NQYLVGSQPL	CEPEPDVAVL TSMLTDPSHI TGETAKRRLA
HCV_K1_S2	RDEVTFFQVGL	NQYVVGSQLP	CEPEPDVAVL TSMLTDPSHI TAEAAKRRLA
HCV_K1_S3	RDEVTFFQVGL	NRYAVGSQPL	CEPEPDVTVI TSMLTDPSHI TAETAARRLA

HCV_L2	REEVTFQVGL	NQYLVGSQLP	CEPEPDVAVL	TSMLTDP SHI	TAETAKRRRLA
HCV_N	RDEVVFQVGL	NQYLVGSQLP	CEPEPDVAVL	TSMLTDP SHI	TAEAAKRRRLA
HCV12083	RDEVTFQVGL	SNYAVGSQLP	CEPEPDVTVV	TSMLTDP THI	TAETAARRLK
HCV1480	REEVTFQVGL	HSYVVGSQLP	CEPEPDVTVL	TSMLSDPAHI	TAETAKRRRLN
HCVPOLYP	RDEVTFQVGL	NQYVVGSQLP	CEPEPDVVVV	TSMLTDP SHI	TAETAKRRRLD
HD_1	RDEVSFQVGL	NHYPVGSQLP	CEPEPDVAVL	TSMLTDP SHI	TAETAKRRRLA
HPCCGAA	REEVSFRVGL	HEYPVGSQLP	CEPEPDVAVL	TSMLTDP SHI	TAEAAAGRRLA
HPCFG	RDEITFSVGL	HSYANGSQLS	CEPEPDVAVL	TSMLRDP AHI	TAATAARRLA
HPCGENANTI	REEVSFQVGL	NQYVVGSQLP	CEPEPDVAVL	TSMLTDP SHI	TAETAKRRRLA
HPCGENOM	REEVVFQVGL	NQYLVGSQLP	CEPEPDVTVL	TSMLTDP SHI	TAETAKRRRLA
HPCHUMR	REEVTFQVGL	NQYLVGSQLP	CEPEPDVAVL	TSMLTDP SHI	TAETAKRRRLA
HPCJ	RDEVSFQVGL	NQYLVGSQLP	CEPEPDVAVL	TSMLTDP SHI	TAETAKRRRLA
HPCJCG	REEVVFQVGL	NQYLVGSQLP	CEPEPDVAVL	TSMLTDP SHI	TAETAKRRRLA
HPCJK046	RDEVTFQVGL	STYVVGSQLP	CEPEPDVLVV	TSMLRDP DHI	TAEAEARRLK
HPCJK049	RDDVTFQVGL	NSYVIGSQLP	CEPEPDVAVV	TSMLQDP SHI	TVETAKRRRLD
HPCJTA	REDVTFQVGL	NQYLVGSQLP	CEPEPDVAVL	TSMLTDP SHI	TAETAKRRRLA
HPCJTB	REDVTFQVGL	NQYLVGSQLP	CEPEPDVAVL	TSMLTDP SHI	TAETAKRRRLA
HPCK3A	RDEITFMVGL	NSYAIGSQLP	CEPEPDVSVL	TSMLRDP SHI	TAETAARRLA
HPCPLYPRE	REEVSFRVGL	HEYPVGSQLP	CEPEPDVAVL	TSMLTDP SHI	TAEAAAGRRLA
HPCPOLP	RDEVSFQVGL	NSFVVGSQLP	CDPEPDVTVL	TSMLTDP SHI	TAETAARRLA
HPCPP	RDEVTFQVGL	NQYTVGSQLP	CEPEPDVTVV	TSMLTDP SHI	TAEAAARRRLA
HPCUNKCD	REEVVFQVGL	HQYLVGSQLP	CEPEPDVAVL	TSMLTDP SHI	TAETAKRRRLA
MKC1A	RDEVTFQVGL	NQYTVGSQLP	CEPEPDVTVV	TSMLTDP SHI	TAETAARRRLA
NDM59	RDEVSFQVGL	NSFVVGSQLP	CDPEPDADVL	TSMLTDP SHI	TAEAAAARRLA
NZLI	RDDITFMVGL	HSYTIGSQLP	CEPEPDVSVL	TSMLRDP SHI	TAETAARRLA
SA13	REEVCFSVGL	HSFVVGSQLP	CEPEPDVTVL	TSMLSDPAHI	TAETAKRRRLD
Th580	RDEVSFQVGL	LEFVVGSQLP	CEPEPDVTVV	TSMLTDP SHI	TAETASARRLK
Type_3a_CB	REEITFSVGL	NSYTIGSQLP	CEPEPDVSVL	TSMLRDP SHI	TAETAARRLA
TypeV_D	RDDITFMVGL	NSYAIGSQLP	CEPEPDVSVL	TSMLRDP SHI	TAETAARRLA
VN004	RDEVSFQVGL	SSYAVGSQLP	CEPEPDVTVV	TSMLIDPSHV	TAEAAAARRLA
VN235	RDDITFSVGL	STYVVGSQLP	CEPEPDVIL	TSMLTDP DHI	TAETAARRLA
VN405	RDEISFLVGL	NSYAIGSQLP	CEPEPDVTVV	TSMLVDPSHL	TAEAAAARRLA

	2201				2250
BEBE1	RGSPPSAASS	SASQLSAPSL	RATCTTHAK.	...CPDIDMV	DANLFCWCTM
D89815	RGSPPSLAGS	SASQLSALS	KATCTTHHG.	...APDTDLI	EANLLWRQEM
ED43type_4	RGSRPSLASS	SASQLSPRL	QATCTAPHD.	...SPGTDLL	EANLLW....
HC_C2	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HC_G9	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	TANLLWRQEM
HCU16326	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_H_CMR	RGSPPSMASS	SASQLSAPSL	KATCTANHD.	...SPDAELI	EANLLWRQEM
HCV_J1	RGSPPSSEASS	SASQLSAPSL	KATCTINHD.	...SPDAELI	EANLLWRQEM
HCV_J483	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_J8	RGSPPSQASS	SASQLSAPSL	KATCTTHKT.	...AYDCDMV	DANLF...M
HCV_JK1	RGSPPSLASS	SASQLSAPSL	KATCTTRHD.	...SPDADLI	EANLLWRQEM
HCV_JS	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_K1_R1	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_K1_R2	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_K1_R3	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_K1_S1	RGSPPSLASS	SASQLSAPSS	KATYITQYD.	...SPDFDLI	EANLLWRQEM
HCV_K1_S2	RGSPPSLASS	SASQLSAPSL	KATCTTRHD.	...SPDADLI	EANLLWRQEM
HCV_K1_S3	RGSPPSLASS	SASQLSAPSL	KATCTTCHD.	...SPDADLI	EANLLWRQEM
HCV_L2	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_N	RGSPPSLASS	SASQLSAPSL	RATCTTHSSY	NLDSPDVL	EANLLWRQEM
HCV12083	KGSPPSLASS	SANQLSAPSL	RATCTTSQK.	...HPPEMEL	QANLLWKHEM
HCV1480	RGSPPSLANS	SASQLSAPSL	KATCTIQGH.	...HPDADLI	KANLLWRQCM
HCVPOLYP	RGSPPSLASS	SASQLSAPSL	KATCTTRHD.	...SPDADLI	EANLLWRQEM
HD_1	RGSPPSLASS	SASQLSAPSL	KATCTTRHD.	...SPDADLI	EAHLLWRQEM
HPCCGAA	RGSPPSMASS	SASQLSAPSL	KATCTANHD.	...SPDAELI	EANLLWRQEM
HPCFG	RGSPPSSEASS	SASQLSAPSL	KATCTQTHRP.	...HPDAELI	DANLLWRQEM
HPCGENANTI	RGSPPSLASS	SASQLSALS	KAACCTTRHT.	...PPDADLI	EANLLWRQEM

HPCGENOM	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HPCHUMR	RGSPPSLASS	SASQLSAPSL	KATCTTHHV.	...SPDADLI	EANLLWRQEM
HPCJ	RGSPPSLASS	SASQLSAPSL	KATCTIHHH.	...SPDADLI	EANLLWRQEM
HPCJCG	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HPCJK046	RGSPPSLASS	SASQLSAPSL	KATCTTHAD.	...HPDAELV	EANLLWRQEM
HPCJK049	RGSPPSLASS	SASQLSAPSR	KATCTTHGR.	...HPDAELI	TANLLWRQEM
HPCJTA	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HPCJTB	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HPCK3A	RGSPPSSEASS	SASQLSAPSL	KATCQTHRP.	...HPDAELV	DANLLWRQEM
HPCPLYPRE	RGSPPSVASS	SASQLSAPSL	KATCTANHD.	...SPDAELI	EANLLWRQEM
HPCPOLP	RGSPPSSEASS	SASQLSAPSL	RATCTTHGK.	...AYDVMV	DANLF...M
HPCPP	RGSPPSLASS	SASQLSAPSL	KATCTTHHG.	...APDTDLI	EANLLWRQEM
HPCUNKCD	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
MKC1A	RGSPPSLASS	SASQLSAPSL	KATCTTHHG.	...APDTDLI	EANLLWRQEM
NDM59	RGSPPSSEASS	SASQLSAPSL	RATCTTHGK.	...AYDVMV	DANLF...M
NZLI	RGSPPSSEASS	SASQLSAPSL	KATCQTHRP.	...HPDAELV	DANLLWRQEM
SA13	RGSPPSLASS	SASQLSAPSL	KATCTTQGH.	...HPDADLI	EANLLWRQCM
Th580	RGSPPSLASS	SASQLSAPSL	KATCTANGD.	...HPDAELI	EANLLWRQEM
Type_3a_CB	RGSPPSSEASS	SASQLSAPSL	KATCQTHRP.	...HPDAELV	NANLLWRQEM
TypeV_D	RGSPPSSEASS	SASQLSAPSL	KATCQTHRP.	...HPDAELV	DANLLWRQEM
VN004	RGSPPSLASS	SASQLSAPSL	KATCTMHGA.	...HPDAELI	EANLLWRQEM
VN235	RGSPPSLASS	SASQLSAPSL	KATCTTAGK.	...HPDAELI	EANLLWRQEV
VN405	RGSPSCASS	LASQLSAPSL	KATCTTHCA.	...HPDADLI	EANLLWRQEV

	2251				2300
BEBE1	GGNMTRIESE	SKVLMVDSFD	PVVDKE.DER	EPSIPSEYLL	PKS.RFPPAL
D89815	GGNITRVESE	NKIVILDSFE	PLRAEE.DER	EVSAABEILR	KTR.KFPAAM
ED43type_4	GSTATRVETD	EKVIILDSFE	SCVAEQNDDR	EVSVAAEILR	PTK.KFPPAL
HC_C2	GGNITRVESE	NKVILDSFE	PLRAEE.DER	EVSVAAEILR	KTR.RFPPAM
HC_G9	GGNITRVESE	NKIVILDSFD	PLVAEE.DDR	EISVPAEILL	KSK.KFPPAM
HCU16326	GGNITRVESE	NKVILDSFD	PLRAED.DEG	EISVPAEILR	KSR.KFPPAL
HCV_H_CMR	GGNITRVESE	NKVILDSFD	PLVAEE.DER	EVSVPAEILR	KSR.RFAPAL
HCV_J1	GGNITRVESE	NKVILDSFD	PLVAEE.DER	EISVPAEILR	KSR.RFTQAL
HCV_J483	GGNITRVESE	NKVILDSFE	PLHAEG.DER	EISVAAEILR	KSR.KFPSAL
HCV_J8	GGDVTRIED	SKVIVLDSLD	SMTEVE.DDR	EPSVPSEYLI	KRR.KFPPAL
HCV_JK1	GGNITRVESE	NKVILDSFE	PLRAEE.DER	EVSVAAEILR	KSR.KFPPAL
HCV_JS	GGNITRVESE	NKVILDSFD	PLHAEE.DER	EVSVAAEILR	KSR.KFPPAL
HCV_K1_R1	GGNITRVESE	NKVIILDSFD	PLRAEE.DER	EVSIPEILR	KSK.KFPPAL
HCV_K1_R2	GGNITRVESE	NKVILDSFE	PLRAEE.DER	EVSLPAEILR	KSR.KFPPAM
HCV_K1_R3	GGNITRVESE	NKVILDSFD	PLRAEE.DER	EVSVAAEILR	KTR.KFPPAL
HCV_K1_S1	GGNITRVESE	NKVITLDSFD	PLRAEE.DER	EVSIPEILR	KSK.KFPSAL
HCV_K1_S2	GGNITRVESE	NKVILDSFE	PLRAEE.DER	EVSLPAEILR	KSR.KFPPAM
HCV_K1_S3	GGNITRVESE	NKVILDSFD	PLRAEE.DER	EVSVAAEILR	KTK.KFPPAL
HCV_L2	GGNITRVESE	SKVILDSFD	PLRAEE.GEG	EVSVAAEILR	KSK.KFPPAL
HCV_N	GGNITRVESE	NKVVLDSFE	PLRAEG.DEN	EISIAAEILR	KSK.KFPAAI
HCV12083	GSHIPRVQSE	NKVVLDSFE	LYPLEY.EER	EISVSVECHR	QPRCKFPFVF
HCV1480	GGNITRVEAE	NKVEILDCFK	PLKEEE.DDR	EISVSADCFK	KGP.AFPPAL
HCVPOLYP	GGNITRVESE	NKVILDSFD	PLRAEE.DER	EVSVAAEILR	KSR.RFPPAM
HD_1	GGNITRVESE	NKVILDSFD	PLRAEE.DER	EVSVPAEILR	KSR.KFPPAM
HPCCGAA	GGNITRVESE	NKVILDSFD	PLVAEE.DER	EVSVPAEILR	KSR.RFAPAL
HPCFG	GSNITRVESE	TKVVILDSFE	PLRAEE.DDT	ELSIPAECFK	KPP.KYPPAL
HPCGENANTI	GGNITRVESE	NKVILDSFD	PLRAEE.DER	EVSVPAEILR	KSR.KFPPAL
HPCGENOM	GGNITRVESE	NKVILDSFD	PLRAEE.DER	EVSVAAEILR	KSR.KFPSAL
HPCHUMR	GGNITRVESE	NKVVLDSFD	PLRAEE.DER	EVSVPAEILR	KSK.KFPAAM
HPCJ	GGNITRVESE	NKVILDSFE	PIRAEE.DER	EVSVPAEILR	RSR.KFPAAM
HPCJCG	GGNITRVESE	NKVILDSFD	PIRAVE.DER	EISVPAEILR	KPR.KFPPAL
HPCJK046	GGNITRVESE	NKIVILDSFE	PLKAEF.DDR	EISVAAECHR	PPRFKYPPAL
HPCJK049	GSNITRVESE	SKVILDSFE	PLRACD.DED	ELSVAAECFK	KPP.KYPPAL
HPCJTA	GGNITRVESE	NKVILDSFD	PLRAEE.DER	EVSVAAEILR	KSK.KFPPAL
HPCJTB	GGNITRVESE	NKVILDSFD	PLRAEE.DER	EVSVAAEILR	KSK.KFPPAL
HPCK3A	GSNITRVESE	TKVVILDSFE	PLRAET.DDA	ELSAAECFK	KPP.KYPPAL

HPCPLYPRE	GGNITRVESE	NKVVILDSFD	PLVAEE.DER	EISVPAEILR	KSR.RFAQAL
HPCPOLP	GGDVTRIESE	SKVVVLDSLD	PMVEER.SDL	EPSIPSEYML	PKK.RFPPAL
HPCPP	GGNITRVESE	NKIVILDSFE	PLRAEE.DER	EVSVAEILR	KTR.KFPAAM
HPCUNKCD	GGNITRVESE	NKVVILDSFD	PLRAED.DEG	EISVPAEILR	KSR.KFPPAL
MKC1A	GGNITRVESE	NKIVILDSFE	PLRAEE.DER	EVSVAEILR	KTR.KFPAAM
NDM59	GGDVTRIESE	SKVVVLDSLD	PMAEER.SDL	EPSIPSEYML	PRN.RFPPAL
NZLI	GSNITRVESE	TKVVVLDSFE	PLRAET.DDV	EPSVAAECFK	KPP.KYPPAL
SA13	GGNITRVEAE	NKVVILDSFE	PLKADD.DDR	EISVSADCFR	RGP.AFPPAL
Th580	GSNITRVESE	TKVVILDSFD	PLVAEY.DDR	EISVSAECHR	PPRPKFPPAL
Type_3a_CB	GSNITRVESE	TKVVILDSFE	PLRAET.DDA	ELSVAAECFK	KPP.KYPPAL
TypeV_D	GSNITRVESE	TKVVILDSFE	PLRAQT.DDA	ELSVAAECFK	KPP.KYPPAL
VN004	GGNITRVESE	NKVVILDSFD	PLVPEF.EER	EMSVPAECHR	PPRPKFPPAL
VN235	GGNITRVESE	NKIIVLDSFD	PLIAET.DDR	EISVGAECFN	PPRPKFPPAL
VN405	GGNITRVESE	NKVIVLDSFD	PLVPEY.DDR	EPSVPAECHR	PNRPKFPPAL

	2301				2350
BEBE1	PPWARPDYNP	PLLETWKRPD	YQPPVVAGCA	LPPPGTTPVP	PPRRRR.AVV
D89815	PVWARPDYNP	PLLESWKNP	YVPPVVHGCP	LPPTKAPP	PPRRKR.TVV
ED43type_4	PIWARPDYNP	PLTETWKQD	YQAPTVMGCA	LPPAKQPPVP	SPRRKR.TVQ
HC_C2	PVWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPP	PPRRKR.TVV
HC_G9	PIWARPDYNP	PLVEPWKRPD	YEPPLVHGCP	LPPPKPTVP	PPRRKR.TVV
HCU16326	PIWAPPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPP	PPRRKR.TVV
HCV_H_CMR	PVWARPDYNP	PLVETWKKPD	YEPPVVHGCP	LPPRSPPVP	PPRRKR.TVV
HCV_J1	PIWARPDYNP	PLIETWKKPN	YEPPVVHGCP	LPPQSPVP	PPRRKR.TVV
HCV_J483	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPP	PPRRKR.TVV
HCV_J8	PPWARPDYNP	VLIETWKRPD	YEPPTVLGCA	LPPTPQTPVP	PPRRRR.AKV
HCV_JK1	PIWARPSYNP	PLLESWKDPD	YVPPVVHGCP	LPPTMAPP	PPRRKR.TVV
HCV_JS	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPP	PPRRKR.TVV
HCV_K1_R1	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPAKAPP	PPRRKR.TVV
HCV_K1_R2	PIWARPDYNP	PLIESWKDPD	YVPPVVHGCP	LPPTKAPP	PPRRKR.TVV
HCV_K1_R3	PIWARPDYNP	PLLEPWKDPD	YAPPVVHGCP	LPPAKDPP	PPRRKR.TVV
HCV_K1_S1	PIWARPDYNP	PLLEPWKDPD	YVPPVVHGCP	LPPAKAPP	PPRRKR.TVV
HCV_K1_S2	PIWARPDYNP	PLIESWKDPD	YVPPVVHGCP	LPPTKAPP	PPRRKR.TVV
HCV_K1_S3	PIWARPDYNP	PLLESWRAPD	YAPPVVHGCP	LPPAKDPP	PPRRKR.TVV
HCV_L2	PEWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPAKAPP	PPRRKR.TVV
HCV_N	PIWARPDYNP	PLLESWKNP	YVPPVVHGCP	LPPVKAPP	PPRRKR.TVV
HCV12083	PVWARPDNNP	PFIQAWQMPG	YEPPVVS	VAPPKPAPVP	PPRRKR.LVH
HCV1480	PVWARPGYDP	PLLETWKRPD	YDPPQVWGCP	IPPAGPPVP	LPRRKRKPM
HCVPOLYP	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPP	PPRRKR.TVV
HD_1	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPP	PPRRKR.TVV
HPCCGAA	PVWARPDYNP	LLVETWKKPD	YEPPVVHGCP	LPPRSPPVP	PPRRKR.TVV
HPCFG	PIWARPDYNP	PLLPWKDPD	YEPPAVHGCA	LPPTRPAPVP	PPRRKR.TIK
HPCGENANTI	PVWARPDYNP	PLLEPWKDPD	YVPPVVHGCP	LPPVKAPP	PPRRKR.TVV
HPCGENOM	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTTAPPVP	PPRRKR.TVV
HPCHUMR	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPIKAPP	PPRRKR.TVV
HPCJ	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAAP	PPRRKR.TIV
HPCJCG	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPSTKAPP	PPRRKR.TVV
HPCJK046	PVWARPDYNP	PLLETWKAPD	YDPPVVS	LPPQGLPPVP	PPRRKR.LVQ
HPCJK049	PIWARPDYNP	PLVEPWKDPD	YVPTVMGCA	LPPQKLPPVP	PPRRKR.TIV
HPCJTA	PIWARPDYNP	PLLESWKSPD	YVPPAVHGCP	LPPTTGPP	PPRRKR.TVV
HPCJTB	PIWARPDYNP	PLLESWKSPD	YVPPAVHGCP	LPPTTGPP	PPRRKR.TVV
HPCK3A	PIWARPDYNP	PLLDWKSPD	YVPTVMGCA	LPPKGAPPVP	PPRRKR.TIQ
HPCPLYPRE	PVWARPDYNP	PLVETWKKPD	YEPPVVHGCP	LPPPKSPPVP	PPRRKR.TVV
HPCPOLP	PAWARPDYNP	PLVESWKRPD	YQPATVAGCA	LPPPKTTP	PPRRRR.TVG
HPCPP	PVWARPDYNP	PLLESWKNP	YVPPVVHGCP	LPPTKAPP	PPRRKR.TVV
HPCUNKCD	PIWAPPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPP	PPRRKR.TVV
MKC1A	PVWARPDYNP	PLLESWKNP	YVPPVVHGCP	LPPTKAPP	PPRRKR.TVV
NDM59	PAWARPDYNP	PLVESWKRPD	YQPTVAGCA	LPPPKTTP	PPRRRR.TVG
NZLI	PIWARPDYNP	PLLDWKAPD	YVPTVMGCA	LPPRGAPPVP	PPRRKR.TIQ
SA13	PIWARPGYDP	PLLETWKQD	YDPPQVSGCP	LPPAGLPPVP	PPRRKRKPVV
Th580	PIWARPDYNP	PLQKQMPG	YEPPVVS	LPPAKTP	PPRRKR.LIQ

Type_3a_CB	PIWARPDYNP	PLLDRWKAPD	YVPPTVHGCA	LPPRGAPPVP	PPRRKR.TIQ
TypeV_D	PIWARPDYNP	PLLDRWKTPD	YVPPTVHGCA	LPPRGAPPVP	PPRRKR.TIQ
VN004	PIWATPGYNP	PVLETWKSPT	YEPPVVHGCA	LPPSGPPPPI	PPRRKR.VVQ
VN235	PVWARPDYNP	PLLQPWKAPD	YEPPLVHGCA	LPPKGLPPVP	PPRKR.VVQ
VN405	PIWARPDYNP	PLLETWKKPD	YAPPLVHGCA	LPSPVQPPVP	PPRRKS.VVH

	2351				2400
BEBE1	LDQSNVGEAL	KELAIKSFGC	PPPSGDPGHS	TGGGTTGETS	KSPPD.EPDD
D89815	LTESTVSSAL	AELATKTFGG	SGS.SAVDSG	TATGPPDQAS	AE....GDAG
ED43type_4	LTESTVSTAL	AELAAKTFGQ	SEP.SSDRDT	DLTTPTETTD	SGPIV.VDDA
HC_C2	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQTS	ND....GDRE
HC_G9	LDESTVSSAL	AELATKTFGS	STT.SGVTSG	EAAESSPAPS	CD....GELD
HCU16326	LTESTVSSAL	AELATKTFGS	SGS.SAIDSG	TATAPPDQAS	GD....GDRE
HCV_H_CMR	LTESTLPTAL	AELATKSFGS	SST.SGITGD	NMTTSSEPAP	SG....CPPD
HCV_J1	LTESTLSTAL	AELAAKSFGS	SST.SGITGD	NTTTSSEPAP	SG....CSPD
HCV_J483	LTESTVSSAL	AELATKTFSS	SGS.SAVDSG	TATALPDQAS	DD....GDKG
HCV_J8	LTQDNVEGVL	REMADKVLSP	LQDNNDGHS	TGADTGGDIV	QQPSD.ETAA
HCV_JK1	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQPS	DD....GDRG
HCV_JS	LTESTVSSAL	AELATKTFGS	SGS.SAADSG	TATAPPDQAS	DD....GDKG
HCV_K1_R1	LTESTVSSAL	AELATKTFGS	SGS.SAADRG	TATAPPDQAS	ND....GDAG
HCV_K1_R2	LTESTVSSAL	AELATKTFGS	SES.SAADSG	TATAPPDQPS	SD....GDAG
HCV_K1_R3	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQTS	ND....GDTG
HCV_K1_S1	LTESTVSSAL	AELATKTFGS	SES.SAADRG	TATAPPDQTS	ND....GDAG
HCV_K1_S2	LTESTVSSAL	AELATKTFGS	SES.SAADSG	TATAPPDQPS	ND....GDAG
HCV_K1_S3	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQPS	ND....GDTG
HCV_L2	LTESTVSSAL	AELAVKTFGS	SES.SAVDSG	TATAPPDQVS	DN....GDKG
HCV_N	LTDSVSSVL	AELATKTFGS	SEL.SAADSG	TATAPPDQTS	DN....GGKD
HCV12083	LDESTVSHAL	AQLADKVFVE	SSNDPGPSSD	SGLSITSPVP	PDPTTPEDAG
HCV1480	LSDSVVSQVM	ADLADARFKV	DTP.SIEGQD	SALGTSSQHD	SGPEEKRDDN
HCVPOLYP	LTESTVSSAL	AELATKTFGS	SES.SAVDSG	TATAPPDQPP	DN....DDTG
HD_1	LTESTVSSAL	AELATKTFGS	SES.SAVDSG	TATAPPGQSS	DD....VDTG
HPCCGAA	LTESTLPTAL	AELATKSFGS	SST.SGITGD	NTTTSSEPAP	SG....CPPD
HPCFG	LDGSNVSAAL	LALAERSFPS	TKPEGTGTSS	SGVGTESTAE	SGDSPETGEE
HPCGENANTI	LTESTVSSAL	AELATKTFGS	SES.SAAGSG	TATAPPDQPS	DD....GDAG
HPCGENOM	LTSSVSSAL	AELATKTFGS	SES.SAVDSG	TATAPPDEAS	GG....GDKG
HPCHUMR	LTSSVSSAL	AELATKTFGS	SES.SAVDSG	TATALPDQAS	DD....GDKG
HPCJ	LTESTVSSAL	AELATKTFGG	SGS.SAADSG	TATAPPDQTS	DD....GDKE
HPCJCG	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATGPPDQAS	DD....GDKG
HPCJK046	LDDSVVGHVL	AQLAEKSFFA	TPDQPQTNSD	SGHGTNGAAS	LPSAE.DDDA
HPCJK049	LSESTVSKAL	ASLAEKSFFQ	PTCSAEDEST	SGVGTQSGSL	TGPVQLDDDD
HPCJTA	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQTS	DD....GDKE
HPCJTB	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQTS	DD....GDKE
HPCK3A	LDGSNVSAAL	AALAEKSFFS	SKPQEENSSS	SGVDTQSSTA	SKVLPSPGEE
HPCPLYPRE	LTESTLSTAL	AELATRSFGS	SST.SGITGD	NTTTSSEPAP	SG....CPPD
HPCPOLP	LSESSIADAL	QQLAIKSFGQ	PPPSGDSGLS	TGADAADSGS	RTPPD.ELAL
HPCPP	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATGPPDQAS	AE....GDAG
HPCUNKCD	LTESTVSSAL	AELATKTFGS	SGS.SAIDSG	TATAPPDQAS	GD....GDRE
MKC1A	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATGPPDQAS	AE....GDAG
NDM59	LNENTIGDAL	QQLAIKAFGQ	PPLSGDSGLS	TGADAADSGS	RTPPD.ESAL
NZLI	LDGSNVSAAL	AALAEKSFFS	SKPQEENSSS	SGVDTQSSTT	SKVPPSPGGE
SA13	LSDSNVSQVL	ADLAHARFKA	DTQ.SIEGQD	SAVGTSSQPD	SGPEEKRDDDD
Th580	LDESAVSQAL	QQLADKVFVE	DTSTSEPSSG	LGGSIAGPSS	PDPTTADDTCT
Type_3a_CB	LDGSNVSAAL	RALAEKSFFS	LKPQEENSSS	SGVDTQSSTT	SKVPPSPGGE
TypeV_D	LDGSNVSAAL	AALAKKSFFS	VNPQDENSSS	SGVDTQSSTT	SKVPPSPGGE
VN004	LDSSNVSAAL	AQLAAKTFET	PSS.PTTGYG	SDQPDHSTES	SEHDRDDGVA
VN235	LDEGSAKRAL	AELAQTSFPP	STATLSEDSG	RETSTLSSDM	TPPREADRA
VN405	LDDSTVATAL	AELAEKSFFPT	QPA.STPDS	SGHPTTSKSS	DQADEGEDTP

	2401				2450
BEBE1	SEAGSVSSMP	PLEGEPGDPD	LEPEQVEHPA	PPQEGGAAPG	SDSGSWSTCS
D89815	SDAESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS

ED43type_4	SDDGSYSSMP	PLEGEPGDPD	LT.....	..SDSWSTVS
HC_C2	SDAESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HC_G9	SEAESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCU16326	SDVESFSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCV_H_CMR	SDVESYSSMP	PLEGEPGDPD	FS.....	..DGSWSTVS
HCV_J1	SDAESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCV_J483	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCV_J8	SEAGSLSSMP	PLEGEPGDPD	LEFEPVGSAP	PSEGECEVID SDSKSWSTVS
HCV_JK1	SDDESYSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCV_JS	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCV_K1_R1	SDVGSYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCV_K1_R2	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCV_K1_R3	SDVGSYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCV_K1_S1	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCV_K1_S2	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCV_K1_S3	SDVGSYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCV_L2	SDAESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCV_N	SDAESCSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HCV12083	SEAESYSSMP	PLEGEPGDPD	LS.....	..SGSWSTVS
HCV1480	SDAASYSSMP	PLEGEPGDPD	LS.....	..SGSWSTVS
HCVPOLYP	SDVESCSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HD_1	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCCGAA	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCFG	SDVESYSSMP	PLEGEPGDPD	LD.....	..ADSWSTVS
HPCGENANTI	SDVESCSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCGENOM	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCHUMR	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCJ	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCJCG	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCJK046	SDADSYSSMP	PLEGEPGDPD	LSDG.....	GGSGSWSTVS
HPCJK049	SDNESHSSMP	PLEGEPGDPD	LS.....	..SGSWSTVS
HPCJTA	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCJTB	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCK3A	SDSESCSSMP	PLEGEPGDPD	LS.....	..CDSWSTVS
HPCPLYPRE	SDAESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCPOLP	SETGSISSMP	PLEGEPGDPD	LEPEQVELQP	PPQGGVVTGP SGSGSWSTCS
HPCPP	SDAESYSSMP	PLEGEPGDPD	LN.....	..DGSWSTVS
HPCUNKCD	SDVESFSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
MKC1A	SDAESYSSMP	PLEGEPGDPD	LN.....	..DGSWSTVS
NDM59	SETGSISSMP	PLEGEPGDPD	LEPEQVELQP	PPQGEEVVPG SDSGSWSTCS
NZLI	SDSESCSSMP	PLEGEPGDPD	LS.....	..CDSWSTVS
SA13	SDAASYSSMP	PLEGEPGDPD	LS.....	..SGSWSTVS
Th580	SDAGSFSSMP	PLEGEPGDPD	LS.....	..TGSWSTVS
Type_3a_CB	SDSESCSSMP	PLEGEPGDPD	LS.....	..CDSWSTVS
TypeV_D	SDSESCSSMP	PLEGEPGDPD	LS.....	..CDSWSTVS
VN004	SEAESYSSMP	PLEGEPGDPD	LS.....	..SGSWSTVS
VN235	SDDGSYSSMP	PLEGEPGDPD	LS.....	..SGSWSTVS
VN405	SEAGSYSSMP	PLEGEPGDPD	LS.....	..SGSWSTVS

2451

2500

BEBE1	DVD..DSVVC	CSMSYSWTGA	LITPCSPEEE	KLPINPLSNS	LLRYHNKVYC
D89815	EEA..SEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNP	LLRHHNMVYS
ED43type_4	GSE...DVVC	CSMSYSWTGA	LVTPCAAEEES	KLPISPLSNS	LLRHHNMVYA
HC_C2	EEA..SGDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HC_G9	SDGGTEDVVC	CSMSYSWTGA	LITPCAAEET	KLPINALSNS	LLRHHNLVYS
HCU16326	EEA..SEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HCV_H_CMR	SGADTEDVVC	CSMSYTWGTGA	LVTPCAAEEQ	KLPINALSNS	LLRHHNLVYS
HCV_J1	SEAGTEDVVC	CSMSYTWGTGA	LITPCAAEEQ	KLPINALSNS	LLRHHNLVYS
HCV_J483	EEA..SEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HCV_J8	DQE..DSVIC	CSMSYSWTGA	LITPCGPEEE	KLPINPLSNS	LMRFHNKVYS
HCV_JK1	EEA..SEDVAC	CSMSYTWGTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA

HCV_JS	EEA.SEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HCV_K1_R1	EEA.GEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_R2	EEA.GEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_R3	EEA.GEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_S1	EEA.GEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_S2	EEA.GEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_S3	EEA.GEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_L2	EEA.SEDVVC	CSMSYSWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_N	EEA.GESVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV12083	DEDD...VVC	CSMSYSWTGA	LITPCAAEEE	KLPINPLSNS	LVRHHNMVYS
HCV1480	GED...NVVC	CSMSYTWGTA	LITPCSAAEE	KLPINPLSNT	LLRHHNLVYS
HCVPOLYP	EEA.SEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HD_1	EEA.NEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HPCCGAA	SGADTEDVVC	CSMSYSWTGA	LVTPCAAEEQ	KLPINALSNS	LLRHHNLVYS
HPCFG	DSE.EQSVVC	CSMSYSWTGA	IITPCSAAEE	KLPISPLSNS	LLRHHNLVYS
HPCGENANTI	EED.GEGVIC	CSMSYTWGTA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HPCGENOM	EEA.SEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HPCHUMR	EEA.SEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HPCJ	EEA.SEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HPCJCG	GEA.GEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINPLSNS	LLRHHSMVYS
HPCJK046	SEETS...VVC	CSMSYSWTGA	LITPCAAEEE	KLPISPLSNT	LIRHHNMVYS
HPCJK049	.GE.EQSVVC	CSMSYSWTGA	LITPCAAEEE	KLPISPLSNS	LLRHHNLVYS
HPCJTA	GEA.SDDIVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HPCJTB	GEA.SDDIVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HPCK3A	DSE.EQSVVC	CSMSYSWTGA	LITPCSAAEE	KLPISPLSNS	LLRHHNLVYS
HPCPLYPRE	SEANAEDVVC	CSMSYSWTGA	LVTPCAAEEQ	KLPINALSNS	LLRHHNLVYS
HPCPOLP	EED...DSVVC	CSMSYSWTGA	LITPCSPEEE	KLPINPLSNS	LLRYHNKVYC
HPCPP	EEA.SEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNP	LLRHHNMVYA
HPCUNKCD	EEA.SEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
MKC1A	EEA.SEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNP	LLRHHNMVYA
NDM59	EED...DSVVC	CSMSYSWTGA	LITPCSPEEE	KLPINPLSNS	LLRYHNKVYC
NZLI	DSE.EQSVVC	CSMSYSWTGA	LITPCSAAEE	KLPISPLSNS	LLRHHNLVYS
SA13	DED...SVVC	CSMSYSWTGA	LITPCSAAEE	KLPINPLSNT	LLRHHNLVYS
Th580	EEDD...VVC	CSMSYTWGTA	LITPCAAEEE	KLPINPLSNS	LIRHHNMVYS
Type_3a_CB	DSE.EQSVVC	CSMSYSWTGA	LITPCSAAEE	KLPISPLSNS	LLRHHNLVYS
TypeV_D	DSE.EQSVVC	CSMSYSWTGA	LITPCSAAEE	KLPISPLSNS	LLRHHNLVYS
VN004	EEGDS...VVC	CSYSYSWTGA	LVTPCAAEEE	KLPINPLSNS	LIRHHNLVYS
VN235	EDHDS...VVC	CSMSYSWTGA	LITPCAAEEE	KLPISPLSNA	LIRHHNLVYS
VN405	EEGDS...VVC	CSMSYSWTGA	LVTPCAAEEE	KLPINPLSNS	LIRHHNLVYS

	2501			2550	
BEBE1	TTSRASQRA	KKVTFDRVQL	LD SHYESVLK	DVKQAATKVS	AKLLSIEEAC
D89815	TTSRASLRQ	KKVTFDRMQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
ED43type_4	TTTRSAVTRQ	KKVTFDRLQV	VDSTYNEVLK	EIKARASRVK	PRLLTTEEAC
HC_C2	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HC_G9	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EAKAKASTVK	AKLLSVEEAC
HCU16326	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_H_CMV	TTSRASQQRQ	KKVTFDRLQV	LD SHYQDVLK	EVKAAASKVK	ANLLSVEEAC
HCV_J1	TTSRASQQRQ	KKVTFDRLQV	LD SHYQDVLK	EVKAAASKVK	ANLLSVEEAC
HCV_J483	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HCV_J8	TTSRASLRA	KKVTFDRVQV	LDAHYDSVLQ	DVKRAASKVS	ARLLTVEEAC
HCV_JK1	TTSRASGLRQ	KKVTFDRLQV	PDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_JS	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HCV_K1_R1	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_K1_R2	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	ARLLSVEEAC
HCV_K1_R3	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_K1_S1	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_K1_S2	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	ARLLSVEEAC
HCV_K1_S3	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_L2	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_N	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC

HCV12083	TTSRSASLRQ	KKVTFDRVQV	FDQHYQDVLK	EIKLRASTVQ	AKLLSIEEAC
HCV1480	TSSRSAGLRQ	KKVTFDRLQV	LDDHYREVVD	EMKRLASKVK	ARLLPLEEAC
HCVPOLYP	TTSRSASQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HD_1	TTSRSASQRQ	KKVTFDRQQV	QDDHYRDVLK	EMKAKASTVK	ARLLSVEEAC
HPCCGAA	TTSRSACQRK	KKVTFDRLQV	LDQHYQDVLK	EVKAAASKVK	ANLLSVEEAC
HPCFG	TSSRSAAARQ	KKVTFDRLQV	LDDHYKNVLK	EVKERASGVK	GRLLSFEEAC
HPCGENANTI	TTSRSASQRQ	KKVTIDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HPCGENOM	TTSRSASLRQ	KKVAFDRMQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HPCHUMR	TTSRSAGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HPCJ	TTSRSASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HPCJCG	TTSRSASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	ARLLSIEEAC
HPCJK046	TTSRSAALRQ	KKVTFDRQQV	VDQHYDVLK	EMKARASTVS	AKLLSVEEAC
HPCJK049	TSSRSAAQRQ	KKVTFDRLQV	LDDHYNTTLK	EIKELASGVK	AELLSVEEAC
HPCJTA	TTSRSASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HPCJTB	TTSRSASLRQ	KKVTFDRLQV	LDDHYRDVLK	EVKAKASTVK	AKLLSVEEAC
HPCK3A	TSSRSASQRQ	KKVTFDRLQV	LDDHYKTALQ	EVKERASRVK	ARMLSIEEAC
HPCPLYPRE	TTSRSACQRQ	KKVTFDRLQV	LDQHYQDVLK	EVKAAASKVK	ANLLSVEEAC
HPCPOLP	TTSKSASLRA	KKVTFDRMQA	LDQHYDSVLK	DIKLAASKVT	ARLLTLEEAC
HPCPP	TTSRSASQRQ	KKVTFDRLQV	LDDHYRDVLK	DMKAKASTVK	AKLLSVEEAC
HPCUNKCD	TTSRSAGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
MKC1A	TTSRSASQRQ	KKVTFDRLQV	LDDHYRDVLK	DMKAKASTVK	AKLLSVEEAC
NDM59	TTSKSASLRA	KKVTFDRMQV	LDQHYDSVLK	DIKLAASKVS	ARLLTLEEAC
NZLI	TSSRSASQRQ	KKVTFDRLQV	LDDHYKTALK	EVKERASRVK	ARMLTIEEAC
SA13	TSSRSAGQRQ	KKVTFDRLQV	LDDHYREVVD	EMKRLASKVK	ARLLPLEEAC
Th580	TTSRSAGLRQ	KKVTFDRLQV	VDQHYQDVLK	EIKLRASTVH	ARLLSTEEAC
Type_3a_CB	TSSRSASQRQ	KKVTFDRLQV	LDDHYKTVLK	EVKERASRVK	ARMLTIEEAC
TypeV_D	TSSRSASQRQ	KKVTFDRLQV	LDDHYKTALK	EVKERASRVK	ARMLTIEEAC
VN004	TSSRSAATRQ	KKVTFDRVQL	LDQHYDVLK	EIKLRASHVK	AQLLSTEEAC
VN235	TTSRSASLRQ	KKVTFDRVQV	VDQHYDVLK	EIKTKASGVS	AKLLSVEEAC
VN405	TTSRSAAMRQ	KKVTFDRLQI	LDQHYNNVVK	EVKLASGVK	AKLLSVEEAC

	2551			2600	
BEBE1	ALTPPHSARS	KYGFGAKEVR	SLSRRAVDHI	KSVWEDLLED	HCSPIDTTIM
D89815	KLTPPHSAKS	KFGYGAKDVR	SLSSRAVNHI	RSVWKDLLED	TDTPPIQTTIM
ED43type_4	DLTPPHSARS	KFGYGKKDVR	SHSRKAINHI	SSVWKDLLED	NNTPIPTTIM
HC_C2	KLTPPHSAKS	KFGYGAKDVR	NLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
HC_G9	SLTPPHSARS	KFGYGAKDVR	SHSSKAIRHI	NSVWQDLLED	NTPPIDTTIM
HCU16326	KLTPPHSAKS	KFGYGAKDVR	SLSSRAVTHI	RSVWKDLLED	TETPISTTIM
HCV_H_CMV	SLTPPHSAKS	KFGYGAKDVR	CHARKAVAH	NSVWKDLLED	SVTPIDTTIM
HCV_J1	SLTPPHSAKS	KFGYGAKDVR	CHARKAVNHI	NSVWKDLLED	SVTPIQTTIM
HCV_J483	KLTPPHSAKS	KFGYGAKDVR	NLSSRAVNHI	RSVWEDLLED	TETPIDTTIM
HCV_J8	ALTPPHSAKS	KYGFGAKEVR	SLSRRAVNHI	RSVWEDLLED	QHTPIDTTIM
HCV_JK1	KLTPPHSAKS	KFGYGAKDVR	NLSSKAVNHI	HSVWKDLLED	TETPIDTTIM
HCV_JS	KLTPPHSAKS	KYGFGAKEVR	NLSSRAVNHI	RSVWEDLLED	TETPIDTTIM
HCV_K1_R1	RLTPPHSAKS	KFGYGAKDVR	NLSSGAVNHI	RSVWKDLLED	TETPIDTTIM
HCV_K1_R2	KLTPPHSAKS	KFGYGAKDVR	NLSSRAINHI	RSVWKDLLED	TETPIDTTIM
HCV_K1_R3	KLTPPHSAKS	KFGYGKKDVR	NLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
HCV_K1_S1	RLTPPHSAKS	KFGYGAKDVR	NLSSGAVNHI	RSVWKDLLED	TETPIDTTIM
HCV_K1_S2	KLTPPHSAKS	KFGYGAKDVR	NLSSRAINHI	RSVWKDLLED	TETPIDTTIM
HCV_K1_S3	KLTPPHSAKS	KFGYGKKDVR	NLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
HCV_L2	KLTPPHSAKS	KFGYGAKDVR	NLSSRAVNHI	RSVWKDLLED	TETPIDTTIM
HCV_N	RLTPPHSAKS	KFGYGAKDVR	NLSSRAINHI	RSVWEDLLED	TVTPIDTTIM
HCV12083	DLTPPHSARS	KYGFGAQDVR	SRASKAVDHI	PSVWEGLED	SDTPIPTTIM
HCV1480	GLTPPHSARS	KYGFGAKEVR	SLDKKALKHI	EGVWQDLLED	SDTPLPTTIM
HCVPOLYP	KLTPPHSARS	KFGYGAKDVR	NLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
HD_1	KLTPPLSARS	KFGYGAKDVR	NLSSKAVNHI	RSVWEDLLED	NVTPIDTTIM
HPCCGAA	SLAPPHSAKS	KFGYGAKDVR	CHARKAVAH	NSVWKDLLED	SVTPIDTTIM
HPCFG	SLVPPHSGRS	KYGYSAKDVR	SLSSKAMNQI	RSVWEDLLED	NSTPIPTTIM
HPCGENANTI	KLTPPHSARS	KFGYGAKDVR	NLSSKAINHI	RSVWKDLLED	TETPIDTTIM
HPCGENOM	KLTPPHSAKS	KFGYGAKDVR	NLSSKAVNHI	RSVWKDLLED	NETPIDTTIM
HPCHUMR	KLTPPHSAKS	KFGYGAKDVR	NLSSKAVNHI	HSVWKDLLED	TVTPIDTTIM

HPCJ	KLTPPHSAKS	KFGYGAKDVR	SLSSRAVNHI	TSVWKDLLED	TKTPIDTTIM
HPCJCG	KLTPPHSAKS	KFGYGAKDVR	SLSSRAVNHI	RSVWEDLLED	TETPIDTTIM
HPCJK046	DLTPAHSARS	KFGYGAKDVR	GRTSKALNHI	NSVWEDLLED	NVTPIPTTIM
HPCJK049	RLVPSHSARS	KFGYGAKEVR	SLSSKAINHI	NSVWEDLLED	NTTPIPTTIM
HPCJTA	KLTPPHSAKS	KFGYGAKDVR	NLSSKAINHI	RSVWKDLLED	TETPIDTTIM
HPCJTB	KLTPPHSAKS	KFGYGAKDVR	NLSSKAINHI	RSVWKDLLED	TETPIDTTIM
HPCK3A	ALVPPHSARS	KFGYSAKDVR	SLSSKAINQI	RSVWEDLLED	TTTPIPTTIM
HPCPLYPRE	SLTPPHSAKS	KFGYGAKDVR	CHARKAVTHI	NSVWKDLLED	NVTPIPTTIM
HPCPOLP	QLTPPHSAKS	KYGFGAKEVR	SLSGRAVNHI	KSVWKDLLED	TQTPIPTTIM
HPCPP	KLTPPHSAKS	KFGYGAKDVR	SLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
HPCUNKCD	KLTPPHSAKS	KFGYGAKDVR	SLSSRAVTHI	RSVWKDLLED	TETPISTTIM
MKC1A	KLTPPHSAKS	KFGYGAKDVR	SLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
NDM59	QLTPPHSAKS	KYGFGAKEVR	SLSGRAVNHI	KSVWKDLLED	SQTPIPTTIM
NZLI	ALVPPHSARS	KFGYSAKDVR	SLSSRAINQI	RSVWEDLLED	TTTPIPTTIM
SA13	GLTPPHSAKS	KYGYGAKEVR	SLDKKALNHI	KGWQDLLED	SDTPLPTTIM
Th580	SLTPPHSAKS	RYGYGARDVR	SHTSKAVKHI	DSVWEDLLED	NATPIPTTIM
Type_3a_CB	ALVPPHSARS	KFGYSAKDVR	SLSSRAINQI	RSVWEDLLED	TTTPIPTTIM
TypeV_D	ALVPPHSARS	KFGYSAKDVR	SLSSRAIDQI	RSVWEDLLED	TTTPIPTTIM
VN004	DLTPPHSAKS	KFGYGAKDVR	SHASKAINHI	NSVWADLLED	TQTPIPTTIM
VN235	ALTTPPHSAKS	KFGYGAKEVR	GLASKAVNHI	NSVWEDLLED	NSTPIPTTIM
VN405	SLTPPHSAKS	KFGYGAKDVR	SHTSKAINHI	NSVWEDLLED	NQTPIPTTIM

	2601			2650	
BEBE1	AKNEVFCVDP	TKGGKKPARL	IVYPDLGVRV	CEKMALYDIT	QKLPVAVMGQ
D89815	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
ED43type_4	AKNEVFAVNP	AKGGRKPARL	IVYPDLGSRV	CEKRALHDVI	KKTALAVMGA
HC_C2	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HC_G9	AKNEVFCVKP	EKGGRKPARL	IVYPDLGVRV	CEKRALYDVV	QQLPIAVMGT
HCU16326	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_H_CMV	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	SKLPLAVMGS
HCV_J1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	SKLPPAVMGS
HCV_J483	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_J8	AKNEVFCIDP	TKGGKKPARL	IVYPDLGVRV	CEKMALYDIA	QKLPKAIMGP
HCV_JK1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_JS	AKSEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_K1_R1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_K1_R2	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGA
HCV_K1_R3	AKNEVFCVQP	EKGGRKAARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_K1_S1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_K1_S2	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGP
HCV_K1_S3	AKNEVFCVQP	EKGGRKAARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_L2	AKSEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGP
HCV_N	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV12083	AKNEVFCVDP	SKGGRKPARL	IVYPDLGVRV	CEKMALYDVT	QKLPQAVMGP
HCV1480	AKNEVFAVEP	SKGGRKPARL	IVYPDLGVRV	CEKRALYDVA	QKLPALMGP
HCVPOLYP	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGP
HD_1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPHTVMGS
HPCCGAA	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	SKLPLAVMGS
HPCFG	AKNEVFSVNP	AKGGRKPARL	IVYPDLGVRV	CEKRALYDVI	QKLSIATMGP
HPCGENANTI	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCGENOM	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCHUMR	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCJ	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCJCG	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGP
HPCJK046	AKNEVFCVDV	SKGGRKPARL	IVYPDLGVRV	CEKRALYDVT	RKLPVAVMGA
HPCJK049	AKNEVFAVAP	HKGGRKPARL	IVYPDLGVRV	CEKRALYDVI	QKLPASAIMGS
HPCJTA	AKSEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCJTB	AKSEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCK3A	AKNEVFCVDP	AKGGRKAARL	IVYPDLGVRV	CEKRALYDVI	QRLSIETMGS
HPCPLYPRE	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	TKLPLAVMGS
HPCPOLP	AKNEVFCVDP	TKGGKKAARL	IVYPDLGVRV	CEKMALYDIT	QKLPQAVMGA

HPCPP	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCUNKCD	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
MKC1A	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
NDM59	AKNEVFCVDP	AKGGKKAARL	IVYPDLGVRV	CEKMALYDVT	QKLPQAVMGA
NZLI	AKNEVFCVDP	AKGGRKPAPL	IVYPDLGVRV	CEKRALYDVI	QKLSIETMGP
SA13	AKNEVFAVEP	SKGGKKPARL	IVYPDLGVRV	CEKRALYDIA	QKLPTALMGP
Th580	AKNEVFCVDP	SKGGRKPAPL	IVYPDLGVRV	CEKMALYDVT	QKLPTVMGS
Type_3a_CB	AKNEVFCVDP	AKGGRKPAPL	IVYPDLGVRV	CEKRALYDVI	QKLAJETIGS
TypeV_D	AKNEVFCVDP	ARGGRKRARL	IVYPDLGVRV	CEKRVLYDVI	QKLSIETMGT
VN004	AKNEVFCVDA	SKGGRKSAARL	IVYPDLGVRV	CEKRALFDVT	RKLPTAIMGD
VN235	AKNEVFCVDA	QKGGRKPARL	IVYPDLGVRV	CEKRALYDVT	QKLPIAVMGA
VN405	AKNEVFCADV	SKGGRKPAPL	IVYPDLGVRV	CEKRALYDVT	RKLPTAIMGD

	2651			2700	
BEBE1	SYGFQYSPAQ	RVDFLQAWK	EKKTPMGFSY	DTRCFDSTVT	ERDIRTEESI
D89815	SYGFQYSPKQ	RVEFLVNTWK	AKKCPMGFSY	DTRCFDSTVT	ENDIRVEESI
ED43type_4	AYGFQYSPAQ	RVEFLLTAWK	SKNDPMGFSY	DTRCFDSTVT	EKDIRVEEEV
HC_C2	SYGFQYSPGQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRIEESI
HC_G9	SYGFQYSPAQ	RVDFLLNAWK	SKKNPMGFSY	DTRCFDSTVT	EADIRTEEDL
HCU16326	SYGFQYSPKQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRVEESI
HCV_H_CMV	SYGFQYSPGQ	RVEFLVQAWK	SKKTPMGFPY	DTRCFDSTVT	ESDIRTEEAI
HCV_J1	SYGFQYSPGQ	RVEFLVQAWK	SKKTPMGFSY	DTRCFDSTVT	ESDIRTEEAI
HCV_J483	SYGFQYSPKQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ESDIRVEESI
HCV_J8	SYGFQYSPAQ	RVDFLKAWG	SKKDPMGFSY	DTRCFDSTVT	ERDIRTEESI
HCV_JK1	SYGFQYSPGQ	RVEFLVNAWK	SKKNPMGFAY	DTRCFDSTVT	ESDIRVEESI
HCV_JS	SYGFQYSPKQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRVEESI
HCV_K1_R1	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ESDIRVEESI
HCV_K1_R2	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ENDIRVEESI
HCV_K1_R3	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFAY	DTRCFDSTVT	ENDIRTEESI
HCV_K1_S1	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ESDIRVEESI
HCV_K1_S2	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ESDIRVEESI
HCV_K1_S3	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFAY	DTRCFDSTVT	ENDIRVEESI
HCV_L2	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFSY	DTRCFDSTVT	ESDIRTEESI
HCV_N	SYGFQYSPGQ	RVEFLVKAWK	SKKNPMGFSY	DTRCFDSTVT	ENDIRVEESI
HCV12083	AYGFQYSPNQ	RVEYLLKMWR	SKKVPMGFSY	DTRCFDSTVT	ERDIRTENDI
HCV1480	SYGFQYSPAQ	RVDFLKAWK	SKKIPMAFSY	DTRCFDSTIT	EHDIMTEESI
HCVPOLYP	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ESDIRVEESI
HD_1	SYGFQYSPGQ	RVEFLVNTWK	SKKCPMGFAY	DTRCFDSTVT	ENDIRVEESI
HPCCGAA	SYGFQYSPGQ	RVEFLVQAWK	SKKTPMGLSY	DTRCFDSTVT	ESDIRTEEAI
HPCFG	AYGFQYSPKQ	RVEHLLKMWT	SKKTPLGFSY	DTRCFDSTVT	EHDIRTEEGI
HPCGENANTI	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFSY	DTRCFDSTVT	ESDIRVEESI
HPCGENOM	SYGFQYSPGQ	RVEFLLNAWK	SKKNPMGFSY	DTRCFDSTVT	QNDIRVEESI
HPCHUMR	SYGFQYSPGQ	RVEFLVNTWK	SKKNPMGFSY	DTRCFDSTVT	ENDIRVEESI
HPCJ	SYGFQYSPGQ	RVEFLVKTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRIEESI
HPCJCG	SYGFQYSPGQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRTEESI
HPCJK046	AYGFQYSPSQ	RVEYLLKIWR	SKKTPMGFSY	DTRCFDSTVT	ERDIRTEESI
HPCJK049	AYGFQYSPKQ	RVEYLLKMWN	SKKTPLGFSY	DTRCFDSTVT	EQDIRVEESI
HPCJTA	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFSY	DTRCFDSTVT	ESDIRVEESI
HPCJTB	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFSY	DTRCFDSTVT	ESDIRVEESI
HPCK3A	AYGFQYSPRQ	RVERLLKMWT	SKKTPLGFSY	DTRCFDSTVT	GQDIRVEEAV
HPCPLYPRE	SYGFQYSPGQ	RVEFLVQAWK	SKKTPMGFSY	DTRCFDSTVT	ESDIRTEEAI
HPCPOLP	SYGFQYSPAQ	RVEFLKAWA	EKKDPMGFSY	DTRCFDSTVT	ERDIRTEESI
HPCPP	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFAY	DTRCFDSTVT	ENDIRTEESI
HPCUNKCD	SYGFQYSPKQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRVEESI
MKC1A	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFAY	DTRCFDSTVT	ENDIRTEESI
NDM59	SYGFQYSPAQ	RVEFLKAWA	EKKDPMGFSY	DTRCFDSTVT	ERDIRTEESI
NZLI	AYGFQYSPQQ	RVERLLKMWT	SKKTPLGFSY	DTRCFDSTVT	EQDIRVEEEI
SA13	SYGFQYSPAQ	RVEFLKAWA	SKKTPMAFSY	DTRCFDSTVT	EHDIMTEESI
Th580	AYGFQYSPSQ	RVEYLLKMWR	SKKTPMGFSY	DTRCFDSTVT	ERDIRTEEDI
Type_3a_CB	AYGFQYSPQQ	RVERLLKMWT	SKKTPLGFSY	DTRCFDSTVT	EQDIRVEEEI
TypeV_D	AYGFQYSPQQ	RVERLLKMWT	SKKTPLGFSY	DTRCFDSTVT	EQDFRVEEEI

VN004	AYGFQYSPQQ	RVDRLKMW	SKKTPMGFSY	DTRCFDSTVT	ERDIRTEQDI
VN235	AYGFQYSPKQ	RVDYLLKMW	SKKTPMGFSY	DTRCFDSTVT	ERDIRTEEDI
VN405	AYGFQYSPKQ	RVDQLLKMWR	SKKTPMGFSY	DTRCFDSTVT	EHDIKTERDV
2701					2750
BEBE1	YLSCSLPEEA	RTAIHSLTER	LYVGGPMTNS	KGQSCGYRRC	RASGVLTTSM
D89815	YQCCDLAPEA	RQAIRSLTER	LYIGGPMTNS	KGQNCGYRRC	RASGVLTTSC
ED43type_4	YQCCDLEPEA	RKVITALTDR	LYVGGPMHNS	KGDLGCGYRRC	RATGVYTTSF
HC_C2	YQCCDLAPEA	KQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HC_G9	YQSCDLVPEA	RAAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCU16326	YQCCDLAPEA	KLAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_H_CM	YQCCDLDPQA	RVAIKSLTER	LYVGGPLTNS	RGENCYRRC	RASGVLTTSC
HCV_J1	YQCCDLDPQA	RVAIRSLTER	LYVGGPLTNS	RGENCYRRC	RASGVLTTSC
HCV_J483	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_J8	YQACSLPQEA	RTVIHSLTER	LYVGGPMTNS	KGQSCGYRRC	RASGVFTTSM
HCV_JK1	YQCCDLAPEA	RQVIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTNC
HCV_JS	YQCCDLAPEA	KLAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_R1	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_R2	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_R3	YQCCDLAPEA	RQVIRSLTER	LYVGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_S1	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_S2	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_S3	YQCCDLAPEA	RQVIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_L2	YQCCDLAPEA	KQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASVVLTTSC
HCV_N	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQSCGYRRC	RASGVLTTSC
HCV12083	YQSCQLDPVA	RRVVSSLTER	LYVGGPMANS	KGQSCGYRRC	RASGVLPTSM
HCV1480	YQSCDLQPEA	RVAIRSLTQR	LYCGGPMYNS	KGQCGYRRC	RASGVFTTSM
HCVPOLYP	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HD_1	YQCCDLGPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCCGAA	YQCCDLDPQA	RVAIKSLTER	LYVGGPLTNS	RGENCYRRC	RASVLTSTSC
HPCFG	YQCCDLEPEA	RKAISALTER	LYIGGPMYNS	KGLQCGYRRC	RASGVLPTSF
HPCGENANTI	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCGENOM	YQCCDLAPEA	RRAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCHUMR	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCJ	YQCCDLAPEA	RQVIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCJCG	YQCCDLAPEA	RQAIRSLTER	LYVGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCJK046	YQCCDLDPVA	RKAISSLTER	LYVGGPMYNS	KGQSCGYRRC	RASGVLPTSM
HPCJK049	YQACDLKDEA	RRVITSLTER	LYCGGPMFNS	KGQHCYRRC	RASGVLPTSF
HPCJTA	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCJTB	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCK3A	YQCCNLEPEP	GQAISSLTER	LYCGGPMNNS	KGAQCGYLR	RASGVLPTSF
HPCPLYPRE	YQCCDLDPQA	RVAIKSLTER	LYVGGPLTNS	RGENCYRRC	RASGVLTTSC
HPCPOLP	YRACSLPEEA	HTAIHSLTER	LYVGGPMFNS	KGQTCGYRRC	RASGVLTTSM
HPCPP	YQCCDLDPQA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RVSGVLTTSC
HPCUNKCD	YQCCDLAPEA	KLAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
MKC1A	YQCCDLDPQA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RVSGVLTTSC
NDM59	YRACSLPEEA	HTAIHSLTER	LYVGGPMLNS	KGQTCGYRRC	RASGVLTTSM
NZLI	YQCCNLEPEA	RKVISSSLTER	LYCGGPMFNS	KGAQCGYRRC	RASGVLPTSF
SA13	YQSCDLQPEA	RAAIRSLTQR	LYCGGPMYNS	KGQCGYRRC	RASGVFTTSM
Th580	YQSCQLDPTA	RKAISSLTER	LYCGGPMFNS	KGESCGYRRC	RASGVLTTSL
Type_3a_CB	YQCCNLEPEA	RKVISSSLTER	LYCGGPMFNS	KGAQCGDRRC	RASGVLPTSF
TypeV_D	YQCCNLEPEA	RKVISSSLTER	LYCGGPMFNS	KGAQCGYRRC	RASGVLPTSF
VN004	YLSCQLDPQA	RKVIESLTER	LYVGGPMYNS	KGQLCGQRR	RASGVLPTSM
VN235	YQCCQLDPVA	KKAITSALTER	LYCGGPMYNS	RGQSCGYRRC	RASGVLTTSL
VN405	YLSCQLDPVA	RKAIESLTER	LYIGGPMYNS	RGQLCGTRRC	RASGVLTTSL
2751					2800
BEBE1	GNTLTCTYVKA	KAACNAAGIV	APTMLVCGDD	LVVISESQGV	EEDERNLRVF
D89815	GNTLTCTYLKA	AAACRAAKLQ	DCTMLVCGDD	LVVICDSAGT	QEDAASLRVF
ED43type_4	GNTLTCTYLKA	TAAIRAAALR	DCTMLVCGDD	LVVIAESDGV	EEDNRALRAF
HC_C2	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF

HC_G9	GNTITCYLKA	SAACRAAKLR	DCTMLVCGDD	LVVICESAGV	QEDAANLRAF
HCU16326	GNTLTCYLKA	TAACRAAKLR	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HCV_H_CMR	GNTLTCYIKA	RAARRAAGLQ	DCTMLVCGDD	LVVICESAGV	QEDAASLRAF
HCV_J1	GNTLTCYIKA	RAACRAAGLQ	DCTMLVCGDD	LVVICESAGV	QEDAASLRAF
HCV_J483	GNTLTCYLKA	TAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAAALRVF
HCV_J8	GNTMTCYIKA	LAACKAAGIV	DPVMLVCGDD	LVVISESQGN	EEDERNLRAF
HCV_JK1	GNTLTCYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_JS	GNTLTCYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_R1	GNTLTCYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_R2	GNTLTCYLKA	TAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_R3	GNTLTCYLKA	AAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_S1	GNTLTCYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_S2	GNTLTCYLKA	TAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_S3	GNTLTCYLKA	AAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_L2	GNTLTCYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAANLRAF
HCV_N	GNTLTCYLKA	SAACRAAKLQ	DCTMLVNGDD	RVVICESAGT	QEDAASLRVF
HCV12083	GNTLTCYLKA	QAACRAANIK	DCDMLVCGDD	LVVICESAGV	QEDTASLRAF
HCV1480	GNTMTCYIKA	LASCRAAKLR	DCTLLVCGDD	LVAICESQGT	HEDEASLRAF
HCVPOLYP	GNTLTCYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HD_1	GNTLTCYLKA	TAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAANLRVF
HPCCGAA	GNTLTRYIKA	RAACRAAGLQ	DCTMLVCGDD	LVVICESAGV	QEDAASLRAF
HPCFG	GNTITCYIKA	TAASRAAGLK	NPSFLVCGDD	LVVISESCGV	EEDRTALRAF
HPCGENANTI	GNTLTCYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HPCGENOM	GNTLTCYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCHUMR	GNTLTCYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCJ	GNTLTCYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCJCG	GNTLTCYLKA	TAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAAALRAF
HPCJK046	GNTLTCYLKA	MAACKAAGLK	NFDMLVCGDD	LVVISESLGV	SEDASALRAF
HPCJK049	GNTVTCYLKA	KAATKAAGIK	DPSFLVCGDD	LVVIAESAGI	DEDKSALRAF
HPCJTA	GNTLTCYLKA	TAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCJTB	GNTLTCYLKA	TAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCK3A	GNTITCYIKA	TAAARAAGLR	NPDFLVCDD	LVVVAESDGV	DEDRAALRAF
HPCPLYPRE	GNTLTCYIKA	RAACRAAGLQ	DCTMLVCGDD	LVVICESAGV	QEDAASLRAF
HPCPOLP	GNTITCYVKA	LAACKAAGII	APTMLVCGDD	LVVISESQGT	EEDERNLRAF
HPCPP	GNTLTCYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICDSAGT	QEDAASLRVF
HPCUNKCD	GNTLTCYLKA	TAACRAAKLR	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
MKC1A	GNTLTCYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICDSAGT	QEDAASLRVF
NDM59	GNTITCYIKA	LAACKAAGIV	APTMLVCGDD	LVVISESQGT	EEDERNLRAF
NZLI	GNTITCYIKA	TAAKAANLR	NPDFLVCDD	LVVVAESDGV	DEDRAALRAF
SA13	GNTMTCYIKA	LASCRAAKLR	DCTLLVCGDD	LVAICESQGT	HEDEASLRAF
Th580	GNTLTCYLKA	QAACRAANIK	NFDMLVCGDD	LVVICESAGV	QEDVVALRAF
Type_3a_CB	GNTITCYIKA	TAAANGAGLR	NPDFLVCDD	LVVVAESDGV	DEDGALRAF
TypeV_D	GNTITCYIKA	TAAKAAGLR	NPDFLVCDD	LVVVAESDGV	DEDRTALRAF
VN004	GNTVTCFLKA	TAACRAAGFT	DYDMLVCGDD	LVVVTESAGV	NEDIANLRAF
VN235	GNTLTCYLKA	QAACRAAKLK	DFDMLVCGDD	LVVISESMGV	AEDASALRAF
VN405	GNTMTCFIKA	EAACRAAGLT	NYDMLVCGDD	LVVIAESAGV	QEDASNLRRAF

	2801				2850
BEBE1	TEAMTRYSAP	PGDPPKAEYD	LELITSCSSN	VSVALDPRGR	RRYYLTRDPT
D89815	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
ED43type_4	TEAMTRYSAP	PGDAPQPAYD	LELITSCSSN	VSVAHDTVTK	KVYYLTRDPE
HC_C2	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HC_G9	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHGAGK	RVYYLTRDPE
HCU16326	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_H_CMR	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHGAGK	RVYYLTRDPT
HCV_J1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHGAGK	RVYYLTRDPT
HCV_J483	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_J8	TEAMTRYSAP	PGDLPRPEYD	LELITSCSSN	VSVALDSRGR	RRYFLTRDPT
HCV_JK1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_JS	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_K1_R1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT

HCV_K1_R2	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HCV_K1_R3	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HCV_K1_S1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HCV_K1_S2	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HCV_K1_S3	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HCV_L2	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HCV_N	TEAMTRYSAP	PGDLPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HCV12083	TDAMTRYSAP	PGDAPQPTYD	LELITSCSSN	VSVAHGNGK	KYYYLTRDCT
HCV1480	TEAMTRYSAP	PGDPPVPAYD	LELVTSCSSN	VSVARDASGN	RIYYLTRDPQ
HCVPOLYP	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HD_1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HPCCGAA	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHGAGK	RVYYLTRDPT
HPCFG	TEAMTRYSAP	PGDAPQPTYD	LELISSCSSN	VSVACDGAGK	RYYYLTRDPE
HPCGENANTI	TEAMTRYSAP	PGDLPQPEYD	QELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HPCGENOM	TEAMTRYSAP	PGDLPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HPCHUMR	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HPCJ	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HPCJCG	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HPCJK046	TDAMTRYSAP	PGDEPHPEYD	LEHITSCSSN	VSVAHDTGQ	RYYYLTRDPT
HPCJK049	TEAMTRYSAP	PGDPPQPTYD	LELITSCSSN	VSVAHGAGK	RYYYLTRDPE
HPCJTA	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HPCJTB	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HPCK3A	TEAMTRYSAP	PGDAPQPTYD	LELITSCSSN	VSVARDDK GK	RYYYLTRDAT
HPCPLYPRE	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHGAGK	RVYYLTRDPT
HPCPOLP	TEAMTRYSAP	PGDPPRPEYD	LELITSCSSN	VSVALGPQGR	RYYYLTRDPT
HPCPP	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
HPCUNKCD	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
MKC1A	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDasGK	RVYYLTRDPT
NDM59	TEAMTRYSAP	PGDPPRPEYD	LELITSCSSN	VSVAXGPQGR	RYYYLTRDPT
NZLI	TEAMTRYSAP	PGDAPQATYD	LELITSCSSN	VSVARDDKGR	RYYYLTRDAT
SA13	TEAMTRYSAP	PGDPPVPAYD	LELVTSCSSN	VSVAHDasGN	RVYYLTRDPQ
Th580	TDAMIRYSAP	PGDAPQPTYD	LELITSCSSN	VSVAHDTGQ	RYYYLTRDCT
Type_3a_CB	TEAMTRYSAP	PGDAPQPTYD	LELITSCSSN	VSVARDDKGR	RYYYLTRDAT
TypeV_D	TEAMTRYSAP	PGDAPQPTYD	LELITSCSSN	VSVALDNK GK	RYYYLTRDAT
VN004	TEAMTRYSAT	PGDEPSPTYD	LELITSCSSN	VSVAHGDGGR	RYYYLTRDPV
VN235	TEAMTRYSAP	PGDDPQPEYD	LELITSCSSN	VSVAHGAGQ	RYYYLTRDPL
VN405	TEAMTRYSAP	PGDEPHPAYD	LELITSCSSN	VSVAHDTGQ	RYYYLTRDPT

	2851				2900
BEBE1	TPLARAAWET	ARHSPVNSWL	GNI IQYAPTV	WVRMVLMT HF	FSVLMAQDTL
D89815	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMT HF	FSILLAQEQL
ED43type_4	TPLARAVWET	VRHTPVNSWL	GNIIVYAPTI	WVRMILMT HF	FSILQSQEAL
HC_C2	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMT HF	FSILLAQEQL
HC_G9	TPLARAAWET	ARHTPVNSWL	GNIIMFAPTL	WVRMVLMT HF	FSILIAQEHL
HCU16326	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMT HF	FSILLAQEQL
HCV_H_CMR	TPLARAAWET	ARHTPVNSWL	GNIIMFAPTL	WARMILMT HF	FSVLIARDQL
HCV_J1	TPLARAAWET	ARHTPVNSWL	GNIIMFAPTL	WARMILMT HF	FSVLIARDQL
HCV_J483	IPLARAAWET	ARHTPVNSWL	GNIIMYAPAL	WARMILMT HF	FSILLAQEQL
HCV_J8	TPITRAAWET	VRHSPVNSWL	GNI IQYAPTI	WVRMVIMT HF	FSILLAQDTL
HCV_JK1	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMT HF	FSILLAQEQL
HCV_JS	TPIARA AWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMT HF	FSILLAQEQL
HCV_K1_R1	TPLARAAWET	AKSTPVNSWL	GNIIMFAPTL	WVRMILMT HF	FSILLAQEQL
HCV_K1_R2	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMT HF	FSILLAQEQL
HCV_K1_R3	TPLARAAWET	ARHTPVNSWL	GNIIMYGPTL	WARMILMT HF	FSNLLAQEYL
HCV_K1_S1	TPLARAAWET	ARSTPVNSWL	GNIIMFAPTL	WVRMILMT HF	FSILLAQEQL
HCV_K1_S2	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMT HF	FSILLAQEQL
HCV_K1_S3	TPLARAAWET	ARHTPVNSWL	GNIIMYGPTL	WARMILMT HF	FSNLLAQEYL
HCV_L2	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMT HF	FSILLAQEQL
HCV_N	TPIARA AWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMT HF	FSILLAQEQL
HCV12083	TPLARA AWET	ARHTPVNSWL	GNIIMFAPTI	WVRMVLMT HF	FSILQSQEQL
HCV1480	VPLAKA AWET	AKHSPVNSWL	GNIIMYAPTL	WARIVLMT HF	FSVLQSQEQL

HCVPOLYP	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
HD_1	TPLARAAWET	ARHTSVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
HPCCGAA	TPLARAAWET	ARHTPVNSWL	GNIIMFAPTL	WARMILMTHF	FSVLIARDQL
HPCFG	TPLARAAWET	ARHTPVNSWL	GNIIMFAPTI	WVRMVLITHF	FSILQAQEQL
HPCGENANTI	TPLARAAWAT	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
HPCGENOM	IPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
HPCHUMR	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
HPCJ	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
HPCJCG	TPLARAAWET	VRHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
HPCJK046	NVLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVLMTTHF	FGILQPQEQL
HPCJK049	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVIMTHF	FSILQAQEQL
HPCJTA	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
HPCJTB	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
HPCK3A	TPLARAAWET	ARHTPVNSWL	GSIIIMYAPTI	WVRMVMMTHF	FSILQSQEIL
HPCPLYPRE	TPLARAAWET	ARHTPVNSWL	GNIIMFAPTL	WARMILMTHF	FSVLIARDQL
HPCPOLP	TPIARAAWET	VRHSPVNSWL	GNI IQYAPTI	WARMVLMTHF	FSILMAQDTL
HPCPP	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
HPCUNKCD	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
MKC1A	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
NDM59	TPLSRAAWET	VRHSPVNSWL	GNI IQYAPTI	WVRMVLMTTHF	FSILMAQDTL
NZLI	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVMMTHF	FSILQSQEIL
SA13	VPLARAAWET	AKHSPVNSWL	GNIIMYAPTL	WARIVLMTHF	FSVLQSQEQL
Th580	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVLMTTHF	FSILQCQEQL
Type_3a_CB	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVMMTHF	FSILQSQEIL
TypeV_D	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVMMTHF	FSILQSQEIL
VN004	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVLMTTHF	FQILQAQETL
VN235	TPLSRAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVLMTTHF	FAILQSQEIL
VN405	TPLSRAAWET	ARHTPVNSWL	GNIIMYAPAI	WVRMVLMTTHF	FQILQAQEQL

	2901				2950
BEBE1	DQDLNFEMYG	AVYSVSPLDL	PAIIERLHGL	EAFSLHSYSP	HELTRVAAAL
D89815	EKALDCQIYG	ATYSIEPLDL	PQIIQRLHGL	SAFSLHSYSP	GEINRVASCL
ED43type_4	EKALDFDIYG	VTYSITPLDL	PAIIQRLHGL	SAFTLHGYS	HELN RVAGAL
HC_C2	EKALECQIYG	ACYSIEPLDL	PQIIERLHGL	SAFSLHSYSP	GEINRVASCL
HC_G9	EKALDCEIYG	AVHSVQPLDL	PEIIQRLHGL	SAFSLHSYSP	GEINRVAACL
HCU16326	EKTLDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFSLHSYSP	GEINRVASCL
HCV_H_CM	EQALNCEIYA	ACYSIEPLDL	PPIIQRLHGL	SAFLLHSYSP	GEVNRVAACL
HCV_J1	EQALDCEIYG	ACYSIEPLDL	PPIIQRLHGL	SAFSLHSYSP	GEINRVAACL
HCV_J483	EQALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFSLHSYSP	GEINRVASCL
HCV_J8	NQNLNFEMYG	AVYSVNPLDL	PAIIERLHGL	EAFSLHTYSP	HELSRVAATL
HCV_JK1	EKALGCQIYG	ATYFIEPLDL	PQIIQRLHGL	SAFSLHSYSP	GEINRVASCL
HCV_JS	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFSLHSYSP	GEINRVASCL
HCV_K1_R1	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFSLHSYSP	GEINRVASCL
HCV_K1_R2	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFSLHSYSP	GEINRVASCL
HCV_K1_R3	DKALDCQIYE	AIYSIGPLDL	PQVIQRLHGL	SAFSLHSYSP	GEINRVASCL
HCV_K1_S1	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFSLHSYSP	GEINRVASCL
HCV_K1_S2	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFSLHSYSP	GEINRVASCL
HCV_K1_S3	DKALDCQIYE	AIYSIGPLDL	PQVIQRLHGL	SAFSLHSYSP	GEINRVASCL
HCV_L2	EKALECQIYG	ACYSIEPLDL	PQIIERLHGL	SAFSLHSYSP	GEINRVASCL
HCV_N	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFSLHSYSP	GEINRVASCL
HCV12083	EKAFDFDIYG	VTYSVSPLDL	PAIIQRLHGM	AAFSLHGYS	VELNRVAGAL
HCV1480	EKTLAFEMYG	SVYSVTPLDL	PAIIQRLHGL	SAFSLHSYSP	SEINRVASCL
HCVPOLYP	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFSLHSYSP	GEINRVASCL
HD_1	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFSLHSYSP	GEINRVASCL
HPCCGAA	EQALNCEIYG	ACYSIEPLDL	PPIIQRLHGL	SAFSLHSYSP	GEINRVAACL
HPCFG	ERALDFEMYG	ATYSVTPLDL	PAIIERLHGL	SAFSLHGYS	TELNRVAGAL
HPCGENANTI	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFSLHSYSP	GEINRVASCL
HPCGENOM	EKALDCQIYG	AYYSIEPLDL	PQIIERLHGL	SAFSLHSYSP	GEINRVASCL
HPCHUMR	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFSLHSYSP	GEINRVASCL
HPCJ	GKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFSLHSYSP	GEINRVASCL
HPCJCG	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFSLHSYSP	GEINRVASCL

HPCJK046	HKALDFDFMYG	VTYNITPLDL	PQIIQRLHGM	AAFSLHGYS	GELNRVGACL
HPCJK049	EKALDFEMYG	AVYSVTPLDL	PAIERLHGL	SAFSLHSYSP	VELNRVAGAL
HPCJTA	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFSLHSYSP	GEINRVASCL
HPCJTB	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFSLHSYSP	GEINRVASSL
HPCK3A	DRPLDFEMYG	ATYSVTPLDL	PAIERLHGL	SAFSVHSYSP	VELNRVAGTL
HPCPLYPRE	EQALDCEIYG	ACYSIEPLDL	PPIIQRLHGL	SAFSLHSYSP	GEINRVAACL
HPCPOLP	DQNLNFEMYG	AVYSVSPLDL	PAIERLHGL	DAFSLHTYTP	HELTRVASAL
HPCPP	EKALDCQIYG	ATYSIEPLDL	PQIIQRLHGL	SAFSLHSYSP	GEINRVASCL
HPCUNKCD	EKTLDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFSLHSYSP	GEINRVASCL
MKC1A	EKALDCQIYG	ATYSIEPLDL	PQIIQRLHGL	SAFSLHSYSP	GEINRVASCL
NDM59	DQNLNFEMYG	XVYSVSPLDL	PAIERLHGL	DAFSLHTYTP	HELTRVASAL
NZLI	DRPLDFEMYG	ATYSVTPLDL	PAIERLHGL	SAFTLHSYSP	VELNRVAGTL
SA13	EKALAFEMYG	SVYSVTPLDL	PAIIQRLHGL	SAFTLHSYSP	SEINRVSSCL
Th580	EALNFDMYG	VTYSVTPLDL	PAIIQRLHGM	AAFSLHGYS	TELNRVGASL
Type_3a_CB	DRPLDFEMYG	ATYSVTPLDL	PAIERLHGL	SAFTLHSYSP	VELNRVAGTL
TypeV_D	DRPLDFEMYG	ATYSVTPLDL	PAIERLHGL	SAFTLHSYSP	VELNRVAGTL
VN004	DRALDFDIYG	VTYSITPLDL	PVIIQRLHGM	AAFSLHGYS	DELNRVASCL
VN235	HKALDFDFMYG	VTYSVTPLDL	PYIIQRLHGM	AAFSLHGYS	GELNRVASCL
VN405	DKVLDFDFMYG	VTYSVSPLQL	PAIIQRLHGM	AAFSLHGYS	TELNRVGACL

	2951		3000		
BEBE1	RKLGAPPLRA	WKSARAVRA	SLISRGGSAA	TCGRYLFNWA	VRTKLKLTPL
D89815	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
ED43type_4	RKLGVPPLRA	WRHRARSVRA	KLIAQGGRAK	ICGIYLFNWA	VTKLKLTP
HC_C2	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HC_G9	RKLGVPPLRA	WRHRARSVRA	TLLSQGGRAA	ICGKYLFNWA	VTKLKLTP
HCU16326	RKLGVPPLRA	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HCV_H_CM	RKLGVPPLRA	WRHRARSVRA	RLLSRGGRAA	ICGKYLFNWA	VRTKLKLTPI
HCV_J1	RKLGVPPLRA	WRHRARSVRA	RLLSRGGRAA	ICGKYLFNWA	VRTKLKLTPI
HCV_J483	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGRYLFNWA	VRTKLKLTPI
HCV_J8	RKLGAPPLRA	WKSARAVRA	SLIAQGARA	ICGRYLFNWA	VTKLKLTP
HCV_JK1	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HCV_JS	RKLGVPPLRV	WRHRARGVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HCV_K1_R1	RKLGVPPLRT	WRHRARSVRA	KLLSQGGRAA	TCGRYLFNWA	VTKLKLTP
HCV_K1_R2	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	ICGKYLFNWA	VRTKLKLTPI
HCV_K1_R3	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
HCV_K1_S1	RKLGVPPLRT	WRHRARSVRA	KLLSQGGRAA	TCGRYLFNWA	VTKLKLTP
HCV_K1_S2	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	ICGKYLFNWA	VRTKLKLTPI
HCV_K1_S3	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
HCV_L2	RKLGVPPLRV	WRHRARRVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HCV_N	RKLGVPPLRV	WRHRARNVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
HCV12083	RKLGVLPSRA	WRHRARAVRA	KLIAQGGKAA	ICGKYLFNWA	VTKLKLTP
HCV1480	RKLGVPPLRA	WRHRARAVRA	KLIAQGGRAA	ICGIYLFNWA	VTKRKLTP
HCVPOLYP	RKLGVPPLRA	WRHRARSVRA	KLLSQGGRAA	TCGRYLFNWA	VTKLKLTP
HD_1	RKLGVPPLRV	WRHRARSVRA	KLLSPGGE	TCGKYLFNWA	VRTKLKLTPI
HPCCGAA	RKLGVPPLRA	WRHRAWVRA	RLLARGGKAA	ICGKYLFNWA	VRTKLKLTPI
HPCFG	RKLGIPPLRA	WRHRARAVRA	KLIAQGGKAR	ICGLYLFNWA	VRTKTKLTPL
HPCGENANTI	RKLGVPPLRA	WRHRARSVRA	KLLSQGGRAA	TCGRYLFNWA	VTKLKLTP
HPCGENOM	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
HPCHUMR	RKLGVPPLRV	WRHRARSVRA	RLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
HPCJ	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HPCJCG	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
HPCJK046	RKLGAPPLRA	WRHRARAVRA	KLIAQGGKAA	ICGMYLFNWA	VTKLKLTP
HPCJK049	RKLGIPPLRA	WRHRARAVRA	KLISQGGKAK	ICGLYLFNWA	VRTKAKLTPL
HPCJTA	RKLGVPPLRV	WRHRARSVRA	RLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HPCJTB	RKLGVPPLRV	WRHRARSVRA	RLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HPCK3A	RKLGCPPLRA	WRHRARAVRA	KLIAQGGRAK	ICGLYLFNWA	VRTKTKLTPL
HPCPLYPRE	RKLGVPPLRA	WRHRARSVRA	RLLARGGRAA	ICGKYLFNWA	VRTKLKLTPI
HPCPOLP	RKLGAPPLRA	WKSARAVRA	SLISRGGSAA	TCGRYLFNWA	VTKLKLTP
HPCPP	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HPCUNKCD	RKLGVPPLRA	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI

MKC1A	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VKTKLKLTP
NDM59	RKLGAPPLRA	WKSRRARAVRA	SLISRGGRAA	ICGRYLFNWA	VKTKLKLTP
NZLI	RKLGCPPLRA	WRHRARAVRA	KLIAQGGKAK	ICGLYLFNWA	VRTKTNLTPL
SA13	RKLGVPPLRA	WRHRARAVRA	KLIAQGGKAA	ICGIYLFNWA	VKTKRKLTP
Th580	RKLGAPPLRA	WRHRARAVRA	KLIAQGGKAA	ICGKYLFNWA	VKTKLKLTP
Type_3a_CB	RKLGCPPLRA	WRHRARAGRA	KLIAQGGKAK	ICGLYLFNWA	VRTKTKLTPL
TypeV_D	RKLGCPPLRA	WRHRARAVRA	KLIAQGGKAK	ICGLYLFNWA	VRTKTNLTPL
VN004	RKLGAPPLRA	WRHRARAVRA	KLIAQGGKAA	VCCKYLFNWA	IKTKLRLTPL
VN235	RKLGAPPLRA	WRHRARAVRA	KLIAQGGKHA	ICGKYLFNWA	VRTKTKLTPL
VN405	RKLGAPPLRA	WRHRARAVRA	KLIAQGGGAA	ICGKYLFNWA	VKTKLKLTP

	3001			3050	
BEBE1	PAARLLDLSS	WFTVSAGGGD	IYHSVSRARP	RLLLLGLLLL	CVGVGIFLLP
D89815	PEASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMWCLLLL	SVGVGIYLLP
ED43type_4	PAAAKLDLSS	WFTVGAGGGD	IYHSMHARP	RYLLLCLLIL	TVGVGIFLLP
HC_C2	PAASRLDLSS	WVAGYGGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HC_G9	PSASQLDLSS	WFTGGYSGGD	IYHSVSHVRP	RWFFWCLLLL	SVGVGIYLLP
HCU16326	PAASRLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HCV_H_CMR	AAAGRLDLSS	WFTAGYSGGD	IYHSVSHARP	RWFWFCLLLL	AAGVGIYLLP
HCV_J1	AAAGRLDLSS	WFTAGYSGGD	IYHSVSHARP	RWFWFCLLLL	AAGVGIYLLP
HCV_J483	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFLCCLLLL	SVGVGIYLLP
HCV_J8	PEASRLDLSS	WFTVGAGGGD	IYHSVSHARP	RLLLLCLLLL	SVGVGIFLLP
HCV_JK1	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMWCLLLL	SVGVGIYLLP
HCV_JS	PAASRLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMWCLLLL	SVGVGIYLLP
HCV_K1_R1	PAASQLDLSS	WVAGYSGGD	VYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HCV_K1_R2	PAASQLDLSS	WVAGYSGGD	IYHSVSRARP	RWFMWCLLLL	SVGVGIYLLP
HCV_K1_R3	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMWCLLLL	SVGVGIYLLP
HCV_K1_S1	PAASQLDLSS	WVAGYSGGD	VYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HCV_K1_S2	PAASQLDLSS	WVAGYSGGD	IYHSVSRARP	RWFMWCLLLL	SVGVGIYLLP
HCV_K1_S3	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMWCLLLL	SVGVGIYLLP
HCV_L2	PAASRLDLSS	WVAGYSGGD	IYHSVSHARP	RWFMLCLLLL	SVGVGIYLLP
HCV_N	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HCV12083	VSASKLDLSS	WVAGYDGGD	IYHSVSQARP	RFLLLGLLLL	TVGVGIFLLP
HCV1480	ADADRLDLSS	WFTVGAGGGD	IYHSMHARP	RNLLLCLLLL	SVGVGIFLLP
HCVPOLYP	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMWCLLLL	SVGVGIYLLP
HD_1	PAAFQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMWCLLLL	SVGVGIYLLP
HPCCGAA	TAAGRLDLSS	WFTAGYSGGD	IYHSVSHARP	RWFWFCLLLL	AAGVGIYLLP
HPCFG	PTAGQLDLSS	WFTVGVGGGD	IYHSVSRARP	RHLLLCLLLL	TVGVGIFLLP
HPCGENANTI	PAASQLDLSS	WVAGYGGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HPCGENOM	PAASRLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HPCCHUMR	PAASRLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HPCJ	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HPCJCG	PAASQLDLSS	WVAGYNGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HPCJK046	RDHRLDLSS	WVAGYSGGD	IFHSVSHARP	RVLLLCLLLL	TVGVGIFLLP
HPCJK049	PQAGLLDLSS	WFTVGAGGGD	IYHSVSRARP	RHLLLGLLLL	TVGVGIFLLP
HPCJTA	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMWCLLLL	SVGVGIYLLP
HPCJTB	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMWCLLLL	SVGVGIYLLP
HPCK3A	PAAGQLDLSS	WFTVGVGGGD	IYHSVSRARP	RYLLLCLLLL	TVGVGIFLLP
HPCPLYPRE	AAAGQLDLSS	WFTAGYSGGD	IYHSVSHARP	RWIWFCLLLL	AAGVGIYLLP
HPCPOLP	PEARLLDLSS	WFTVGAGGGD	IYHSVSRARP	RLLLLGLLLL	FVGVLFLLP
HPCPP	PEASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMWCLLLL	SVGVGIYLLP
HPCUNKCD	PAASRLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
MKC1A	PEASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMWCLLLL	SVGVGIYLLP
NDM59	PEARLLDLSS	WFTVGAGGGD	IYHSVSRARP	RLLLLSLLLL	LVGVGLFLLP
NZLI	PAAGQLDLSS	WFTVGVGGGD	IYHSVSRARP	RHLLLCLLLL	TVGVGIFLLP
SA13	ADADRLDLSS	WFTVGAGGGD	IYHSMHARP	RCILLCLLLL	TVGVGIFLLP
Th580	AAASQLDLSS	WVAGYDGGD	IYHSVSRARP	RLLLLGLLLL	TVGVGIFLLP
Type_3a_CB	PRAGQLDLSS	WFTVGVGGGD	IYHSVSRARP	RYLLLCLLLL	TVGVGIFLLP
TypeV_D	PATGQLDLSS	WFTVGVGGGD	IYHSVSRARP	RYLLLCLLLL	TVGVGIFLLP
VN004	RGASALDLSS	WFTSGYGGGD	VYHSASRARP	RFLLLCLLLL	SVGVGIFLLP
VN235	RGAANLDLSS	WVSGSGGGD	IFHSVSRARP	RNLLLCLLLL	TVGVGIFLLP

VN405	PDAARLDLSG WFISGFSGGD IYHSVSRARP RIFLLCLLLL SVGVGIFLLP
	3051
BEBE1	AR
D89815	NR
ED43type_4	AR
HC_C2	NR
HC_G9	NR
HCU16326	NR
HCV_H_CMR	NR
HCV_J1	NR
HCV_J483	NR
HCV_J8	AR
HCV_JK1	NR
HCV_JS	NR
HCV_K1_R1	NR
HCV_K1_R2	NR
HCV_K1_R3	NR
HCV_K1_S1	NR
HCV_K1_S2	NR
HCV_K1_S3	NR
HCV_L2	NR
HCV_N	N.
HCV12083	AR
HCV1480	AR
HCVPOLYP	NR
HD_1	NR
HPCCGAA	NR
HPCFG	AR
HPCGENANTI	NR
HPCGENOM	NR
HPCHUMR	NR
HPCJ	NR
HPCJCG	NR
HPCJK046	PR
HPCJK049	AR
HPCJTA	NR
HPCJTB	NR
HPCK3A	AR
HPCPLYPRE	NR
HPCPOLP	AR
HPCPP	NR
HPCUNKCD	NR
MKC1A	NR
NDM59	AR
NZLI	AR
SA13	AR
Th580	AR
Type_3a_CB	AR
TypeV_D	AR
VN004	AR
VN235	AR
VN405	AR

Table 23. HIV Fusion Construct

SEQ ID NO: 1934

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA
 GGAAAGCTGGTGGGCAAACCTCAACTGGGCCGGAGCTGCAATCCTGAAGGAGCCCGTCCACGG
 GGTGAATGCCGCTTGCCCTAAAGTCAGCTTCGAACCAATTAAGATCCCCATTCTACTGTGC
 ACCTGCCAAAGCTAAGTTTGTGGCCGCTTGGACCCTCAAGGCCGCTGCAAAAGCCTTCCCAGT
 GAGGCCCCAGGTGCCTCTGGGCGCCGCTAAACTCACACCACTGTGCGTCACTCTGGGAGCCGC
 TGCAGTGCTGGCAGAGGCCATGTCCCAAGTGAAGGTGTATCTGGCTTGGGTGCCCCGCCACAA
 GGGGGCCGCTGCAGCCATCTTTCAGTCTAGCATGACCAAGAAAACAACCTCTGTTCTGTGCCTC
 CGACGCTAAGAACATCCCTTATAATCCACAGTCTCAGGGCGTGGTCAAGCATCCCGTGCACGC
 CGGACCTATTGCTAACGTGACCGTGTACTATGGGGTCCCAGTGTGGAAGAAAGCCGCTGCACA
 GATGGCCGTGTTTATTACAAATTTCAAAAACGCCGCTGCATACCCCTCGCCAGCCTGAGATC
 CCTCTTCAACCTGACATTTCGGCTGGTGCTTTAAGCTGAACCGGATCCTGCAGCAACTGCTCTTT
 ATCAATGCTAAAATCCAGAACTTCCGCGTCTACTATAGGAAGGCTGCAGTGACTATCAAAATT
 GGCGGACAACTGAAGAAAGTGCCTCTCCAGCTGCCCCCTCTCAAGGCAATGACCAACAATCC
 CCTATCCCAGTCTGA

EP-HIV-1090 SEQ ID NO: 1935

MGMQVQIQSLFLLLLWVPGSRGKLVGKLNWAGAAILKEPVHGVNAACPKVSFEPKIPHYCAPA
 KAKFVAAWTLKAAAKAFPVRPQVPLGAAKLTPLCVTLGAAAVLAEAMSQVKVYLAWVPAHKG
 AAAAIFQSSMTKKTTLFCASDAKNIPYNPQSQGVVKHPVHAGPIANVTVYYGVPVWKAAAQMA
 VFIHNFKNAAA YPLASLRSLFNLTFGWCFKLNRI LQQLFINAKIQNFRVYYRKA AVTIKIGGQLKK
 VPLQLPPLKAMTNNPPIPV

Table 24. HBV GCR-3697 Fusion Construct

<p>GCR-3697</p> <p>SEQ ID NO: 1936</p>	<p><i>Polynucleotide</i></p> <p>1 Start ↑***</p> <p>ATGGGCATGTCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTGCTGTGGGTGCCAGGAAGCAGAGGCTTTCTCCTGTGCCCTGGGCATCCACCTGAACGCCGCTGCAAAGTACACCAGCTTCCCTGGCTGCTCAACGCCGCTGCCCGGTTACGCTGGCTGTCCCTGCTCGTGCCCTTCAACGCAGCCTTCCCCACTGCCTGGCCTTACGCTACATGA AAGCAGCCCTGGTGGTGGTCTGCTCCAGTTCAAGCCGGGGAGCCATCCTGCTCCTGTGCCTGATCTTTCTGCT CAACGCCGCTGCCCCACACCCTGTGGAAGGCTGGCATCCTGTACAAGAAAGCCTGGATGATGTGGTACTGGG GACCCAGCCTGTACAAGGCATATCCAGCCCTGATGCCCTGTACGCCCTGCATCGGAGCTGCCGCATGGCTGA GCCTCCTGGTGCCCTTCGTGAACGCCGCTGCCGGGTTCTGTGACAAGAATCCTGACCATCAACGCCGCAG CCATTCTATCCCTCCAGCTGGGCCTTCAAGGCAGCCGCCGAGTACCTGGTGAGCTTCGGAGTCTGGAACC TGCCCAGCGACTTCTTTCCAGCGTGAAAGCCGCAGCCTTCTGCCCTCCGACTTCTTTCCAGCGTGAAGGC CGCAGCCGATCTCCTGGACACCGCTAGCGCCCTGTACAACAGCTGGCCCAAGTTCGCCGTGCCCAACCTGAA GGCCGCAGCCAGCGCCATCTGCAGCGTGGTCAGACGGAAGCTGTCCCTCGATGTGAGCGCCGCTTTCTACAA CGCCGCCGCAAAGTTCGTGGCCGCCTGGACCCTGAAAGCCGCTGCCAAGGCAGCCAACGTGAGCATCCCTT GGACCCACAAAGGAGCCGAGGACTGAGCCGCTATGTGGCCAGACTGAACGCCGCTGCCAGCACCCCTGCC GAGACCACAGTGGTCAGACGGAAGCACCCCGCCGATGCCCCACCTGCTGAAGGCCGCGAGCCCGGTGGAT GTGCCTCAGACGGTTATCATCAACGCTTCTTCTGTGGCAGCCCTACAAGGCCGCTACATGGATGACGT GGTCTTGGGAGTGAACGCCCTCTGGTTCCACATCAGCTGCCTGACCTTCAAAGCCGCTGCCACACCCGCAAG AGTGACCGGAGGCGTGTTCAGGCTGCAGCCCTGACCTTCGCCCGGAGACCGTGTGGAGTACAAGCAGG CCTTACCTTACGCCCCACCTACAAGAAGCCGGCACCAGCTTTGTGTACGTCCCAAGCGCCCTGAATCCCG CAGACGGCCCCGGCCCCGACTGTGCCAGGTGTTCCCGATGCCACACCAACCGGATGGGGCCTGGGCCCT GGACCCGCGACACTACCTGCATACCCTGTGGAAGGCAGGAATCCTGTACAAGGCCCGGCCCTGGACC CCATCACACCGCTCTGCGGCAGGCCATCCTGTGCTGGGGCAGCTCATGACTCTGGCAGGACCCGGCCCCGG CGAATCCAGGCTGGTGGTGGACTTTAGCCAGTTCTCCAGAGGCAACGGACCCGGCCAGGACCCCTCTGTCT CGCCAGTTACCCAGCGCCATCTGCAGCGTGGTCGGACCTGGCCAGGACTGGTGCCTTCGTGCAGTGGTT CGTCGGCCTCAGCCCCACCGTCGGACCTGGCCCCGGCCTGCACCTCTACAGCCACCTATCATTCTGGGCTT CAGAAAGATCGGACCAGGCCCGGCTCCAGCAACCTGTCTGGCTCAGCCTGGACGTCAGCGCAGCCTTCG GACCCGGCCCTGGCCTGCAGAGCCTGACCAACCTGTCAAGCAACCTCAGCTGGCTGGGCCCAAGGACCC GGGCAGGCTTCTTTCTGCTCACCAGAATCCTGACCATCCCTCAGAGCGGCCCGGACCCAGGCTGAGCTTC GGCGTGTGGATTTCGACTCTCTCCCGCTACAGACCCCAATGCCCCATCGGCCAGGACCCGGCGCTCGGA CCTCTGACTGTGAACGAGAAGCGGAGACTGAAGCTGATCGGCCCGGACCCAGGCAACAGTGCTTCAGGAA GCTCCCTGTGAACAGACCTATCAGACTGGGGCCCCGGACCCGGCGCAGCCAACCTGGATTCTGAGAGGCACCA GCTTCGTGTACGTCCCTGGACCCGGCCTGGCAAGCAAGCCTTACCTTACGCCCCACCTACAAGGCATTCC TGTGCGGA</p> <p>↓ Stop 2232</p>
<p>GCR-3697</p> <p>SEQ ID NO: 1937</p>	<p><i>Polypeptide</i></p> <p>1 ↑</p> <p>MGMQVQIQSLFLLLLWVPGSRGFLLSLGIHLNAAAKYTSFPWLLNAAARFWSLLVPFNAAFPHCLAFSYMKA ALVVDQSFSRGAILLCLIFLLNAAAHTLWKAGILYKKAWMWYWGPSLYKAYPALMPLYACIGAAAWLSLL VPFVNAAAGFLLTRILTINAAAIPISSWAFKAAAEYLVSGVWNLPSDFFPVSKAAAFPSDFFPVSKAADLLD TASALYNSWPKFAVPNLKAAASAICSVVRRKLSLDVSAAFYNAAAKFVAAWTLKAAAKAANVSIPWTHKGAA GLSRYVARLNAAASTLPETTVVRRKHPAAMPHLLKAAARWMCLRRFIINASFCGSPYKAA YMDDVVGLVNAL WFHISCLTFKAAATPARVTGGVFKAALTFGRETVLEYKQAFTFSPYKNAFTSFVYVPSALNPADGPGPLCQ VFADATPTGWGLGPGPRHYLHTLWKAGILYKGP GPGPHHTALRQAILCWGELMTLAGPGPGESRLVVDQSFS RGNPGPGPFLLAQFTSAICSVVGPGLVPFVQWFGVLSPTVGPGLHLYSHPIILGFRKIGPGPGSSNLSWLSL DVSAAFGPGPLQSLTNLSSNLSWLGPGGAGFFLLTRILTIPQSGPGPGVSFGVWIRTPPAYRPPNAPIGPGPV GPLTVNEKRRLKLIGPGPKQCFRKL P VNRPIDWGP GPGGAANWILRGTSFVYVPGPGPKQAFTFSPYKAFLCG</p> <p>↓ 744</p>

Table 25. HBV AOSIb2 Fusion Construct

HBV AOSIb2	<i>Polynucleotide</i>
SEQ ID NO: 1938	<p>1 Start ↑</p> <p>ATG GGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACAC CCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCT GCCTAGCGATTTCTTTCCTAGCGTGAACCTTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTG CTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCTGCTGACCAGAATCCTGACCATCTCCACCCTG CCAGAGACCACCGTGGTGAGGAGGCAGGCCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCT GAGCCTGCTGGTGCCCTTTGTGAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGAC CGGAGGAGTGTTTAAGGTGGGAACTTCACCGGCCTGTATAACCTGCCAGCGATTTCTTTCCTAGCGTGAA GACCCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCGCTCTGG TGGTGGACTTTTCCCAGTTCAGCAGAAATCCGCTATCTGCTCCGTGGTGAGGAGAGCTCTGATGCCACTGT ATGCCTGTATC TGA</p> <p>↓ Stop 657</p>
HBV AOSIb2	<i>Polypeptide</i>
SEQ ID NO: 1939	<p>1 ↑</p> <p>MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFPSDFFPSVNFLLSLGIHLYMDDVVL GVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAWLSLLVPFVNIPSSWAFKTPARVTGGVFKV GNFTGLYNLPSDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVDFSQFSRNSAICSVVRRALMPLYACI</p> <p>↓ 219</p>

Table 26. HCV Fusion Construct

HCV 4312(1P) (SEQ ID NO: 1940)

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVK
YLLPRRGPRNLNLCGFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFP
DLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPPRRNGYLVAYQATVAAALLFLLADALIFCHS
KKKYLVTNRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKKAAAVLVGGVLAA
AFLLADARVLSAFSLHSYILAGYGAGVWMNRLAFANAAAKFVAAWTLKAAA

(SEQ ID NO: 1941)

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCCGGCTCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAAAC
AAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTCTTTCAGCATCTTTAATGACCTCAT
GGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGGGGCCCTCGCCTGAACACTCTCTG
TGGATTTGCTGATCTGATGGGGTACAGGATGTATGTCGGCGGAGTCGAACACAGAAAACCTGCT
CTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCG
GAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGA
ATTTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCCAA
GACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGCTGCAGCTCTGCTCTTCCTGCTCC
TGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACG
TGCTGGGGTTTGGCGCCTACATGAGCAAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGT
GGAACCTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGGAATTTTAAGAAAGCCGCTGCAG
TCCTGGTGGGCGGCGTCCTGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTG
CCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGA
TCGCCTTTGCCAATGCTGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAG
GATCC

Table 27. *Plasmodium falciparum* Fusion Construct

Pf33 (SEQ ID NO: 1942)

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVK
YLLPRRGPRNLNLCGFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFP
DLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPRRNGYLVAYQATVAAALLFLLLADALIFCHS
KKKYLVTTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKKAAAVLVGGVLAA
AFLLLADARVLSAFSLHSYILAGYGAGVWMNRLAFANAAAKFVAAWTLKAAA

(SEQ ID NO: 1943)

GCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCC
GGATCCAGAGGATTTATGAAAGCTGTCTGTGTAGAGGTGAATGTAACATGCGGTAACGGAAT
TCAGGTGAGAAAGGGACTCATCATGGTACTCAGCTTTCTGAACGCAGCCCTGTTCCACATCTT
TGACGGAGACAATGAAATCAAAGCCGCATTGCTCGCCTGTGCCGACTAGCCTATAAAAAGA
GTTTCCTTTTCGTTGAAGCACTATTTAACGCAGCACCCAGTGACGGTAAATGCAACCTATATA
AAGCAGCTCAGACTAATTTCAAAAGCCTGTTAAGAAATCTGCCCTCAGAGAATGAAAGGGGT
TACAAAGCCGCGCGGTGTCCGAGAATATTTTCCTGAAGAACGCCGCTGCTTATTTTATACTC
GTGAATCTACTCATAAAGGCAGCCGCAATCCTTTCAGTGTCCAGCTTTCTGTTTGTTAACACAC
CATATGCGGGCGAGCCGGCTCCTTTCAAGGCTGCAGCAAAAATACAAGCTTGCCACATCAGTAT
TGAAAGCAGCTGTGTTTTTGATATTCTTTGATCTTTTTTTAACTACTACATACCTCATCAGTCT
AGTCTTAAAGCAGCCGGGCTACTGGGGAACGTCTCTACTGTGGGGGCGCTTACTTGGAGGA
GTTGGCCTCGTGTTGAACCTCGCGTGCGCAGGTCTGGCCTACAAAAAAGCGAAATTCATCAAG
TCTCTGTTCCACATTTTTAAAGCCGCATTCTATTTCACTAGTGAACCTTCTCAAAGCTTTCCT
GATCTTCTTCGATCTATTCCTCGTAAAAGCGCTATTCTTCATTATCTTTAACAAAAATTATTAC
GGCAAGCAAGAAAATTGGTACTACTCAAGTTTGTAGAAGCTCTGTTCCAGGAATACAACGCC
GCTGCTAAATTTCGTTGCAGCTTGGACCCTGAAAGCAGCTGCAAAGATCCTATCGGTCTTCTTTC
TCGCTAATGCCGTATTAGCAGGACTTCTAGGCAACGTGAACCTTCAAGACGAAGAGAATATAG
GCATCTACAAAGCCGCAGCACTGTACATTTCACTTCTACTTCATCAAGGCCTTCATACTGGTCAA
CCTTCTGATATTTTATAATGCAGCACTGCCATATGGGAGAACCAACTTGAAAGCGGCCACGT
GTTGAGCCACAACCTCCTACGAGAAGAACGCGCCGCGAAATATCTCGTCATTGTCTTCCTGAT
TTGA

Table 28. *Mycobacterium tuberculosis* Fusion Construct

TB.1 (SEQ ID NO: 1944)

MQVQIQSLFLLLLWVPGSRGRMSRVTTFTVKALVLLMLPVVNL
MIGTAAAVVKALVLLMLPVGA
GLMTAVYLVGAAAMALLRLPVKRMFAANLGVNSLYFGGICVGR
LPLVLPVNA
AAAKFVAAWT
LKAAAKAAARLMIGTAAAGFVVALIPLV
NAMTYAAPLFV
GAAAAMALLRLPLV

(SEQ ID NO: 1945)

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTG
CCCCGGATCCAGAGGAAGG
ATGAGCAGAGTGACCACATTCACTGTCAAGGCCCTGGTGCTCCTG
ATGCTCCCCGTCGTGAAC
CTGATGATCGGCACCGCTGCAGCCGTCGTGAAAGCTCTCGTCCTG
CTCATGCTCCCTGTGGGA
GCAGGGCTGATGACAGCCGTGTACCTGGTCGGCGCTGCAGCCATGG
CCCTCCTGCGGCTGCCA
GTGAAGCGCATGTTTGCTGCAAATCTGGGAGTCAACTCCCTCTATT
TCGGGGGCATTTGCGTG
GGAAGGCTGCCCCCTCGTGCTGCCTGCTGTGAATGCAGCCGCTGCC
AAATTTGTCGCCGCTTGG
ACTCTGAAGGCAGCCGCTAAGGCCGCTGCAAGACTGATGATCGGGAC
CGCCGCTGCCGGCTT
CGTGGTCGCCCTGATTCCCCTGGTGAACGCCATGACATACGCAGCTC
CTCTGTTTGTGGGAGC
CGCTGCAGCCATGGCTCTCCTGCGGCTGCCACTGGTGTGA

Table 29. Hepatitis B Virus Core Protein (SEQ ID NO: 1946)

MQLFHLCLIISCSCPTVQASKLCLGWLWGMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTAS
ALYREALSPEHCSPHHTALRQAILCWGELMTLATWVGVNLEDPASRDLVVS YVNTNMGLKF
RQLLWFHISCLTFGRETVIEYLVSFSGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTP
SPRRRRSQSPRRRRSQSRESQC